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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 15:26:23 ; Search time 14 Seconds
(without alignments)
3.750 Million cell updates/sec

Title: us-10-008-789-3
Perfect score: 1755
Sequence: 1 cgcgcggcaggtcccaaaa.....aaaaaaaaaaaaaaaaaaaa 1755

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 843 seqs, 14956 residues

Total number of hits satisfying chosen parameters: 1686

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 843 summaries

Database : ruidb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.4	1.3	24	1	US-09-164-249B-6 Sequence 6, Appli
C 2	21.4	1.2	24	1	US-08-996-306-10 Sequence 10, Appl
C 3	21.4	1.2	24	1	US-09-338-907-10 Sequence 10, Appl
C 4	21.4	1.2	24	1	US-09-218-207-10 Sequence 10, Appl
C 5	21.4	1.2	26	1	US-08-621-914A-1 Sequence 1, Appli
C 6	21.4	1.2	26	1	US-09-522-217-38 Sequence 38, Appl
C 7	21.4	1.2	26	1	US-09-527-345-7 Sequence 7, Appli
C 8	21.4	1.2	26	1	US-09-923-246-38 Sequence 38, Appl
C 9	21.4	1.2	26	1	US-10-295-723-38 Sequence 38, Appl
C 10	21.4	1.2	27	1	US-09-475-947A-153 Sequence 153, App
C 11	21	1.2	25	1	US-08-113-646A-42 Sequence 42, Appl
C 12	21	1.2	26	1	US-08-621-914A-3 Sequence 3, Appli
C 13	20.6	1.2	26	1	US-09-527-345-6 Sequence 6, Appli
C 14	20.6	1.2	26	1	US-09-167-513-10 Sequence 10, Appl
C 15	20.6	1.2	26	1	US-09-161-939A-43 Sequence 43, Appl
16	20.4	1.2	22	1	US-08-123-449A-19 Sequence 19, Appl
17	20.4	1.2	22	1	US-08-458-050-19 Sequence 19, Appl
18	20.4	1.2	22	1	US-08-847-844A-94 Sequence 94, Appl
19	20.4	1.2	22	1	US-08-950-196-19 Sequence 19, Appl
20	20.4	1.2	22	1	US-09-720-201A-25 Sequence 25, Appl
21	20.4	1.2	24	1	US-08-014-943A-25 Sequence 25, Appl
22	20.4	1.2	24	1	US-08-486-421-50 Sequence 50, Appl
23	20.4	1.2	24	1	US-08-470-911-50 Sequence 50, Appl
24	20.4	1.2	24	1	US-08-735-381-1 Sequence 1, Appli
25	20.4	1.2	24	1	US-08-486-809-50 Sequence 50, Appl
26	20.4	1.2	24	1	US-09-183-619-7 Sequence 7, Appli
27	20.4	1.2	24	1	US-09-201-674-1 Sequence 1, Appli
28	20.4	1.2	24	1	US-09-536-936-11 Sequence 11, Appl
29	20.4	1.2	24	1	US-09-025-639-4 Sequence 4, Appli
30	20.4	1.2	24	1	US-09-333-237-4 Sequence 4, Appli
31	20.4	1.2	24	1	US-09-732-067-1 Sequence 1, Appli
C 32	20.4	1.2	24	1	US-09-475-947A-134 Sequence 134, App
33	20.4	1.2	24	1	US-10-043-415-4 Sequence 4, Appli

34	20.4	1.2	24	1	US-09-854-317-1 Sequence 1, Appli
C 35	20.4	1.2	24	1	US-09-721-154-1 Sequence 1, Appli
C 36	20.4	1.2	24	1	US-09-721-154-4 Sequence 4, Appli
C 37	20.4	1.2	25	1	US-08-341-148-2 Sequence 2, Appli
C 38	20.4	1.2	25	1	US-08-460-130-2 Sequence 2, Appli
C 39	20.4	1.2	25	1	US-08-969-813-1 Sequence 1, Appli
C 40	20.4	1.2	25	1	US-09-183-619-5 Sequence 5, Appli
C 41	20.4	1.2	25	1	US-09-282-734-23 Sequence 23, Appl
C 42	20.4	1.2	25	1	PCT-US94-14096-2 Sequence 2, Appli
C 43	20.4	1.2	26	1	US-08-621-914A-2 Sequence 2, Appli
C 44	20.4	1.2	26	1	US-08-873-437-2 Sequence 2, Appli
C 45	20.4	1.2	26	1	US-09-197-951-5 Sequence 5, Appli
C 46	20.4	1.2	26	1	US-09-522-217-39 Sequence 39, Appl
C 47	20.4	1.2	26	1	US-09-593-312-2 Sequence 2, Appli
C 48	20.4	1.2	26	1	US-09-923-246-39 Sequence 39, Appl
C 49	20.4	1.2	26	1	US-09-658-077-1 Sequence 1, Appli
C 50	20.4	1.2	26	1	US-10-295-723-39 Sequence 39, Appl
C 51	20.4	1.2	27	1	US-08-208-486-79 Sequence 79, Appl
C 52	20.4	1.2	27	1	US-09-325-554-18 Sequence 18, Appl
C 53	20	1.1	20	1	US-08-146-504-16 Sequence 16, Appl
C 54	20	1.1	20	1	US-08-379-593-5 Sequence 5, Appli
C 55	20	1.1	20	1	US-08-725-976-16 Sequence 16, Appl
C 56	20	1.1	20	1	US-08-997-080-83 Sequence 83, Appl
C 57	20	1.1	20	1	US-08-997-362-83 Sequence 83, Appl
C 58	20	1.1	20	1	US-08-965-780-1 Sequence 1, Appli
C 59	20	1.1	20	1	US-08-873-970-83 Sequence 83, Appl
C 60	20	1.1	20	1	US-08-765-340-96 Sequence 96, Appl
C 61	20	1.1	20	1	US-09-095-855-83 Sequence 83, Appl
C 62	20	1.1	20	1	US-09-407-675-1 Sequence 1, Appli
C 63	20	1.1	20	1	US-09-250-075-1 Sequence 1, Appli
C 64	20	1.1	20	1	US-09-173-936B-14 Sequence 14, Appl
C 65	20	1.1	20	1	US-09-454-704A-13 Sequence 13, Appl
C 66	20	1.1	20	1	US-09-324-542-83 Sequence 83, Appl
C 67	20	1.1	20	1	US-09-205-426-83 Sequence 83, Appl
C 68	20	1.1	20	1	US-09-619-103-26 Sequence 26, Appl
C 69	20	1.1	20	1	US-09-726-096A-1 Sequence 1, Appli
C 70	20	1.1	20	1	US-09-603-830-55 Sequence 55, Appl
C 71	20	1.1	20	1	US-09-976-978A-55 Sequence 55, Appl
C 72	20	1.1	20	1	US-09-344-260A-10 Sequence 10, Appl
C 73	20	1.1	20	1	US-09-961-949A-55 Sequence 55, Appl
C 74	20	1.1	20	1	US-09-966-491A-55 Sequence 55, Appl
C 75	20	1.1	20	1	US-09-957-313A-55 Sequence 55, Appl
C 76	20	1.1	20	1	US-09-966-312-55 Sequence 55, Appl
C 77	20	1.1	20	1	US-09-975-062A-55 Sequence 55, Appl
C 78	20	1.1	20	1	US-09-976-971A-55 Sequence 55, Appl
C 79	20	1.1	20	1	PCT-US93-07603-6 Sequence 6, Appli
C 80	20	1.1	21	1	US-08-146-504-2 Sequence 2, Appli
C 81	20	1.1	21	1	US-08-455-896-13 Sequence 13, Appl
C 82	20	1.1	21	1	US-08-933-149-13 Sequence 13, Appl
C 83	20	1.1	21	1	US-08-725-976-2 Sequence 2, Appli
C 84	20	1.1	21	1	US-09-082-343-13 Sequence 13, Appl
C 85	20	1.1	21	1	US-08-863-639A-10 Sequence 10, Appl
C 86	20	1.1	21	1	US-08-863-639A-13 Sequence 13, Appl
C 87	20	1.1	21	1	US-08-416-214A-12 Sequence 12, Appl
C 88	20	1.1	21	1	US-09-082-253-13 Sequence 13, Appl
C 89	20	1.1	21	1	US-08-271-882B-2 Sequence 2, Appli
C 90	20	1.1	21	1	US-08-726-278-2 Sequence 2, Appli
C 91	20	1.1	21	1	US-09-162-622-13 Sequence 13, Appl
C 92	20	1.1	21	1	US-09-509-015-13 Sequence 13, Appl
C 93	20	1.1	21	1	PCT-US96-08235-13 Sequence 13, Appl
C 94	19.2	1.1	24	1	US-08-031-147A-52 Sequence 52, Appl
C 95	19.2	1.1	24	1	US-08-403-888A-35 Sequence 35, Appl
C 96	19.2	1.1	24	1	US-08-403-888A-43 Sequence 43, Appl
C 97	19.2	1.1	24	1	US-08-403-888A-109 Sequence 109, App
C 98	19.2	1.1	24	1	US-08-403-888A-116 Sequence 116, App
C 99	19.2	1.1	24	1	US-08-729-598-3 Sequence 3, Appli
C 100	19.2	1.1	24	1	US-08-819-867-29 Sequence 29, Appl
C 101	19.2	1.1	24	1	US-08-819-867-32 Sequence 32, Appl
C 102	19.2	1.1	24	1	US-08-819-867-34 Sequence 34, Appl
C 103	19.2	1.1	24	1	US-09-378-535-29 Sequence 29, Appl
C 104	19.2	1.1	24	1	US-09-378-535-32 Sequence 32, Appl
C 105	19.2	1.1	24	1	US-09-378-535-34 Sequence 34, Appl
C 106	19.2	1.1	24	1	PCT-US94-02471-52 Sequence 52, Appl

C 107	19.2	1.1	25	1	US-08-403-888A-33	Sequence 33, Appl	C 180	19	1.1	19	1	US-10-121-135-5	Sequence 5, Appli
C 108	19.2	1.1	25	1	US-08-403-888A-34	Sequence 34, Appl	C 181	19	1.1	19	1	US-10-121-135-26	Sequence 26, Appl
C 109	19	1.1	19	1	US-08-756-728A-1	Sequence 1, Appli	C 182	19	1.1	19	1	US-09-142-212A-10	Sequence 10, Appl
C 110	19	1.1	19	1	US-08-469-852A-2	Sequence 2, Appli	C 183	19	1.1	19	1	US-09-349-040A-3	Sequence 3, Appli
C 111	19	1.1	19	1	US-08-271-882B-16	Sequence 16, Appl	C 184	19	1.1	19	1	US-09-349-040A-4	Sequence 4, Appli
C 112	19	1.1	19	1	US-08-295-509B-2	Sequence 2, Appli	C 185	19	1.1	19	1	US-09-349-040A-5	Sequence 5, Appli
C 113	19	1.1	19	1	US-09-234-237-1	Sequence 1, Appli	C 186	19	1.1	19	1	US-09-409-926-17	Sequence 17, Appl
C 114	19	1.1	19	1	US-09-016-520-20	Sequence 20, Appl	C 187	19	1.1	19	1	US-09-409-926-18	Sequence 18, Appl
C 115	19	1.1	19	1	US-09-016-520-21	Sequence 21, Appl	C 188	19	1.1	19	1	US-10-123-597-1	Sequence 1, Appli
C 116	19	1.1	19	1	US-09-016-520-22	Sequence 22, Appl	C 189	19	1.1	19	1	US-10-123-597-2	Sequence 2, Appli
C 117	19	1.1	19	1	US-09-016-520-23	Sequence 23, Appl	C 190	19	1.1	19	1	US-10-123-597-3	Sequence 3, Appli
C 118	19	1.1	19	1	US-09-016-520-24	Sequence 24, Appl	C 191	19	1.1	19	1	US-10-123-597-4	Sequence 4, Appli
C 119	19	1.1	19	1	US-09-016-520-25	Sequence 25, Appl	C 192	19	1.1	19	1	US-10-123-597-5	Sequence 5, Appli
C 120	19	1.1	19	1	US-09-016-520-26	Sequence 26, Appl	C 193	19	1.1	19	1	US-10-123-597-6	Sequence 6, Appli
C 121	19	1.1	19	1	US-09-016-520-27	Sequence 27, Appl	C 194	19	1.1	19	1	US-10-123-597-7	Sequence 7, Appli
C 122	19	1.1	19	1	US-09-016-520-31	Sequence 31, Appl	C 195	19	1.1	19	1	US-10-123-597-8	Sequence 8, Appli
C 123	19	1.1	19	1	US-09-016-520-33	Sequence 33, Appl	C 196	19	1.1	19	1	US-10-123-597-12	Sequence 12, Appl
C 124	19	1.1	19	1	US-09-016-520-34	Sequence 34, Appl	C 197	19	1.1	19	1	US-10-123-597-14	Sequence 14, Appl
C 125	19	1.1	19	1	US-09-016-520-44	Sequence 44, Appl	C 198	19	1.1	19	1	US-10-123-597-15	Sequence 15, Appl
C 126	19	1.1	19	1	US-09-378-568-4	Sequence 4, Appli	C 199	19	1.1	19	1	US-10-123-597-25	Sequence 25, Appl
C 127	19	1.1	19	1	US-09-130-973-20	Sequence 20, Appl	C 200	19	1.1	19	1	US-09-349-033A-1	Sequence 1, Appli
C 128	19	1.1	19	1	US-09-130-973-21	Sequence 21, Appl	C 201	19	1.1	19	1	US-09-435-806-6	Sequence 6, Appli
C 129	19	1.1	19	1	US-09-130-973-22	Sequence 22, Appl	C 202	19	1.1	20	1	US-08-482-918-32	Sequence 32, Appl
C 130	19	1.1	19	1	US-09-130-973-23	Sequence 23, Appl	C 203	19	1.1	20	1	US-09-224-681-32	Sequence 32, Appl
C 131	19	1.1	19	1	US-09-130-973-24	Sequence 24, Appl	C 204	19	1.1	20	1	US-08-336-728A-32	Sequence 32, Appl
C 132	19	1.1	19	1	US-09-130-973-25	Sequence 25, Appl	C 205	19	1.1	21	1	US-08-359-295C-23	Sequence 23, Appl
C 133	19	1.1	19	1	US-09-130-973-26	Sequence 26, Appl	C 206	19	1.1	21	1	US-08-485-105A-23	Sequence 23, Appl
C 134	19	1.1	19	1	US-09-130-973-27	Sequence 27, Appl	C 207	19	1.1	21	1	US-09-183-650-23	Sequence 23, Appl
C 135	19	1.1	19	1	US-09-130-973-31	Sequence 31, Appl	C 208	19	1.1	23	1	PCT-US94-05407-7	Sequence 7, Appli
C 136	19	1.1	19	1	US-09-130-973-33	Sequence 33, Appl	C 209	19	1.1	23	1	PCT-US94-05407-8	Sequence 8, Appli
C 137	19	1.1	19	1	US-09-130-973-34	Sequence 34, Appl	C 210	19	1.1	24	1	US-09-721-154-6	Sequence 6, Appli
C 138	19	1.1	19	1	US-09-477-902-44	Sequence 44, Appl	C 211	18.8	1.1	24	1	US-09-721-154-2	Sequence 2, Appli
C 139	19	1.1	19	1	US-09-477-902-20	Sequence 20, Appl	C 212	18.4	1.0	20	1	US-08-482-918-33	Sequence 33, Appl
C 140	19	1.1	19	1	US-09-477-902-21	Sequence 21, Appl	C 213	18.4	1.0	20	1	US-08-482-918-34	Sequence 34, Appl
C 141	19	1.1	19	1	US-09-477-902-22	Sequence 22, Appl	C 214	18.4	1.0	20	1	US-09-224-681-33	Sequence 33, Appl
C 142	19	1.1	19	1	US-09-477-902-23	Sequence 23, Appl	C 215	18.4	1.0	20	1	US-09-224-681-34	Sequence 34, Appl
C 143	19	1.1	19	1	US-09-477-902-24	Sequence 24, Appl	C 216	18.4	1.0	20	1	US-08-336-728A-33	Sequence 33, Appl
C 144	19	1.1	19	1	US-09-477-902-25	Sequence 25, Appl	C 217	18.4	1.0	20	1	US-08-336-728A-34	Sequence 34, Appl
C 145	19	1.1	19	1	US-09-477-902-26	Sequence 26, Appl	C 218	18.4	1.0	20	1	US-09-588-950A-5	Sequence 5, Appli
C 146	19	1.1	19	1	US-09-477-902-27	Sequence 27, Appl	C 219	18.4	1.0	21	1	US-09-475-947A-119	Sequence 119, App
C 147	19	1.1	19	1	US-09-477-902-31	Sequence 31, Appl	C 220	18.2	1.0	19	1	US-08-881-784-18	Sequence 18, Appl
C 148	19	1.1	19	1	US-09-477-902-33	Sequence 33, Appl	C 221	18.2	1.0	19	1	US-09-292-768-18	Sequence 18, Appl
C 149	19	1.1	19	1	US-09-477-902-34	Sequence 34, Appl	C 222	18	1.0	18	1	US-08-621-914A-16	Sequence 16, Appl
C 150	19	1.1	19	1	US-09-477-902-44	Sequence 44, Appl	C 223	18	1.0	18	1	US-08-346-429-3	Sequence 3, Appli
C 151	19	1.1	19	1	US-08-726-278-16	Sequence 16, Appl	C 224	18	1.0	18	1	US-08-358-556A-12	Sequence 12, Appl
C 152	19	1.1	19	1	US-09-123-108-6	Sequence 515, App	C 225	18	1.0	18	1	US-08-358-556A-18	Sequence 18, Appl
C 153	19	1.1	19	1	US-09-338-907-515	Sequence 5, Appli	C 226	18	1.0	18	1	US-08-469-852A-4	Sequence 4, Appli
C 154	19	1.1	19	1	US-09-378-665A-5	Sequence 4, Appli	C 227	18	1.0	18	1	US-08-295-509B-4	Sequence 9, Appli
C 155	19	1.1	19	1	US-09-202-294-4	Sequence 515, App	C 228	18	1.0	18	1	US-08-884-029-9	Sequence 30, Appl
C 156	19	1.1	19	1	US-09-218-207-515	Sequence 15, Appl	C 229	18	1.0	18	1	US-08-941-445A-30	Sequence 6, Appli
C 157	19	1.1	19	1	US-09-303-586-15	Sequence 16, Appl	C 230	18	1.0	18	1	US-09-637-751A-6	Sequence 9, Appli
C 158	19	1.1	19	1	US-09-303-586-16	Sequence 17, Appl	C 231	18	1.0	18	1	US-09-545-225-9	Sequence 24, Appl
C 159	19	1.1	19	1	US-09-303-586-17	Sequence 18, Appl	C 232	18	1.0	18	1	US-09-619-103-24	Sequence 14, Appl
C 160	19	1.1	19	1	US-09-303-586-18	Sequence 26, Appl	C 233	18	1.0	18	1	US-09-370-541-14	Sequence 9, Appli
C 161	19	1.1	19	1	US-09-303-586-26	Sequence 1, Appli	C 234	18	1.0	18	1	US-10-125-295-9	Sequence 4, Appli
C 162	19	1.1	19	1	US-09-227-782-1	Sequence 2, Appli	C 235	18	1.0	18	1	PCT-US94-05407-4	Sequence 7, Appli
C 163	19	1.1	19	1	US-09-227-782-2	Sequence 3, Appli	C 236	18	1.0	19	1	US-09-435-806-7	Sequence 1, Appli
C 164	19	1.1	19	1	US-09-227-782-3	Sequence 4, Appli	C 237	18	1.0	22	1	US-08-123-449A-1	Sequence 2, Appli
C 165	19	1.1	19	1	US-09-227-782-4	Sequence 5, Appli	C 238	18	1.0	22	1	US-08-123-449A-2	Sequence 1, Appli
C 166	19	1.1	19	1	US-09-227-782-5	Sequence 6, Appli	C 239	18	1.0	22	1	US-08-458-050-1	Sequence 2, Appli
C 167	19	1.1	19	1	US-09-227-782-6	Sequence 7, Appli	C 240	18	1.0	22	1	US-08-458-050-2	Sequence 1, Appli
C 168	19	1.1	19	1	US-09-227-782-7	Sequence 8, Appli	C 241	18	1.0	22	1	US-08-950-196-1	Sequence 2, Appli
C 169	19	1.1	19	1	US-09-227-782-8	Sequence 12, Appl	C 242	18	1.0	22	1	US-08-950-196-2	Sequence 82, Appl
C 170	19	1.1	19	1	US-09-227-782-12	Sequence 14, Appl	C 243	18	1.0	24	1	US-08-906-156A-82	Sequence 20, Appl
C 171	19	1.1	19	1	US-09-227-782-14	Sequence 15, Appl	C 244	17.4	1.0	20	1	US-07-912-900-20	Sequence 20, Appl
C 172	19	1.1	19	1	US-09-227-782-15	Sequence 25, Appl	C 245	17.4	1.0	20	1	US-08-285-309-20	Sequence 11, Appl
C 173	19	1.1	19	1	US-09-227-782-25	Sequence 25, Appl	C 246	17.4	1.0	20	1	US-08-313-075A-11	Sequence 20, Appl
C 174	19	1.1	19	1	US-09-619-103-25	Sequence 1, Appli	C 247	17.4	1.0	20	1	US-08-502-046-20	Sequence 4, Appli
C 175	19	1.1	19	1	US-09-288-679-1	Sequence 3, Appli	C 248	17.4	1.0	21	1	US-08-108-591B-4	Sequence 7, Appli
C 176	19	1.1	19	1	US-09-612-531-3	Sequence 7, Appli	C 249	17.4	1.0	21	1	US-08-704-966-7	Sequence 7, Appli
C 177	19	1.1	19	1	US-09-612-531-7	Sequence 13, Appl	C 250	17.4	1.0	21	1	US-08-705-438-7	Sequence 1, Appli
C 178	19	1.1	19	1	US-09-612-531-13	Sequence 5, Appli	C 251	17.2	1.0	19	1	US-09-130-079-1	Sequence 36, Appl
C 179	19	1.1	19	1	US-10-121-135-5		C 252	17.2	1.0	22	1	US-08-403-888A-36	

253	17.2	1.0	22	1	US-08-403-888A-44	Sequence 44, Appl	C 326	15.2	0.9	20	1	US-09-295-026-22	Sequence 22, Appl
254	17.2	1.0	22	1	US-08-403-888A-110	Sequence 110, App	327	15.2	0.9	20	1	US-09-780-173A-93	Sequence 93, Appl
255	17.2	1.0	22	1	US-08-403-888A-117	Sequence 117, App	328	15.2	0.9	20	1	US-09-422-978-6563	Sequence 6563, Ap
C 256	17	1.0	17	1	US-08-851-843A-132	Sequence 132, App	C 329	15.2	0.9	20	1	US-09-422-978-10187	Sequence 10187, A
C 257	17	1.0	17	1	US-09-250-075-5	Sequence 5, Appli	330	15.2	0.9	20	1	US-09-823-634A-18	Sequence 18, Appl
C 258	17	1.0	17	1	US-08-854-050-132	Sequence 132, App	331	15.2	0.9	20	1	US-09-823-647B-18	Sequence 18, Appl
C 259	17	1.0	17	1	US-09-430-323-132	Sequence 132, App	332	15.2	0.9	20	1	US-09-112-580-72	Sequence 72, Appl
C 260	17	1.0	17	1	US-09-619-103-23	Sequence 23, Appl	333	15	0.9	15	1	US-08-452-196A-6	Sequence 6, Appli
C 261	17	1.0	17	1	US-09-726-096A-5	Sequence 5, Appli	C 334	15	0.9	15	1	US-07-971-978-1	Sequence 1, Appli
C 262	17	1.0	18	1	US-09-637-751A-5	Sequence 5, Appli	335	15	0.9	15	1	US-08-756-728A-2	Sequence 2, Appli
C 263	17	1.0	19	1	US-08-973-857-6	Sequence 6, Appli	C 336	15	0.9	15	1	US-08-663-918-3	Sequence 3, Appli
264	16.8	1.0	20	1	US-08-031-147A-55	Sequence 55, Appl	337	15	0.9	15	1	US-08-663-918-4	Sequence 4, Appli
265	16.8	1.0	20	1	US-08-403-888A-37	Sequence 37, Appl	C 338	15	0.9	15	1	US-08-292-620A-361	Sequence 361, App
266	16.8	1.0	20	1	US-08-403-888A-45	Sequence 45, Appl	C 339	15	0.9	15	1	US-08-292-620A-362	Sequence 3, Appli
267	16.8	1.0	20	1	US-08-403-888A-114	Sequence 114, App	C 340	15	0.9	15	1	US-08-771-789-3	Sequence 4, Appli
268	16.8	1.0	20	1	US-08-403-888A-118	Sequence 118, App	341	15	0.9	15	1	US-08-771-789-4	Sequence 4, Appli
C 269	16.8	1.0	20	1	US-09-490-692-68	Sequence 68, Appl	C 342	15	0.9	15	1	US-08-358-556A-10	Sequence 10, Appl
270	16.8	1.0	20	1	US-09-228-942-7	Sequence 7, Appli	343	15	0.9	15	1	US-08-358-556A-16	Sequence 16, Appl
271	16.8	1.0	20	1	PCT-US94-02471-55	Sequence 55, Appl	C 344	15	0.9	15	1	US-08-922-170B-5	Sequence 5, Appli
C 272	16.4	0.9	20	1	US-09-198-452A-2140	Sequence 2140, Ap	345	15	0.9	15	1	US-08-863-639A-5	Sequence 5, Appli
C 273	16	0.9	16	1	US-07-971-978-36	Sequence 36, Appl	346	15	0.9	15	1	US-08-863-639A-7	Sequence 7, Appli
C 274	16	0.9	16	1	US-07-971-978-42	Sequence 42, Appl	C 347	15	0.9	15	1	US-08-863-639A-9	Sequence 9, Appli
C 275	16	0.9	16	1	US-07-971-978-60	Sequence 60, Appl	C 348	15	0.9	15	1	US-08-693-831-1	Sequence 1, Appli
C 276	16	0.9	16	1	US-08-415-370-2	Sequence 2, Appli	C 349	15	0.9	15	1	US-08-832-021-61	Sequence 61, Appl
C 277	16	0.9	16	1	US-08-687-551-15	Sequence 15, Appl	C 350	15	0.9	15	1	US-09-183-619-4	Sequence 4, Appli
C 278	16	0.9	16	1	US-09-141-764-2	Sequence 2, Appli	C 351	15	0.9	15	1	US-09-071-845-361	Sequence 361, App
279	16	0.9	16	1	US-08-851-843A-131	Sequence 131, App	C 352	15	0.9	15	1	US-09-071-845-362	Sequence 362, App
280	16	0.9	16	1	US-08-854-050-131	Sequence 131, App	353	15	0.9	15	1	US-09-167-375-1	Sequence 1, Appli
281	16	0.9	16	1	US-09-430-323-131	Sequence 131, App	C 354	15	0.9	15	1	US-08-150-156A-19	Sequence 19, Appl
C 282	16	0.9	16	1	US-09-507-345A-2	Sequence 2, Appli	355	15	0.9	15	1	US-08-150-156A-20	Sequence 20, Appl
283	16	0.9	16	1	US-09-619-103-22	Sequence 22, Appl	C 356	15	0.9	15	1	US-08-108-591B-17	Sequence 17, Appl
C 284	16	0.9	16	1	US-09-739-928-2	Sequence 2, Appli	357	15	0.9	15	1	US-08-108-591B-18	Sequence 18, Appl
C 285	16	0.9	17	1	US-08-821-827C-30	Sequence 30, Appl	358	15	0.9	15	1	US-09-619-103-21	Sequence 21, Appl
C 286	16	0.9	17	1	US-09-290-202B-30	Sequence 30, Appl	C 359	15	0.9	15	1	US-09-300-958A-68	Sequence 68, Appl
C 287	16	0.9	17	1	US-08-584-040-2550	Sequence 2550, Ap	C 360	15	0.9	15	1	US-08-988-024C-9	Sequence 9, Appli
C 288	16	0.9	17	1	US-08-584-040-2551	Sequence 2551, Ap	C 361	15	0.9	15	1	US-09-435-739-5	Sequence 5, Appli
C 289	16	0.9	17	1	US-09-788-338-3	Sequence 3, Appli	C 362	15	0.9	15	1	US-10-091-231-2	Sequence 2, Appli
C 290	16	0.9	17	1	US-09-300-958A-64	Sequence 64, Appl	C 363	15	0.9	15	1	US-09-930-218-5	Sequence 5, Appli
C 291	16	0.9	17	1	US-09-371-772B-1074	Sequence 1074, Ap	C 364	15	0.9	16	1	US-09-507-345A-3	Sequence 3, Appli
C 292	16	0.9	17	1	US-09-371-772B-1075	Sequence 1075, Ap	C 365	15	0.9	16	1	US-09-507-345A-4	Sequence 4, Appli
C 293	16	0.9	18	1	US-09-637-751A-7	Sequence 7, Appli	C 366	15	0.9	16	1	US-09-507-345A-5	Sequence 5, Appli
C 294	16	0.9	20	1	US-09-658-687A-47	Sequence 47, Appl	C 367	15	0.9	16	1	US-09-507-345A-6	Sequence 6, Appli
C 295	16	0.9	21	1	US-09-228-942-8	Sequence 8, Appli	C 368	15	0.9	16	1	US-09-507-345A-7	Sequence 7, Appli
C 296	15.8	0.9	20	1	US-08-063-167A-57	Sequence 57, Appl	C 369	15	0.9	16	1	US-09-507-345A-8	Sequence 8, Appli
C 297	15.8	0.9	20	1	US-08-007-997A-57	Sequence 57, Appl	C 370	15	0.9	16	1	US-09-739-928-3	Sequence 3, Appli
C 298	15.8	0.9	20	1	US-08-440-740A-57	Sequence 57, Appl	C 371	15	0.9	16	1	US-09-739-928-4	Sequence 4, Appli
C 299	15.8	0.9	20	1	US-08-344-155C-57	Sequence 57, Appl	C 372	15	0.9	16	1	US-09-739-928-5	Sequence 5, Appli
C 300	15.8	0.9	20	1	US-08-982-845B-57	Sequence 57, Appl	C 373	15	0.9	16	1	US-09-739-928-6	Sequence 6, Appli
C 301	15.8	0.9	20	1	US-09-344-001-12	Sequence 12, Appl	C 374	15	0.9	16	1	US-09-739-928-7	Sequence 7, Appli
C 302	15.8	0.9	20	1	US-08-991-525B-57	Sequence 57, Appl	C 375	15	0.9	16	1	US-09-739-928-8	Sequence 8, Appli
C 303	15.8	0.9	20	1	US-09-085-759-57	Sequence 57, Appl	C 376	15	0.9	17	1	US-08-292-620A-1682	Sequence 1682, Ap
C 304	15.8	0.9	20	1	US-09-128-496-57	Sequence 57, Appl	377	15	0.9	17	1	US-08-985-162-35	Sequence 35, Appl
C 305	15.8	0.9	20	1	US-09-009-490A-57	Sequence 57, Appl	C 378	15	0.9	17	1	US-09-071-845-1682	Sequence 1682, Ap
C 306	15.8	0.9	20	1	PCT-US93-08101-57	Sequence 57, Appl	C 379	15	0.9	17	1	US-08-584-040-2549	Sequence 2549, Ap
C 307	15.8	0.9	21	1	US-09-422-978-10471	Sequence 10471, A	C 380	15	0.9	17	1	US-08-584-040-2552	Sequence 2552, Ap
C 308	15.6	0.9	17	1	US-08-937-067-17	Sequence 17, Appl	C 381	15	0.9	17	1	US-09-475-947A-118	Sequence 118, App
309	15.4	0.9	18	1	US-08-715-202A-7	Sequence 7, Appli	C 382	15	0.9	17	1	US-09-300-958A-63	Sequence 63, Appl
310	15.4	0.9	18	1	US-09-328-775-7	Sequence 7, Appli	C 383	15	0.9	17	1	US-09-371-772B-1073	Sequence 1073, Ap
311	15.4	0.9	18	1	US-09-994-177-7	Sequence 7, Appli	C 384	15	0.9	17	1	US-09-371-772B-1076	Sequence 1076, Ap
C 312	15.4	0.9	18	1	PCT-US91-03680-73	Sequence 73, Appl	385	15	0.9	17	1	US-09-401-063-35	Sequence 35, Appl
C 313	15.4	0.9	18	1	PCT-US91-03680-74	Sequence 74, Appl	386	15	0.9	18	1	US-09-437-076-1	Sequence 1, Appli
C 314	15.4	0.9	20	1	US-08-715-461-3	Sequence 3, Appli	C 387	15	0.9	18	1	US-09-437-076-2	Sequence 2, Appli
C 315	15.4	0.9	20	1	US-08-715-461-4	Sequence 4, Appli	C 388	15	0.9	19	1	US-09-349-035-2	Sequence 2, Appli
C 316	15.4	0.9	20	1	US-08-715-461-5	Sequence 5, Appli	C 389	15	0.9	20	1	US-08-534-479-1	Sequence 1, Appli
C 317	15.4	0.9	20	1	US-08-275-951-49	Sequence 49, Appl	C 390	15	0.9	20	1	US-09-676-610B-116	Sequence 116, App
C 318	15.2	0.9	17	1	US-09-390-324B-2	Sequence 2, Appli	C 391	15	0.9	20	1	US-09-965-599-4	Sequence 4, Appli
C 319	15.2	0.9	17	1	US-10-015-593-2	Sequence 253, App	392	14.8	0.8	18	1	US-08-031-147A-57	Sequence 57, Appl
C 320	15.2	0.9	20	1	US-08-117-952-253	Sequence 22, Appl	C 393	14.8	0.8	18	1	US-08-482-115B-36	Sequence 36, Appl
C 321	15.2	0.9	20	1	US-08-767-979-22	Sequence 12, Appl	C 394	14.8	0.8	18	1	US-08-482-115B-37	Sequence 37, Appl
322	15.2	0.9	20	1	US-09-357-071-12	Sequence 3, Appli	395	14.8	0.8	18	1	US-08-403-888A-38	Sequence 38, Appl
323	15.2	0.9	20	1	US-08-954-536-3	Sequence 10, Appl	396	14.8	0.8	18	1	US-08-403-888A-54	Sequence 54, Appl
324	15.2	0.9	20	1	US-08-765-340-10	Sequence 2, Appli	397	14.8	0.8	18	1	US-08-403-888A-111	Sequence 111, App
325	15.2	0.9	20	1	US-09-407-675-2	Sequence 2, Appli	C 398	14.8	0.8	18	1	US-08-472-802C-35	Sequence 35, Appl

C 399	14.8	0.8	18	1	US-08-472-802C-36	Sequence 36, Appl	C 472	13.8	0.8	17	1	US-08-584-040-7819	Sequence 7819, Ap
C 400	14.8	0.8	18	1	US-09-161-015-26	Sequence 26, Appl	C 473	13.8	0.8	17	1	US-08-584-040-7820	Sequence 7820, Ap
C 401	14.8	0.8	18	1	US-09-214-178-9	Sequence 9, Appli	C 474	13.8	0.8	17	1	US-08-584-040-7821	Sequence 7821, Ap
C 402	14.8	0.8	18	1	US-08-584-040-3043	Sequence 3043, Ap	C 475	13.8	0.8	17	1	US-08-584-040-7823	Sequence 7823, Ap
C 403	14.8	0.8	18	1	US-09-387-341-169	Sequence 169, App	C 476	13.8	0.8	17	1	US-08-679-645-881	Sequence 881, App
C 404	14.8	0.8	18	1	US-08-275-951-32	Sequence 32, Appl	C 477	13.8	0.8	17	1	US-09-903-915-3	Sequence 3, Appli
C 405	14.8	0.8	18	1	US-08-275-951-33	Sequence 33, Appl	C 478	13.8	0.8	17	1	US-09-474-432B-467	Sequence 467, App
C 406	14.8	0.8	18	1	US-09-057-351-35	Sequence 35, Appl	C 479	13.8	0.8	17	1	US-09-474-432B-564	Sequence 564, App
C 407	14.8	0.8	18	1	US-09-057-351-36	Sequence 36, Appl	C 480	13.8	0.8	17	1	US-09-371-772B-675	Sequence 675, App
C 408	14.8	0.8	18	1	US-09-371-772B-1471	Sequence 1471, Ap	C 481	13.8	0.8	17	1	US-09-371-772B-1078	Sequence 1078, Ap
C 409	14.8	0.8	18	1	PCT-US94-02471-57	Sequence 57, Appl	C 482	13.8	0.8	17	1	US-09-371-772B-1079	Sequence 1079, Ap
C 410	14.8	0.8	19	1	US-09-672-717-2	Sequence 2, Appli	C 483	13.8	0.8	17	1	US-09-371-772B-3602	Sequence 3602, Ap
C 411	14.4	0.8	16	1	US-09-050-159-12	Sequence 12, Appl	C 484	13.8	0.8	17	1	US-09-371-772B-3603	Sequence 3603, Ap
C 412	14.4	0.8	17	1	US-09-866-108A-7877	Sequence 7877, Ap	C 485	13.8	0.8	17	1	US-09-371-772B-3604	Sequence 3604, Ap
C 413	14.4	0.8	17	1	US-09-866-108A-7878	Sequence 7878, Ap	C 486	13.8	0.8	17	1	US-09-371-772B-3605	Sequence 3605, Ap
C 414	14.4	0.8	18	1	US-09-161-244-71	Sequence 71, Appl	C 487	13.8	0.8	17	1	US-09-371-772B-3607	Sequence 3607, Ap
C 415	14.4	0.8	18	1	US-09-920-760-49	Sequence 49, Appl	C 488	13.8	0.8	17	1	US-09-371-772B-5015	Sequence 5015, Ap
C 416	14.4	0.8	18	1	US-09-077-619-6	Sequence 6, Appli	C 489	13.8	0.8	17	1	US-09-476-387-466	Sequence 466, App
C 417	14.4	0.8	18	1	US-09-663-834A-35	Sequence 35, Appl	C 490	13.8	0.8	17	1	US-09-476-387-563	Sequence 563, App
C 418	14.4	0.8	19	1	US-09-053-293-4	Sequence 4, Appli	C 491	13.8	0.8	17	1	US-09-827-998-484	Sequence 484, App
C 419	14.4	0.8	19	1	US-09-422-375-42	Sequence 42, Appl	C 492	13.8	0.8	17	1	US-09-866-108A-896	Sequence 896, App
C 420	14.4	0.8	19	1	US-09-526-193A-148	Sequence 148, App	C 493	13.8	0.8	17	1	US-09-866-108A-7879	Sequence 7879, Ap
C 421	14.2	0.8	15	1	US-08-882-649A-7	Sequence 7, Appli	C 494	13.8	0.8	17	1	US-09-866-108A-10022	Sequence 10022, A
C 422	14	0.8	14	1	US-08-173-489C-75	Sequence 75, Appl	C 495	13.8	0.8	17	1	US-09-866-108A-10502	Sequence 10502, A
C 423	14	0.8	14	1	US-08-173-489C-76	Sequence 76, Appl	C 496	13.8	0.8	17	1	US-09-866-108A-10504	Sequence 10504, A
C 424	14	0.8	14	1	US-08-832-021-16	Sequence 16, Appl	C 497	13.8	0.8	17	1	US-09-866-108A-10505	Sequence 10505, A
C 425	14	0.8	14	1	US-08-724-466B-14	Sequence 14, Appl	C 498	13.8	0.8	17	1	US-09-866-108A-10506	Sequence 10506, A
C 426	14	0.8	14	1	US-09-019-095A-26	Sequence 26, Appl	C 499	13.8	0.8	18	1	US-08-632-673B-9	Sequence 9, Appli
C 427	14	0.8	14	1	US-08-882-164D-14	Sequence 14, Appl	C 500	13.8	0.8	18	1	US-08-752-844-52	Sequence 52, Appl
C 428	14	0.8	14	1	US-09-462-569B-1	Sequence 1, Appli	C 501	13.8	0.8	18	1	US-08-591-196-52	Sequence 52, Appl
C 429	14	0.8	14	1	US-09-619-103-20	Sequence 20, Appl	C 502	13.8	0.8	18	1	US-09-280-409-13	Sequence 13, Appl
C 430	14	0.8	14	1	5453496-4	Patent No. 5453496	C 503	13.8	0.8	18	1	US-09-280-409-92	Sequence 92, Appl
C 431	14	0.8	14	1	5453496-5	Patent No. 5453496	C 504	13.8	0.8	18	1	US-09-306-595C-30	Sequence 30, Appl
C 432	14	0.8	15	1	US-08-452-196A-3	Sequence 3, Appli	C 505	13.8	0.8	18	1	US-08-584-040-8372	Sequence 8372, Ap
C 433	14	0.8	15	1	US-08-291-932A-16	Sequence 4, Appli	C 506	13.8	0.8	18	1	US-09-686-179A-2	Sequence 2, Appli
C 434	14	0.8	15	1	US-08-292-620A-56	Sequence 56, Appl	C 507	13.8	0.8	18	1	US-09-194-842A-48	Sequence 48, Appl
C 435	14	0.8	15	1	US-08-292-620A-360	Sequence 360, App	C 508	13.8	0.8	18	1	US-09-360-545-60	Sequence 60, Appl
C 436	14	0.8	15	1	US-08-292-620A-363	Sequence 363, App	C 509	13.8	0.8	18	1	US-09-293-533-52	Sequence 52, Appl
C 437	14	0.8	15	1	US-08-292-620A-597	Sequence 597, App	C 510	13.8	0.8	18	1	US-09-371-772B-4028	Sequence 4028, Ap
C 438	14	0.8	15	1	US-08-832-021-62	Sequence 62, Appl	C 511	13.8	0.8	18	1	US-09-925-388-30	Sequence 30, Appl
C 439	14	0.8	15	1	US-08-832-021-63	Sequence 63, Appl	C 512	13.8	0.8	18	1	US-09-981-621-2	Sequence 2, Appli
C 440	14	0.8	15	1	US-08-832-021-64	Sequence 64, Appl	C 513	13.8	0.8	18	1	5182262-6	Patent No. 5182262
C 441	14	0.8	15	1	US-09-071-845-56	Sequence 56, Appl	C 514	13.4	0.8	15	1	US-08-242-664-19	Sequence 19, Appl
C 442	14	0.8	15	1	US-09-071-845-360	Sequence 360, App	C 515	13.4	0.8	15	1	US-08-484-138-19	Sequence 19, Appl
C 443	14	0.8	15	1	US-09-071-845-363	Sequence 363, App	C 516	13.4	0.8	15	1	US-08-854-041-4	Sequence 4, Appli
C 444	14	0.8	15	1	US-09-071-845-597	Sequence 597, App	C 517	13.4	0.8	15	1	US-08-863-639A-8	Sequence 8, Appli
C 445	14	0.8	15	1	US-09-475-947A-158	Sequence 158, App	C 518	13.4	0.8	15	1	US-08-893-204C-2	Sequence 2, Appli
C 446	14	0.8	15	1	US-08-087-387-6	Sequence 6, Appli	C 519	13.4	0.8	15	1	US-08-832-021-17	Sequence 17, Appl
C 447	14	0.8	16	1	US-08-455-627-6	Sequence 6, Appli	C 520	13.4	0.8	15	1	US-08-832-021-25	Sequence 25, Appl
C 448	14	0.8	16	1	US-08-461-271-6	Sequence 6, Appli	C 521	13.4	0.8	15	1	US-08-832-021-37	Sequence 37, Appl
C 449	14	0.8	16	1	US-08-689-856-6	Sequence 6, Appli	C 522	13.4	0.8	15	1	US-08-832-021-44	Sequence 44, Appl
C 450	14	0.8	16	1	US-08-822-028-23	Sequence 23, Appl	C 523	13.4	0.8	15	1	US-08-832-021-48	Sequence 48, Appl
C 451	14	0.8	16	1	US-08-822-028-39	Sequence 39, Appl	C 524	13.4	0.8	15	1	US-08-832-021-49	Sequence 49, Appl
C 452	14	0.8	16	1	US-09-070-477-6	Sequence 6, Appli	C 525	13.4	0.8	15	1	US-08-832-021-52	Sequence 52, Appl
C 453	14	0.8	16	1	US-08-479-285-39	Sequence 39, Appl	C 526	13.4	0.8	15	1	US-08-832-021-53	Sequence 53, Appl
C 454	14	0.8	16	1	US-08-882-649A-8	Sequence 8, Appli	C 527	13.4	0.8	15	1	US-08-832-021-55	Sequence 55, Appl
C 455	14	0.8	16	1	US-09-503-653A-23	Sequence 23, Appl	C 528	13.4	0.8	15	1	US-08-832-021-56	Sequence 56, Appl
C 456	14	0.8	16	1	US-08-584-040-2548	Sequence 2548, Ap	C 529	13.4	0.8	15	1	US-08-832-021-57	Sequence 57, Appl
C 457	14	0.8	17	1	US-08-584-040-2553	Sequence 2553, Ap	C 530	13.4	0.8	15	1	US-08-832-021-59	Sequence 59, Appl
C 458	14	0.8	17	1	US-09-371-772B-1077	Sequence 1077, Ap	C 531	13.4	0.8	15	1	US-08-832-021-60	Sequence 60, Appl
C 459	14	0.8	17	1	US-08-373-124A-196	Sequence 196, App	C 532	13.4	0.8	15	1	US-09-475-947A-164	Sequence 164, App
C 460	14	0.8	17	1	US-08-437-350-3	Sequence 3, Appli	C 533	13.4	0.8	15	1	US-09-335-629-7	Sequence 7, Appli
C 461	14	0.8	17	1	US-09-334-938-3	Sequence 3, Appli	C 534	13.4	0.8	15	1	PCT-US91-03680-19	Sequence 19, Appl
C 462	14	0.8	17	1	US-08-584-040-2130	Sequence 2130, Ap	C 535	13.4	0.8	15	1	PCT-US95-06379-19	Sequence 19, Appl
C 463	14	0.8	17	1	US-08-584-040-2554	Sequence 2554, Ap	C 536	13.4	0.8	16	1	US-08-952-376-2	Sequence 2, Appli
C 464	13.8	0.8	17	1	US-08-373-124A-196	Sequence 196, App	C 537	13.4	0.8	17	1	US-08-233-608-12	Sequence 12, Appl
C 465	13.8	0.8	17	1	US-09-317-350-3	Sequence 3, Appli	C 538	13.4	0.8	17	1	US-08-531-747-4	Sequence 4, Appli
C 466	13.8	0.8	17	1	US-08-584-040-2130	Sequence 2130, Ap	C 539	13.4	0.8	17	1	US-08-373-124A-194	Sequence 194, App
C 467	13.8	0.8	17	1	US-08-584-040-2554	Sequence 2554, Ap	C 540	13.4	0.8	17	1	US-08-531-749-4	Sequence 4, Appli
C 468	13.8	0.8	17	1	US-08-584-040-2555	Sequence 2555, Ap	C 541	13.4	0.8	17	1	US-08-178-476A-16	Sequence 16, Appl
C 469	13.8	0.8	17	1	US-08-584-040-2555	Sequence 2555, Ap	C 542	13.4	0.8	17	1	US-08-781-432-4	Sequence 4, Appli
C 470	13.8	0.8	17	1	US-08-584-040-2555	Sequence 7818, Ap	C 543	13.4	0.8	17	1	US-08-257-073-135	Sequence 135, App
C 471	13.8	0.8	17	1	US-08-584-040-7818	Sequence 7818, Ap	C 544	13.4	0.8	17	1	US-08-887-480-12	Sequence 12, Appl

C 545	13.4	0.8	17	1	US-08-435-628-194	Sequence 194, Appl	618	13	0.7	16	1	US-08-711-417C-119	Sequence 119, Appl
C 546	13.4	0.8	17	1	US-08-722-187-12	Sequence 12, Appl	C 619	13	0.7	16	1	US-08-275-951-42	Sequence 42, Appl
C 547	13.4	0.8	17	1	US-08-964-020-2	Sequence 2, Appl	620	13	0.7	16	1	US-09-723-909-119	Sequence 119, Appl
C 548	13.4	0.8	17	1	US-09-083-366-16	Sequence 16, Appl	621	13	0.7	16	1	PCT-US93-08743-119	Sequence 119, Appl
C 549	13.4	0.8	17	1	US-08-584-040-2776	Sequence 2776, Ap	C 622	13	0.7	17	1	US-08-292-620A-1639	Sequence 1639, Ap
C 550	13.4	0.8	17	1	US-08-584-040-2777	Sequence 2777, Ap	C 623	13	0.7	17	1	US-08-292-620A-1790	Sequence 1790, Ap
C 551	13.4	0.8	17	1	US-08-584-040-2778	Sequence 2778, Ap	C 624	13	0.7	17	1	US-08-292-620A-1801	Sequence 1801, Ap
C 552	13.4	0.8	17	1	US-09-370-644B-23	Sequence 23, Appl	C 625	13	0.7	17	1	US-08-292-620A-1823	Sequence 1823, Ap
C 553	13.4	0.8	17	1	US-09-371-772B-1300	Sequence 1300, Ap	C 626	13	0.7	17	1	US-08-292-620A-1868	Sequence 1868, Ap
C 554	13.4	0.8	17	1	US-09-371-772B-1301	Sequence 1301, Ap	C 627	13	0.7	17	1	US-09-071-845-1639	Sequence 1639, Ap
C 555	13.4	0.8	17	1	US-09-371-772B-1302	Sequence 1302, Ap	C 628	13	0.7	17	1	US-09-071-845-1790	Sequence 1790, Ap
556	13.4	0.8	17	1	US-09-371-772B-5090	Sequence 5090, Ap	C 629	13	0.7	17	1	US-09-071-845-1801	Sequence 1801, Ap
557	13.4	0.8	17	1	US-09-866-108A-6390	Sequence 6390, Ap	C 630	13	0.7	17	1	US-09-071-845-1823	Sequence 1823, Ap
558	13.4	0.8	17	1	US-09-866-108A-6391	Sequence 6391, Ap	C 631	13	0.7	17	1	US-09-071-845-1868	Sequence 1868, Ap
559	13.4	0.8	17	1	US-09-866-108A-6392	Sequence 6392, Ap	632	13	0.7	17	1	US-09-434-131A-12	Sequence 12, Appl
560	13.4	0.8	17	1	US-09-866-108A-7876	Sequence 7876, Ap	C 633	13	0.7	17	1	US-08-584-040-2547	Sequence 2547, Ap
561	13.4	0.8	17	1	US-09-866-108A-7880	Sequence 7880, Ap	C 634	13	0.7	17	1	US-09-371-772B-1071	Sequence 1071, Ap
562	13.4	0.8	17	1	US-09-866-108A-7881	Sequence 7881, Ap	635	13	0.7	17	1	US-09-371-772B-5091	Sequence 5091, Ap
563	13.4	0.8	17	1	US-09-866-108A-10020	Sequence 10020, A	C 636	13	0.7	17	1	US-09-371-772B-5092	Sequence 5092, Ap
564	13.4	0.8	17	1	US-09-866-108A-10021	Sequence 10021, A	C 637	13	0.7	17	1	US-09-866-108A-1381	Sequence 1381, Ap
C 565	13.4	0.8	17	1	US-09-866-108A-10281	Sequence 10281, A	C 638	13	0.7	17	1	US-09-866-108A-1382	Sequence 1382, Ap
C 566	13.4	0.8	17	1	US-09-866-108A-10282	Sequence 10282, A	C 639	13	0.7	17	1	US-09-866-108A-1383	Sequence 1383, Ap
C 567	13.4	0.8	17	1	US-09-866-108A-10283	Sequence 10283, A	C 640	13	0.7	17	1	US-09-866-108A-1384	Sequence 1384, Ap
568	13.4	0.8	17	1	US-09-866-108A-10500	Sequence 10500, A	C 641	13	0.7	17	1	US-09-866-108A-1385	Sequence 1385, Ap
569	13.4	0.8	17	1	US-09-866-108A-10501	Sequence 10501, A	642	12.8	0.7	16	1	US-08-126-564A-46	Sequence 46, Appl
570	13.4	0.8	17	1	US-09-866-108A-10503	Sequence 10503, A	643	12.8	0.7	16	1	US-08-031-147A-56	Sequence 56, Appl
C 571	13.4	0.8	17	1	PCT-US91-03680-7	Sequence 7, Appl	C 644	12.8	0.7	16	1	US-08-455-627-16	Sequence 16, Appl
C 572	13.4	0.8	17	1	PCT-US95-04712-12	Sequence 12, Appl	645	12.8	0.7	16	1	US-08-748-591-18	Sequence 18, Appl
C 573	13.2	0.8	14	1	US-09-300-958A-65	Sequence 65, Appl	646	12.8	0.7	16	1	US-08-748-591-20	Sequence 20, Appl
C 574	13	0.7	13	1	US-08-745-269-3	Sequence 3, Appl	C 647	12.8	0.7	16	1	US-08-689-856-16	Sequence 16, Appl
C 575	13	0.7	13	1	US-08-745-269-4	Sequence 4, Appl	C 648	12.8	0.7	16	1	US-08-412-376-5	Sequence 5, Appl
576	13	0.7	13	1	US-09-305-223-1	Sequence 1, Appl	649	12.8	0.7	16	1	US-08-403-888A-39	Sequence 39, Appl
577	13	0.7	13	1	US-09-068-860-15	Sequence 15, Appl	650	12.8	0.7	16	1	US-08-403-888A-55	Sequence 55, Appl
C 578	13	0.7	13	1	US-09-352-540A-6	Sequence 6, Appl	651	12.8	0.7	16	1	US-08-403-888A-112	Sequence 112, Appl
C 579	13	0.7	13	1	US-09-799-645-6	Sequence 6, Appl	C 652	12.8	0.7	16	1	US-08-739-069-1	Sequence 1, Appl
580	13	0.7	13	1	US-09-619-103-19	Sequence 19, Appl	653	12.8	0.7	16	1	US-08-656-906-2	Sequence 2, Appl
C 581	13	0.7	13	1	US-10-002-528-6	Sequence 6, Appl	C 654	12.8	0.7	16	1	US-08-757-024-858	Sequence 858, Appl
582	13	0.7	13	1	US-09-475-947A-29	Sequence 29, Appl	655	12.8	0.7	16	1	US-07-808-452-11	Sequence 11, Appl
583	13	0.7	14	1	US-08-455-627-8	Sequence 8, Appl	C 656	12.8	0.7	16	1	US-07-808-452-12	Sequence 12, Appl
C 584	13	0.7	14	1	US-08-486-955A-2	Sequence 2, Appl	C 657	12.8	0.7	16	1	US-09-313-121-1	Sequence 1, Appl
585	13	0.7	14	1	US-08-294-424-33	Sequence 33, Appl	C 658	12.8	0.7	16	1	US-09-217-847-2	Sequence 2, Appl
586	13	0.7	14	1	US-08-689-856-8	Sequence 8, Appl	C 659	12.8	0.7	16	1	US-08-750-088A-38	Sequence 38, Appl
C 587	13	0.7	14	1	US-08-371-377-8	Sequence 8, Appl	C 660	12.8	0.7	16	1	US-09-633-848-1	Sequence 1, Appl
C 588	13	0.7	14	1	US-08-832-021-13	Sequence 13, Appl	661	12.8	0.7	16	1	US-08-754-477A-37	Sequence 37, Appl
C 589	13	0.7	14	1	US-08-832-021-14	Sequence 14, Appl	662	12.8	0.7	16	1	US-09-474-432B-1	Sequence 1, Appl
C 590	13	0.7	14	1	US-08-832-021-15	Sequence 15, Appl	663	12.8	0.7	16	1	US-09-474-432B-21	Sequence 21, Appl
C 591	13	0.7	14	1	US-08-724-466B-12	Sequence 12, Appl	C 664	12.8	0.7	16	1	US-09-829-855-40	Sequence 40, Appl
C 592	13	0.7	14	1	US-08-724-466B-13	Sequence 13, Appl	C 665	12.8	0.7	16	1	US-09-829-855-115	Sequence 115, Appl
C 593	13	0.7	14	1	US-08-724-466B-15	Sequence 15, Appl	666	12.8	0.7	16	1	US-09-476-387-1	Sequence 1, Appl
594	13	0.7	14	1	US-08-787-321-8	Sequence 8, Appl	667	12.8	0.7	16	1	US-09-476-387-21	Sequence 21, Appl
C 595	13	0.7	14	1	US-08-882-164D-12	Sequence 12, Appl	C 668	12.8	0.7	16	1	US-09-722-319-38	Sequence 38, Appl
C 596	13	0.7	14	1	US-08-882-164D-13	Sequence 13, Appl	669	12.8	0.7	16	1	PCT-US92-10770-11	Sequence 11, Appl
C 597	13	0.7	14	1	US-08-882-164D-15	Sequence 15, Appl	C 670	12.8	0.7	16	1	PCT-US92-10770-12	Sequence 12, Appl
C 598	13	0.7	14	1	US-09-475-947A-94	Sequence 94, Appl	671	12.8	0.7	16	1*	PCT-US92-10792-9	Sequence 9, Appl
C 599	13	0.7	14	1	US-09-151-771B-18	Sequence 18, Appl	C 672	12.8	0.7	16	1	PCT-US92-10792-10	Sequence 10, Appl
C 600	13	0.7	14	1	US-09-151-771B-20	Sequence 20, Appl	673	12.8	0.7	16	1	PCT-US94-02471-56	Sequence 56, Appl
C 601	13	0.7	15	1	US-08-292-620A-359	Sequence 359, App	674	12.8	0.7	16	1	PCT-US94-09143-46	Sequence 46, Appl
C 602	13	0.7	15	1	US-08-832-021-26	Sequence 364, App	C 675	12.8	0.7	17	1	US-08-152-313-67	Sequence 67, Appl
C 603	13	0.7	15	1	US-08-832-021-26	Sequence 26, Appl	C 676	12.8	0.7	17	1	US-08-373-124A-2149	Sequence 2149, Ap
C 604	13	0.7	15	1	US-08-832-021-27	Sequence 27, Appl	C 677	12.8	0.7	17	1	US-08-579-223-67	Sequence 67, Appl
C 605	13	0.7	15	1	US-08-832-021-28	Sequence 28, Appl	C 678	12.8	0.7	17	1	US-08-309-512-16	Sequence 16, Appl
C 606	13	0.7	15	1	US-08-832-021-36	Sequence 36, Appl	C 679	12.8	0.7	17	1	US-08-758-306-83	Sequence 83, Appl
C 607	13	0.7	15	1	US-08-832-021-38	Sequence 38, Appl	C 680	12.8	0.7	17	1	US-08-758-306-1067	Sequence 1067, Ap
C 608	13	0.7	15	1	US-08-832-021-39	Sequence 39, Appl	C 681	12.8	0.7	17	1	US-08-435-628-2149	Sequence 2149, Ap
C 609	13	0.7	15	1	US-08-832-021-40	Sequence 40, Appl	C 682	12.8	0.7	17	1	US-08-292-620A-1770	Sequence 1770, Ap
C 610	13	0.7	15	1	US-08-832-021-50	Sequence 50, Appl	C 683	12.8	0.7	17	1	US-08-292-620A-1894	Sequence 1894, Ap
C 611	13	0.7	15	1	US-08-832-021-51	Sequence 51, Appl	C 684	12.8	0.7	17	1	US-08-292-620A-1884	Sequence 1884, Ap
C 612	13	0.7	15	1	US-09-071-845-359	Sequence 359, App	C 685	12.8	0.7	17	1	US-08-173-489C-96	Sequence 96, Appl
C 613	13	0.7	15	1	US-09-071-845-364	Sequence 364, App	C 686	12.8	0.7	17	1	US-08-757-024-847	Sequence 847, App
614	13	0.7	15	1	US-09-081-646-842	Sequence 842, App	C 687	12.8	0.7	17	1	US-08-757-024-857	Sequence 857, App
C 615	13	0.7	15	1	US-09-531-000-54	Sequence 54, Appl	C 688	12.8	0.7	17	1	US-08-665-259-42	Sequence 42, Appl
616	13	0.7	16	1	US-08-284-484A-4	Sequence 4, Appl	C 689	12.8	0.7	17	1	US-08-665-259-55	Sequence 55, Appl
617	13	0.7	16	1	US-08-465-590-119	Sequence 119, App	C 690	12.8	0.7	17	1	US-08-762-500-42	Sequence 42, Appl

C 691	12.8	0.7	17	1	US-08-762-500-55	Sequence 55, Appl	C 764	12.4	0.7	14	1	US-08-832-021-7	Sequence 7, Appli
C 692	12.8	0.7	17	1	US-08-463-903-89	Sequence 89, Appl	C 765	12.4	0.7	14	1	US-08-832-021-8	Sequence 8, Appli
C 693	12.8	0.7	17	1	US-08-998-099-91	Sequence 91, Appl	C 766	12.4	0.7	14	1	US-08-832-021-11	Sequence 11, Appl
C 694	12.8	0.7	17	1	US-09-071-845-1770	Sequence 1770, Ap	C 767	12.4	0.7	14	1	US-08-832-021-12	Sequence 12, Appl
C 695	12.8	0.7	17	1	US-09-071-845-1894	Sequence 1894, Ap	C 768	12.4	0.7	14	1	US-08-724-466B-16	Sequence 16, Appl
C 696	12.8	0.7	17	1	US-09-071-845-1984	Sequence 1984, Ap	C 769	12.4	0.7	14	1	US-08-724-466B-17	Sequence 17, Appl
C 697	12.8	0.7	17	1	US-09-021-701-74	Sequence 74, Appl	C 770	12.4	0.7	14	1	US-08-724-466B-18	Sequence 18, Appl
C 698	12.8	0.7	17	1	US-09-021-701-75	Sequence 75, Appl	C 771	12.4	0.7	14	1	US-08-724-466B-20	Sequence 20, Appl
C 699	12.8	0.7	17	1	US-08-957-351-28	Sequence 28, Appl	C 772	12.4	0.7	14	1	US-08-724-466B-22	Sequence 22, Appl
700	12.8	0.7	17	1	US-07-935-695-89	Sequence 89, Appl	773	12.4	0.7	14	1	US-08-871-678C-9	Sequence 9, Appli
C 701	12.8	0.7	17	1	US-08-584-040-2519	Sequence 2519, Ap	C 774	12.4	0.7	14	1	US-08-991-789A-130	Sequence 130, App
C 702	12.8	0.7	17	1	US-08-584-040-2556	Sequence 2556, Ap	C 775	12.4	0.7	14	1	US-08-882-164D-16	Sequence 16, Appl
C 703	12.8	0.7	17	1	US-08-584-040-2740	Sequence 2740, Ap	C 776	12.4	0.7	14	1	US-08-882-164D-17	Sequence 17, Appl
C 704	12.8	0.7	17	1	US-08-584-040-7822	Sequence 7822, Ap	C 777	12.4	0.7	14	1	US-08-882-164D-18	Sequence 18, Appl
C 705	12.8	0.7	17	1	US-08-584-040-7824	Sequence 7824, Ap	C 778	12.4	0.7	14	1	US-08-882-164D-20	Sequence 20, Appl
C 706	12.8	0.7	17	1	US-08-679-645-880	Sequence 880, App	C 779	12.4	0.7	14	1	US-08-882-164D-22	Sequence 22, Appl
C 707	12.8	0.7	17	1	US-08-679-645-882	Sequence 882, App	C 780	12.4	0.7	14	1	US-09-062-451-130	Sequence 130, App
C 708	12.8	0.7	17	1	US-09-593-012-23	Sequence 23, Appl	C 781	12.4	0.7	14	1	US-09-303-069-10	Sequence 10, Appl
C 709	12.8	0.7	17	1	US-09-474-432B-526	Sequence 526, App	C 782	12.4	0.7	14	1	US-09-134-250-10	Sequence 10, Appl
C 710	12.8	0.7	17	1	US-09-474-432B-558	Sequence 558, App	C 783	12.4	0.7	14	1	US-09-598-326-130	Sequence 130, App
C 711	12.8	0.7	17	1	US-09-474-432B-559	Sequence 559, App	C 784	12.4	0.7	14	1	US-09-370-838-47	Sequence 47, Appl
C 712	12.8	0.7	17	1	US-09-474-432B-568	Sequence 568, App	C 785	12.4	0.7	14	1	US-09-475-947A-310	Sequence 310, App
C 713	12.8	0.7	17	1	US-09-474-432B-825	Sequence 825, App	C 786	12.4	0.7	14	1	US-09-289-198-130	Sequence 130, App
C 714	12.8	0.7	17	1	US-08-415-658-6	Sequence 6, Appli	C 787	12.4	0.7	14	1	US-09-429-755-130	Sequence 130, App
C 715	12.8	0.7	17	1	US-09-371-772B-1043	Sequence 1043, Ap	C 788	12.4	0.7	15	1	US-08-041-599-2	Sequence 2, Appli
C 716	12.8	0.7	17	1	US-09-371-772B-1080	Sequence 1080, Ap	C 789	12.4	0.7	15	1	US-08-337-025-2	Sequence 2, Appli
C 717	12.8	0.7	17	1	US-09-371-772B-1264	Sequence 1264, Ap	790	12.4	0.7	15	1	US-08-363-240A-141	Sequence 141, App
C 718	12.8	0.7	17	1	US-09-371-772B-3606	Sequence 3606, Ap	791	12.4	0.7	15	1	US-08-363-240A-142	Sequence 142, App
C 719	12.8	0.7	17	1	US-09-371-772B-3608	Sequence 3608, Ap	C 792	12.4	0.7	15	1	US-08-363-240A-757	Sequence 757, App
C 720	12.8	0.7	17	1	US-09-371-772B-5343	Sequence 5343, Ap	C 793	12.4	0.7	15	1	US-08-585-684B-159	Sequence 159, App
C 721	12.8	0.7	17	1	US-09-371-772B-5476	Sequence 5476, Ap	C 794	12.4	0.7	15	1	US-08-819-867-68	Sequence 68, Appl
C 722	12.8	0.7	17	1	US-09-371-772B-5562	Sequence 5562, Ap	C 795	12.4	0.7	15	1	US-08-832-021-18	Sequence 18, Appl
C 723	12.8	0.7	17	1	US-09-371-772B-6785	Sequence 6785, Ap	C 796	12.4	0.7	15	1	US-08-832-021-19	Sequence 19, Appl
C 724	12.8	0.7	17	1	US-09-371-772B-6956	Sequence 6956, Ap	C 797	12.4	0.7	15	1	US-08-832-021-20	Sequence 20, Appl
C 725	12.8	0.7	17	1	US-09-476-387-525	Sequence 525, App	C 798	12.4	0.7	15	1	US-08-832-021-41	Sequence 41, Appl
C 726	12.8	0.7	17	1	US-09-476-387-557	Sequence 557, App	C 799	12.4	0.7	15	1	US-08-832-021-42	Sequence 42, Appl
C 727	12.8	0.7	17	1	US-09-476-387-558	Sequence 558, App	C 800	12.4	0.7	15	1	US-08-832-021-43	Sequence 43, Appl
728	12.8	0.7	17	1	US-09-476-387-567	Sequence 567, App	C 801	12.4	0.7	15	1	US-08-832-021-45	Sequence 45, Appl
C 729	12.8	0.7	17	1	US-09-476-387-824	Sequence 824, App	C 802	12.4	0.7	15	1	US-08-832-021-46	Sequence 46, Appl
730	12.8	0.7	17	1	US-09-827-998-376	Sequence 376, App	C 803	12.4	0.7	15	1	US-08-832-021-47	Sequence 47, Appl
731	12.8	0.7	17	1	US-09-827-998-377	Sequence 377, App	C 804	12.4	0.7	15	1	US-08-832-021-54	Sequence 54, Appl
732	12.8	0.7	17	1	US-09-827-998-483	Sequence 483, App	C 805	12.4	0.7	15	1	US-08-832-021-58	Sequence 58, Appl
733	12.8	0.7	17	1	US-09-827-998-485	Sequence 485, App	C 806	12.4	0.7	15	1	US-09-038-073-159	Sequence 159, App
C 734	12.8	0.7	17	1	US-09-866-108A-645	Sequence 645, App	C 807	12.4	0.7	15	1	US-09-446-765-4	Sequence 4, Appli
C 735	12.8	0.7	17	1	US-09-866-108A-646	Sequence 646, App	808	12.4	0.7	15	1	US-09-344-667-37	Sequence 37, Appl
736	12.8	0.7	17	1	US-09-866-108A-895	Sequence 895, App	809	12.4	0.7	15	1	US-08-464-011B-58	Sequence 58, Appl
737	12.8	0.7	17	1	US-09-866-108A-897	Sequence 897, App	810	12.4	0.7	15	1	US-09-693-352-37	Sequence 37, Appl
738	12.8	0.7	17	1	US-09-866-108A-1424	Sequence 1424, Ap	811	12.4	0.7	15	1	US-09-693-005A-37	Sequence 37, Appl
739	12.8	0.7	17	1	US-09-866-108A-1425	Sequence 1425, Ap	812	12.4	0.7	15	1	US-09-603-830-37	Sequence 37, Appl
740	12.8	0.7	17	1	US-09-866-108A-1530	Sequence 1530, Ap	813	12.4	0.7	15	1	US-09-976-978A-37	Sequence 37, Appl
741	12.8	0.7	17	1	US-09-866-108A-1531	Sequence 1531, Ap	814	12.4	0.7	15	1	US-09-378-535-68	Sequence 68, Appl
742	12.8	0.7	17	1	US-09-866-108A-1638	Sequence 1638, Ap	815	12.4	0.7	15	1	US-09-961-949A-37	Sequence 37, Appl
743	12.8	0.7	17	1	US-09-866-108A-1639	Sequence 1639, Ap	C 816	12.4	0.7	15	1	US-09-402-048-3	Sequence 3, Appli
C 744	12.8	0.7	17	1	US-09-866-108A-2252	Sequence 2252, Ap	C 817	12.4	0.7	15	1	US-09-402-048-6	Sequence 6, Appli
C 745	12.8	0.7	17	1	US-09-866-108A-2253	Sequence 2253, Ap	818	12.4	0.7	15	1	US-09-966-491A-37	Sequence 37, Appl
C 746	12.8	0.7	17	1	US-09-866-108A-6140	Sequence 6140, Ap	819	12.4	0.7	15	1	US-09-957-313A-37	Sequence 37, Appl
C 747	12.8	0.7	17	1	US-09-866-108A-6141	Sequence 6141, Ap	C 820	12.4	0.7	15	1	US-09-898-210-1	Sequence 1, Appli
C 748	12.8	0.7	17	1	US-09-866-108A-7436	Sequence 7436, Ap	821	12.4	0.7	15	1	US-09-966-312-37	Sequence 37, Appl
C 749	12.8	0.7	17	1	US-09-866-108A-7437	Sequence 7437, Ap	822	12.4	0.7	15	1	US-09-975-062A-37	Sequence 37, Appl
750	12.8	0.7	17	1	US-09-866-108A-10023	Sequence 10023, A	823	12.4	0.7	15	1	US-09-976-971A-37	Sequence 37, Appl
751	12.8	0.7	17	1	US-09-866-108A-10028	Sequence 10028, A	824	12.4	0.7	16	1	US-08-152-313-15	Sequence 15, Appl
752	12.8	0.7	17	1	US-09-866-108A-10229	Sequence 10229, A	825	12.4	0.7	16	1	US-08-579-223-15	Sequence 15, Appl
753	12.8	0.7	17	1	US-09-866-108A-10507	Sequence 10507, A	826	12.4	0.7	16	1	US-08-282-197C-20	Sequence 20, Appl
C 754	12.8	0.7	17	1	US-09-866-108A-10742	Sequence 10742, A	827	12.4	0.7	16	1	US-07-792-600-27	Sequence 27, Appl
C 755	12.8	0.7	17	1	US-09-866-108A-10743	Sequence 10743, A	828	12.4	0.7	16	1	US-09-157-021-27	Sequence 27, Appl
C 756	12.8	0.7	17	1	PCT-US94-12947A-67	Sequence 67, Appl	829	12.4	0.7	16	1	US-09-156-842-27	Sequence 27, Appl
C 757	12.4	0.7	14	1	US-08-332-838-3	Sequence 3, Appli	C 830	12.4	0.7	16	1	US-09-102-528-15	Sequence 15, Appl
758	12.4	0.7	14	1	US-08-435-684A-9	Sequence 9, Appli	C 831	12.4	0.7	16	1	US-08-626-285-19	Sequence 19, Appl
759	12.4	0.7	14	1	US-08-373-127B-9	Sequence 9, Appli	C 832	12.4	0.7	16	1	US-09-300-958A-58	Sequence 58, Appl
C 760	12.4	0.7	14	1	US-08-494-577-10	Sequence 10, Appl	C 833	12.4	0.7	16	1	US-09-300-958A-84	Sequence 84, Appl
C 761	12.4	0.7	14	1	US-08-795-868-10	Sequence 10, Appl	C 834	12.4	0.7	16	1	US-09-527-972-17	Sequence 17, Appl
762	12.4	0.7	14	1	US-08-934-877A-9	Sequence 9, Appli	835	12.4	0.7	16	1	US-09-591-514-27	Sequence 27, Appl
C 763	12.4	0.7	14	1	US-08-832-021-5	Sequence 5, Appli	836	12.4	0.7	16	1	PCT-US94-12947A-15	Sequence 15, Appl

c 837 12.2 0.7 13 1 US-08-351-748-2 Sequence 2, Appli
c 838 12.2 0.7 13 1 US-08-430-536A-2 Sequence 2, Appli
c 839 12.2 0.7 13 1 US-08-684-547-2 Sequence 2, Appli
c 840 12.2 0.7 13 1 PCT-US93-02246-2 Sequence 2, Appli
c 841 12.2 0.7 14 1 US-09-042-225-4 Sequence 4, Appli
c 842 12.2 0.7 14 1 US-09-390-324B-1 Sequence 1, Appli
c 843 12.2 0.7 14 1 US-10-015-593-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-164-249B-6
; Sequence 6, Application US/09164249B
; Patent No. 6322971
; GENERAL INFORMATION:
; APPLICANT: Chetverin, Alexander B.
; APPLICANT: Kramer, Fred Russel
; TITLE OF INVENTION: NOVEL OLIGONUCLEOTIDE ARRAYS AND THEIR USE FOR SORTING,
; TITLE OF INVENTION: ISOLATING, SEQUENCING, AND MANIPULATING NUCLEIC ACIDS
; FILE REFERENCE: 07763-004003
; CURRENT APPLICATION NUMBER: US/09/164,249B
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 08/473,010
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/247,530
; PRIOR FILING DATE: 1994-05-23
; PRIOR APPLICATION NUMBER: US 07/838,607
; PRIOR FILING DATE: 1992-02-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically derived DNA
US-09-164-249B-6

Query Match 1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 41;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1731 TTACAAAAA 1754
Db 1 TTAAAAA 24

RESULT 2
US-08-996-306-10/c
; Sequence 10, Application US/08996306
; Patent No. 5945522
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/996,306
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: GENSET.018A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PGRT32
; LOCATION: complement 5198..5221
; OTHER INFORMATION: Location relative to seqID3
US-08-996-306-10
Query Match 1.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 57;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1732 TTACAAAAA 1754
Db 23 TTTCAAAAA 1

RESULT 3
US-09-338-907-10/c
; Sequence 10, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 10
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..24
; OTHER INFORMATION: primer oligonucleotide PGRT32
US-09-338-907-10

Query Match 1.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 57;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1732 TTACAAAAA 1754
Db 23 TTTCAAAAA 1


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; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-527-345-7

Query Match          1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 64;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 8
US-09-923-246-38/c
; Sequence 38, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-923-246-38

Query Match          1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 64;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 9
US-10-295-723-38/c
; Sequence 38, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
```

```
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-10-295-723-38

Query Match          1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 64;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 10
US-09-475-947A-153/c
; Sequence 153, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
; LENGTH: 27
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-153

Query Match          1.2%; Score 21.4; DB 1; Length 27;
Best Local Similarity 95.7%; Pred. No. 68;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 24 TAAAAA 2

RESULT 11
US-08-113-646A-42
; Sequence 42, Application US/08113646A
; Patent No. 5578468
; GENERAL INFORMATION:
; APPLICANT: PICKUP, David J.
; APPLICANT: PATEL, Dhaval Kumar
```

APPLICANT: ANTCAK, James B.
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/084,406
FILING DATE: 10-AUG-1987
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-113-646A-42

Query Match 1.2%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1754
Db 5 ACACAAAAA 25

RESULT 12
US-08-621-914A-3/c
Sequence 3, Application US/08621914A
Patent No. 5707807
GENERAL INFORMATION:
APPLICANT: KATO, KIKUYA
TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
TITLE OF INVENTION: ANALYSIS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,914A
FILING DATE: 26-MAR-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: LAWRENCE III, STANTON T.
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-107-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: other nucleic acid
US-08-621-914A-3

Query Match 1.2%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA 1755
Db 26 CAAAAA 6

RESULT 13
US-09-527-345-6/c
Sequence 6, Application US/09527345
Patent No. 6331413
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Adler, David A.
TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
FILE REFERENCE: 97-71
CURRENT APPLICATION NUMBER: US/09/527,345
CURRENT FILING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: US 60/124,820
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-527-345-6

Query Match 1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 83;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 BAAAAA 4

RESULT 14
US-09-167-513-10/c
Sequence 10, Application US/09167513
Patent No. 6388064
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Blumberg, Hal
TITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, Z219A
FILE REFERENCE: 97-63
CURRENT APPLICATION NUMBER: US/09/167,513
CURRENT FILING DATE: 1998-10-06
EARLIER APPLICATION NUMBER: US 60/061,712
EARLIER FILING DATE: 1997-10-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 10
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-167-513-10

Query Match          1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 83;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 26 BAAAAA 4

RESULT 15
US-09-161-939A-43/c
; Sequence 43, Application US/09161939A
; Patent No. 6486299
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: Genes and Proteins Predictive for
; TITLE OF INVENTION: Stroke, Hypertension, Diabetes, and Obesity
; FILE REFERENCE: 15966-527
; CURRENT APPLICATION NUMBER: US/09/161,939A
; CURRENT FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligo(dT)<25>V
US-09-161-939A-43

Query Match          1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 83;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 26 BAAAAA 4

RESULT 16
US-08-123-449A-19
; Sequence 19, Application US/08123449A
; Patent No. 5583032
; GENERAL INFORMATION:
; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,449A
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; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: miscellaneous feature
; LOCATION: 1-4
; OTHER INFORMATION: A is linked by 2',5'-linkage
; FEATURE:
; NAME/KEY: miscellaneous feature
; LOCATION: 4
; OTHER INFORMATION: A is linked at 2' end to following
; OTHER INFORMATION: base through a linker moiety
US-08-123-449A-19

Query Match          1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAA 1755
Db 1 AAAAAA 22

RESULT 17
US-08-458-050-19
; Sequence 19, Application US/08458050
; Patent No. 5677289
; GENERAL INFORMATION:
; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,050
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,449
; FILING DATE: 17-SEP-1993
```



```
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: miscellaneous feature
; LOCATION: 1-4
; OTHER INFORMATION: A is linked by 2',5'-linkage
; FEATURE:
; NAME/KEY: miscellaneous feature
; LOCATION: 4
; OTHER INFORMATION: A is linked at 2' end to following
; OTHER INFORMATION: base through a linker moiety
;
US-08-458-050-19

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 18
US-08-847-844A-94
; Sequence 94, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; MAMMALIAN RETROTRANSPOSONS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831

; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; US-08-847-844A-94

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 19
US-08-950-196-19
; Sequence 19, Application US/08950196
; Patent No. 6271369
; GENERAL INFORMATION:
; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,449
; FILING DATE:
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
```


TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-486-421-50
Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 23
US-08-470-911-50
Sequence 50, Application US/08470911
Patent No. 5756684
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-470-911-50
Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 24

US-08-735-381-1
Sequence 1, Application US/08735381
Patent No. 5853993
GENERAL INFORMATION:
APPLICANT: Dellinger, Douglas J.
APPLICANT: Dahm, SueAnn
APPLICANT: Troll, Mark
TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hewlett-Packard Company, Legal Dept.,
ADDRESSEE: Intellectual Property
STREET: 1501 Page Mill Road, MS 4U-10
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1126
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,381
FILING DATE: 21-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10950427-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-857-4125
TELEFAX: 650-852-8063
TELEX: 348-461
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
US-08-735-381-1
Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 25
US-08-486-809-50
Sequence 50, Application US/08486809
Patent No. 5869622
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,809
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-486-809-50

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAACAAAAA 1755
Db 1 AAAAAA 22

RESULT 26

US-09-183-619-7
Sequence 7, Application US/09183619
Patent No. 6103474
GENERAL INFORMATION:
APPLICANT: DELLINGER, DOUGLAS J.
APPLICANT: DAHM, SUEANN C.
APPLICANT: ILSLEY, DIANE D.
APPLICANT: ACH, ROBERT A.
APPLICANT: TROLL, MARK A.
TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
FILE REFERENCE: 10981619-1
CURRENT APPLICATION NUMBER: US/09/183,619
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 08/735,381
EARLIER FILING DATE: 1996-10-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 24
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: poly A-RNA target
OTHER INFORMATION: analyte
US-09-183-619-7

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAACAAAAA 1755
Db 1 AAAAAA 22

RESULT 27

US-09-201-674-1

Sequence 1, Application US/09201674
Patent No. 6110682
GENERAL INFORMATION:
APPLICANT: Dellinger, Douglas J.
Dahm, SueAnn
Troll, Mark
TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hewlett-Packard Company, Legal Dept.,
Intellectual Property
STREET: 1501 Page Mill Road, MS 4U-10
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1126
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,674
FILING DATE: 30-No. 6110682-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,381
FILING DATE: 21-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10950427-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-857-4125
TELEFAX: 650-852-8063
TELEX: 348-461
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-201-674-1

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAACAAAAA 1755
Db 1 AAAAAA 22

RESULT 28

US-09-536-936-11
Sequence 11, Application US/09536936
Patent No. 6346384
GENERAL INFORMATION:
APPLICANT: Pollner, Reinhold
TITLE OF INVENTION: Real Time Monitoring of PCR Using LOCI
FILE REFERENCE: BEH-7438
CURRENT APPLICATION NUMBER: US/09/536,936
CURRENT FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Oligonucleotide attached to beads
US-09-536-936-11

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 29
US-09-025-639-4
; Sequence 4, Application US/09025639
; Patent No. 6365346
; GENERAL INFORMATION:
; APPLICANT: Kurn, Nurith
; APPLICANT: Patel, Rajesh D.
; TITLE OF INVENTION: Quantitative Determination of Nucleic
; TITLE OF INVENTION: Acid Amplification Products
; FILE REFERENCE: BEH-7408
; CURRENT APPLICATION NUMBER: US/09/025,639
; CURRENT FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)...(24)
; OTHER INFORMATION: Synthetic DNA Probe
US-09-025-639-4

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 30
US-09-333-237-4
; Sequence 4, Application US/09333237
; Patent No. 6406667
; GENERAL INFORMATION:
; APPLICANT: Singh, Sharat
; APPLICANT: Ullman, Edwin F.
; TITLE OF INVENTION: Chemiluminescent Compositions For Use In
; TITLE OF INVENTION: Detection Of Multiple Analytes
; FILE REFERENCE: BEH-7383A
; CURRENT APPLICATION NUMBER: US/09/333,237
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 09/025,624
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: detection probe bound to sensitizer particle
US-09-333-237-4

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 31
US-09-732-067-1
; Sequence 1, Application US/09732067
; Patent No. 6457426
; GENERAL INFORMATION:
; APPLICANT: Ullman, Edwin
; APPLICANT: Singh, Rajendra
; APPLICANT: DeKeczer, Steve
; APPLICANT: Davalian, Dariush
; TITLE OF INVENTION: Amplified Luminescent Homogeneous
; TITLE OF INVENTION: Immunoassay
; FILE REFERENCE: BEH-7385
; CURRENT APPLICATION NUMBER: US/09/732,067
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hybridization oligo
US-09-732-067-1

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 32
US-09-475-947A-134/c
; Sequence 134, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 24
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-134

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 23 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 33
US-10-043-415-4
; Sequence 4, Application US/10043415
; Patent No. 6573054
; GENERAL INFORMATION:
```



```
; APPLICANT: Kurn, Nurith
; APPLICANT: Patel, Rajesh D.
; TITLE OF INVENTION: Quantitative Determination of Nucleic
; TITLE OF INVENTION: Acid Amplification Products
; FILE REFERENCE: BEH-7408
; CURRENT APPLICATION NUMBER: US/10/043,415
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US/09/025,639
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)...(24)
; OTHER INFORMATION: Synthetic DNA Probe
US-10-043-415-4

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 34
US-09-854-317-1
; Sequence 1, Application US/09854317
; Patent No. 6582938
; GENERAL INFORMATION:
; APPLICANT: Su, Xing
; APPLICANT: Dong, Helin
; APPLICANT: Ryder, Thomas B.
; TITLE OF INVENTION: Amplification of Nucleic Acids
; FILE REFERENCE: 3234.2
; CURRENT APPLICATION NUMBER: US/09/854,317
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-854-317-1

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 35
US-09-721-154-1/c
; Sequence 1, Application US/09721154
; Patent No. 6651008
; GENERAL INFORMATION:
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Adams, Cynthia
; APPLICANT: Sabry, James
; APPLICANT: Crompton, Anne
; TITLE OF INVENTION: Database system including computer code
; FILE REFERENCE: CytoP007C2
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; CURRENT APPLICATION NUMBER: US/09/721,154
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/311,996
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Psuedo-sequence
US-09-721-154-1

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 23 ATAAAAAAAAAAAAAAAAAAAAA 2

RESULT 36
US-09-721-154-4/c
; Sequence 4, Application US/09721154
; Patent No. 6651008
; GENERAL INFORMATION:
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Adams, Cynthia
; APPLICANT: Sabry, James
; APPLICANT: Crompton, Anne
; TITLE OF INVENTION: Database system including computer code
; FILE REFERENCE: CytoP007C2
; CURRENT APPLICATION NUMBER: US/09/721,154
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/311,996
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Psuedo-sequence
US-09-721-154-4

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 37
US-08-341-148-2/c
; Sequence 2, Application US/08341148
; Patent No. 5610287
; GENERAL INFORMATION:
; APPLICANT: NIKIFOROV, THEO
; APPLICANT: KNAPP, MICHAEL
; TITLE OF INVENTION: METHOD FOR THE IMMOBILIZATION OF NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
```

; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/341,148
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 639-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Equus caballus
; IMMEDIATE SOURCE:
; CLONE: Biotin-T25
; US-08-341-148-2

Query Match 1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 84;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 38
US-08-460-130-2/c
; Sequence 2, Application US/08460130
; Patent No. 5734020
; GENERAL INFORMATION:
; APPLICANT: Yuan N. Wong
; TITLE OF INVENTION: Production and Use
; TITLE OF INVENTION: of Magnetic Porous Inorganic Materials
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CPG, Inc.
; STREET: 3 Borinski Road
; CITY: Lincoln Park
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07035
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density
; MEDIUM TYPE: 5 1/4" diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,130
; FILING DATE: 2 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/307,307
; FILING DATE: 16 September 1994
; APPLICATION NUMBER: 07/794,910

; FILING DATE: 20 No. 5734020ember 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: Wong
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 626-3564
; TELEFAX: (202) 783-6031
; TELEX: No. 5734020e
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25
; TYPE: Nucleotide
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; US-08-460-130-2

Query Match 1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 84;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 39
US-08-969-813-1/c
; Sequence 1, Application US/08969813
; Patent No. 6060246
; GENERAL INFORMATION:
; APPLICANT: Summerton, James E.
; APPLICANT: Weller, Dwight D.
; APPLICANT: Wages, John M.
; TITLE OF INVENTION: Reagent and Method for Isolation
; TITLE OF INVENTION: and Detection of Selected Nucleic Acid Sequences
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,813
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,963
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gorthey, LeeAnn
; REGISTRATION NUMBER: 37,337
; REFERENCE/DOCKET NUMBER: 0450-0013.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-969-813-1

Query Match 1.2%; Score 20.4; DB 1; Length 25;

Best Local Similarity 95.5%; Pred. No. 84;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 40

US-09-183-619-5/c
; Sequence 5, Application US/09183619
; Patent No. 6103474
; GENERAL INFORMATION:
; APPLICANT: DELLINGER, DOUGLAS J.
; APPLICANT: DAHM, SUEANN C.
; APPLICANT: ILSLEY, DIANE D.
; APPLICANT: ACH, ROBERT A.
; APPLICANT: TROLL, MARK A.
; TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
; FILE REFERENCE: 10981619-1
; CURRENT APPLICATION NUMBER: US/09/183,619
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 08/735,381
; EARLIER FILING DATE: 1996-10-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Reporter probe
US-09-183-619-5

Query Match 1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 84;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 41

US-09-282-734-23/c
; Sequence 23, Application US/09282734A
; Patent No. 6537749
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis et al.
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
; FILE REFERENCE: 50036/009002
; CURRENT APPLICATION NUMBER: US/09/282,734A
; CURRENT FILING DATE: 1999-03-03
; EARLIER APPLICATION NUMBER: 60/080,686
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Capture probe sequence
US-09-282-734-23

Query Match 1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 84;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 42
PCT-US94-14096-2/c
; Sequence 2, Application PC/TUS9414096
; GENERAL INFORMATION:
; APPLICANT: NIKIFOROV, THEO
; APPLICANT: KNAPP, MICHAEL
; TITLE OF INVENTION: METHOD FOR THE IMMOBILIZATION OF NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14096
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 639-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Equus caballus
; IMMEDIATE SOURCE:
; CLONE: Biotin-T25
PCT-US94-14096-2

Query Match 1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 84;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 43

US-08-621-914A-2/c
; Sequence 2, Application US/08621914A
; Patent No. 5707807
; GENERAL INFORMATION:
; APPLICANT: KATO, KIKUYA
; TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
; TITLE OF INVENTION: ANALYSIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,914A
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAWRENCE III, STANTON T.
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
; US-08-621-914A-2

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 44
US-08-873-437-2/c
; Sequence 2, Application US/08873437
; Patent No. 6124092
; GENERAL INFORMATION:
; APPLICANT: O'Neill, Roger A.
; APPLICANT: Chen, Jer-Kang
; APPLICANT: Chiesa, Claudia
; APPLICANT: -Fry, George
; TITLE OF INVENTION: Multiplex Polynucleotide Capture
; TITLE OF INVENTION: Methods and Compositions
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PE Applied Biosystems
; STREET: 850 Lincoln Centre Drive
; CITY: Foster City
; STATE: CA
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,437
; FILING DATE: 12-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,832
; FILING DATE: 04-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bortner, Scott R
; REGISTRATION NUMBER: 34,298
; REFERENCE/DOCKET NUMBER: 4294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-638-6245
; TELEFAX: 415-638-6071
; INFORMATION FOR SEQ ID NO: 2:
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-873-437-2

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 45
US-09-197-951-5/c
; Sequence 5, Application US/09197951
; Patent No. 6197554
; GENERAL INFORMATION:
; APPLICANT: LIN, SHI-LUNG
; CHUONG, CHENG-MING
; YING, SHAO-YAO
; TITLE OF INVENTION: Method for Generating Full-Length cDNA
; Library from Single Cells
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David & Raymond Patent Firm
; STREET: 108 N. Ynez Ave., Suite 128
; CITY: Monterey Park
; STATE: CA
; COUNTRY: USA
; ZIP: 91754
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,951
; FILING DATE: 20-NO. 6197554-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chan, Raymond Y.C.
; REGISTRATION NUMBER: 37,484
; REFERENCE/DOCKET NUMBER: USP8462A-SL(3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 571-9812
; TELEFAX: (626) 571-9813
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
; US-09-197-951-5

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 46
```

```
US-09-522-217-39/c
; Sequence 39, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764b
US-09-522-217-39
Query Match          1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 47
US-09-593-312-2/c
; Sequence 2, Application US/09593312
; Patent No. 6514699
; GENERAL INFORMATION:
; APPLICANT: O'Neill, Roger A.
; APPLICANT: Chen, Jer-Kang
; APPLICANT: Chiesa, Claudia
; APPLICANT: Fry, George
; TITLE OF INVENTION: Multiplex Polynucleotide Capture
; TITLE OF INVENTION: Methods and Compositions
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PE Applied Biosystems
; STREET: 850 Lincoln Centre Drive
; CITY: Foster City
; STATE: CA
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/593,312
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/873,437
; FILING DATE:

US-09-522-217-39/c
; ATTORNEY/AGENT INFORMATION:
; NAME: Bortner, Scott R
; REGISTRATION NUMBER: 34,298
; REFERENCE/DOCKET NUMBER: 4294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-638-6245
; TELEFAX: 415-638-6071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-593-312-2
Query Match          1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 48
US-09-923-246-39/c
; Sequence 39, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764b
US-09-923-246-39
Query Match          1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 49
US-09-658-077-1/c
; Sequence 1, Application US/09658077
; Patent No. 6627748
; GENERAL INFORMATION:
```



```

; APPLICANT: Ju, Jingyue
; APPLICANT: et al.
; TITLE OF INVENTION: Combinatorial Fluoresence Energy Transfer Tags And
; TITLE OF INVENTION: Their Applications For Multiplex Genetic Analyses
; FILE REFERENCE: 0575/62238/JPW/ADM
; CURRENT APPLICATION NUMBER: US/09/658,077
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scaffold
US-09-658-077-1

Query Match          1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 25 AAAAAAAAA 4

RESULT 50
US-10-295-723-39/c
; Sequence 39, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764b
US-10-295-723-39

Query Match          1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 25 AAAAAAAAA 4

RESULT 51
```

```

US-08-208-486-79
; Sequence 79, Application US/08208486
; Patent No. 5389531
; GENERAL INFORMATION:
; APPLICANT: Ito, Junetsu
; APPLICANT: Yoo, Seung-Ku
; TITLE OF INVENTION: METHODS TO REPLICATE DNA in vitro USING
; TITLE OF INVENTION: PRD1-CATALYZED DNA REPLICATION SYSTEMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cahill, Sutton & Thomas
; STREET: 155 Park One, 2141 E. Highland Ave.
; CITY: Phoenix
; STATE: Arizona
; COUNTRY: U.S.A.
; ZIP: 85016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
; COMPUTER: Packard Bell (IBM PC/AT compatible)
; OPERATING SYSTEM: MS-Dos, Version 5.0
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,486
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/869,916
; FILING DATE: April 14, 1992
; APPLICATION NUMBER: Japan 240525/91
; FILING DATE: August 26, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janelle Faunce Raupp
; REGISTRATION NUMBER: 30,485
; REFERENCE/DOCKET NUMBER: #3954-A-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (602) 956-7000
; TELEFAX: (602) 495-9475
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-208-486-79

Query Match          1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 94;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 1 AAAAAAAAA 22

RESULT 52
US-09-325-554-18/c
; Sequence 18, Application US/09325554
; Patent No. 6410235
; GENERAL INFORMATION:
; APPLICANT: Weindel, Kurt
; APPLICANT: Brand, Joachim
; TITLE OF INVENTION: DNA DETECTION BY MEANS OF A STRAND REASSOCIATION COMPLEX
; FILE REFERENCE: 024420-00008
; CURRENT APPLICATION NUMBER: US/09/325,554
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 198-24-900.4
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent-In version 3.1
; SEQ ID NO 18
; LENGTH: 27
; TYPE: DNA
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```
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: (27)..(27)
; OTHER INFORMATION: Y means incorporation of Aminolinker-phosphoramidite subsequently
; OTHER INFORMATION: esterified with 3-O carboxymethyl digoxigenin
US-09-325-554-18

Query Match          1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 94;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 53
US-08-146-504-16/c
; Sequence 16, Application US/08146504
; Patent No. 5605662
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES FOR
; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND
; TITLE OF INVENTION: DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,504
; FILING DATE: No. 5605662ember 1, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 203/218
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-146-504-16

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
```

```
RESULT 54
US-08-379-593-5/c
; Sequence 5, Application US/08379593
; Patent No. 5849480
; GENERAL INFORMATION:
; APPLICANT: Cros, Philippe
; APPLICANT: Kurfurst, Robin
; APPLICANT: Battail, Nicole
; APPLICANT: Piga, Nadia
; TITLE OF INVENTION: HAPTEN ASSAY DEVICE AND USE THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Floppy disk, 1.44M storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,593
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA"
; FEATURE:
; OTHER INFORMATION: consists of nucleosides with an alpha anomer and carries
US-08-379-593-5

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 55
US-08-725-976-16/c
; Sequence 16, Application US/08725976
; Patent No. 5929208
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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COMPUTER: IBM compatible
OPERATING SYSTEM: WINDOWS (VERSION 3.0)
SOFTWARE: WordPerfect (Version 6.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,976
FILING DATE: October 4, 1996
CLASSIFICATION: 422
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/146,504
FILING DATE: No. 5929208ember 1, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, David B.
REGISTRATION NUMBER: 31,125
REFERENCE/DOCKET NUMBER: 222/211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-725-976-16

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 56
US-08-997-080-83
Sequence 83, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
US-08-997-080-83

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 57
US-08-997-362-83
Sequence 83, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
US-08-997-362-83

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 58

US-08-965-780-1/c
; Sequence 1, Application US/08965780
; Patent No. 5986084
; GENERAL INFORMATION:
; APPLICANT: Pitsch, Stefan
; APPLICANT: Weiss, Patrick A.
; APPLICANT: Jenny, Luzi
; TITLE OF INVENTION: RIBONUCLEOSIDE-DERIVATIVE AND METHOD FOR
; TITLE OF INVENTION: PREPARING THE SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KUBOVCIK & KUBOVCIK
; STREET: 900 17th Street, N.W., Suite 990
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,780
; FILING DATE: 07-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 01931/97
; FILING DATE: 18-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubovcik, Ronald J.
; REGISTRATION NUMBER: 25,401
; REFERENCE/DOCKET NUMBER: FREI-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-9023
; TELEFAX: 202-887-9093
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligoribonucleotide"
US-08-965-780-1

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 59

US-08-873-970-83
; Sequence 83, Application US/08873970
; Patent No. 6001361
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,970
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-873-970-83

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 60

US-08-765-340-96/c
; Sequence 96, Application US/08765340
; Patent No. 6150092
; GENERAL INFORMATION:
; APPLICANT: UCHIDA, K.
; APPLICANT: UCHIDA, T.
; APPLICANT: TANAKA, Y.
; APPLICANT: MATSUDA, Y.
; APPLICANT: KONDO, S.
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
; TITLE OF INVENTION: COMPOUND
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version

SOFTWARE: #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 145146/94
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 311130/94
FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-765-340-96

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 61

US-09-095-855-83
Sequence 83, Application US/09095855
Patent No. 6160093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
US-09-095-855-83

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 62

US-09-407-675-1
Sequence 1, Application US/09407675
Patent No. 6169176
GENERAL INFORMATION:
APPLICANT: Bruice, Thomas C.
APPLICANT: Arya, Dev P.
TITLE OF INVENTION: DEOXYNUCLEIC ALKYL THIUREA COMPOUNDS AND USES THEREOF
FILE REFERENCE: 30448.65US02
CURRENT APPLICATION NUMBER: US/09/407,675
CURRENT FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 09/347,443
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/091,481
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/111,800
PRIOR FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Oligo 1
US-09-407-675-1

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 63

US-09-250-075-1/c
Sequence 1, Application US/09250075
Patent No. 6207819
GENERAL INFORMATION:
APPLICANT: Manoharan, Muthiah
APPLICANT: Maier, Martin A
TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of
Mixed Backbone Oligomeric Compounds
FILE REFERENCE: ISIS3299
CURRENT APPLICATION NUMBER: US/09/250,075
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 12


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; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-205-426-83

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 68
US-09-619-103-26
; Sequence 26, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-26

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 69
US-09-726-096A-1/c
; Sequence 1, Application US/09726096A
; Patent No. 6462184
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Martin A.
; TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of Mixed Back
; TITLE OF INVENTION: Oligomeric Compounds
; FILE REFERENCE: ISIS4528
; CURRENT APPLICATION NUMBER: US/09/726,096A
; CURRENT FILING DATE: 2000-11-29

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: 2'-methoxyethoxy (MOE)
US-09-726-096A-1

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 70
US-09-603-830-55
; Sequence 55, Application US/09603830
; Patent No. 6506564
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 4149-1-1-1-1
; CURRENT APPLICATION NUMBER: US/09/603,830
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-603-830-55

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 71
US-09-976-978A-55
; Sequence 55, Application US/09976978A
; Patent No. 6532097
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```

; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i17
; CURRENT APPLICATION NUMBER: US/09/976,978A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-976-978A-55

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 72
US-09-344-260A-10/c
; Sequence 10, Application US/09344260A
; Patent No. 6576752
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Lonnberg, Harri
; APPLICANT: Salo, Harri
; APPLICANT: Virta, Pasi
; TITLE OF INVENTION: Aminoxy Functionalized Oligomers
; FILE REFERENCE: ISIS-3508
; CURRENT APPLICATION NUMBER: US/09/344,260A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576752el Sequence
US-09-344-260A-10

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 73
US-09-961-949A-55
; Sequence 55, Application US/09961949A
; Patent No. 6582921
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i1
; CURRENT APPLICATION NUMBER: US/09/961,949A
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-961-949A-55

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 74
US-09-966-491A-55
; Sequence 55, Application US/09966491A
; Patent No. 6610491
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i4
; CURRENT APPLICATION NUMBER: US/09/966,491A
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667

```

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; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-966-491A-55
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```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
        |||||
Db       1 AAAAAAAAAAAAAAAAAAAAAA 20
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RESULT 75
US-09-957-313A-55
; Sequence 55, Application US/09957313A
; Patent No. 6645721
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-13
; CURRENT APPLICATION NUMBER: US/09/957,313A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-957-313A-55
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Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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```
Db       1 AAAAAAAAAAAAAAAAAAAAAA 20
        |||||
RESULT 76
US-09-966-312-55
; Sequence 55, Application US/09966312
; Patent No. 6673548
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i5
; CURRENT APPLICATION NUMBER: US/09/966,312
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-966-312-55
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Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
        |||||
Db       1 AAAAAAAAAAAAAAAAAAAAAA 20
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RESULT 77
US-09-975-062A-55
; Sequence 55, Application US/09975062A
; Patent No. 6677122
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-111
; CURRENT APPLICATION NUMBER: US/09/975,062A
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
```

; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-09-975-062A-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 78

US-09-976-971A-55
; Sequence 55, Application US/09976971A
; Patent No. 6682895
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR

; FILE REFERENCE: 00-713-118
; CURRENT APPLICATION NUMBER: US/09/976,971A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-09-976-971A-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 79

PCT-US93-07603-6
; Sequence 6, Application PC/TUS9307603
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NUCLEIC ACID RECOGNITION AND TRANSPORT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07603
; FILING DATE: 19930813
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,087
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0636/7007WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Synthetic RNA oligonucleotide.
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-07603-6

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 80

US-08-146-504-2
; Sequence 2, Application US/08146504
; Patent No. 5605662
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; MICROELECTRONIC SYSTEMS AND DEVICES FOR
; MOLECULAR BIOLOGICAL ANALYSIS AND
; DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA

RESULT 83
US-08-725-976-2
; Sequence 2, Application US/08725976
; Patent No. 5929208
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM compatible
; SOFTWARE: WordPerfect (Version 6.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,976
; FILING DATE: October 4, 1996
; CLASSIFICATION: 422
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/146,504
; FILING DATE: No. 5929208ember 1, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, David B.
; REGISTRATION NUMBER: 31,125
; REFERENCE/DOCKET NUMBER: 222/211
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-725-976-2
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 84
US-08-725-976-2
; Sequence 13, Application US/09082343
; Patent No. 5968754
; GENERAL INFORMATION:
; APPLICANT: WATSON, MARK A.
; APPLICANT: FLEMING, TIMOTHY P.
; TITLE OF INVENTION: DNA SEQUENCE AND ENCODED
; TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAERKAMP
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105-1817
; COMPUTER READABLE FORM: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,343
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/455,896
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 952726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-082-343-13
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2
RESULT 85
US-08-863-639A-10
; Sequence 10, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-10

Query Match          1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 86
US-08-863-639A-13/c
; Sequence 13, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863.639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-13

Query Match          1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 87
US-08-416-214A-12/c
; Sequence 12, Application US/08416214A
; Patent No. 5998596
; GENERAL INFORMATION:

```

```

; APPLICANT: Bergan, Raymond; Neckers, Len
; TITLE OF INVENTION: Inhibition Of Protein
; TITLE OF INVENTION: Kinase Activity By Aptameric Action Of
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,214A
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Kathryn M.
; REGISTRATION NUMBER: 34,556
; REFERENCE/DOCKET NUMBER: 2026-4166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: Yes
; ANTI-SENSE: No
US-08-416-214A-12

Query Match          1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 88
US-09-082-253-13/c
; Sequence 13, Application US/09082253
; Patent No. 6004756
; GENERAL INFORMATION:
; APPLICANT: WATSON, MARK A.
; APPLICANT: FLEMING, TIMOTHY P.
; TITLE OF INVENTION: DNA SEQUENCE AND ENCODED
; TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAERKAMP
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,253
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/455,896
; APPLICATION NUMBER: 08/455,896
; FILING DATE: 05/31/1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 952726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-082-253-13

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 89
US-08-271-882B-2
; Sequence 2, Application US/08271882B
; Patent No. 6017696
; GENERAL INFORMATION:
; APPLICANT: Michael J. Heller
; APPLICANT: Eugene Tu
; APPLICANT: Glen A. Evans
; APPLICANT: Ronald G. Sosnowski
; TITLE OF INVENTION: SELF-ADDRESSABLE
; TITLE OF INVENTION: SELF-ASSEMBLING
; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND
; TITLE OF INVENTION: DEVICES FOR
; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS
; TITLE OF INVENTION: AND DIAGNOSTICS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,882B
; FILING DATE: July 7, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,504
; FILING DATE: No. 6017696member 1, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, David B.
; REGISTRATION NUMBER: 31,125
; REFERENCE/DOCKET NUMBER: 207/263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
```

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; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-271-882B-2

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 90
US-08-726-278-2
; Sequence 2, Application US/08726278
; Patent No. 6238624
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Evans, Glen A.
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC TRANSPORT IN MOLECULAR
; TITLE OF INVENTION: BIOLOGICAL ANALYSIS AND DIAGNOSTICS
; FILE REFERENCE: DAVID B. MURPHY/NANOGEN: 222-210
; CURRENT APPLICATION NUMBER: US/08/726,278
; CURRENT FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: 08/271,882
; PRIOR FILING DATE: 1994-07-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequences for
; OTHER INFORMATION: Labeling
; US-08-726-278-2

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 91
US-09-162-622-13/c
; Sequence 13, Application US/09162622
; Patent No. 6566072
; GENERAL INFORMATION:
; APPLICANT: WATSON, MARK A
; APPLICANT: FLEMING, TIMOTHY P
; TITLE OF INVENTION: Mammaglobin, A Secreted Mammary-Specific Breast Cancer
; TITLE OF INVENTION: Protein
; FILE REFERENCE: 6029-5134
; CURRENT APPLICATION NUMBER: US/09/162,622
; CURRENT FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 08/933,149
; EARLIER FILING DATE: 1997-09-18
; EARLIER APPLICATION NUMBER: PCT/US96/08235
; EARLIER FILING DATE: 1996-05-31
; EARLIER APPLICATION NUMBER: 08/455,896
; EARLIER FILING DATE: 1995-05-31
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: WORDPERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/031.147A
/ FILING DATE: March 12, 1993
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 485,297
/ FILING DATE: February 26, 1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 852,132
/ FILING DATE: April 28, 1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 954,185
/ FILING DATE: September 29, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jane Massey Licata
/ REGISTRATION NUMBER: 32,257
/ REFERENCE/DOCKET NUMBER: ISIS-0469
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 52:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ ANTI-SENSE: yes
/
/ US-08-031-147A-52

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Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred.No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGGTTGTGG 1042
|||
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24
|||

RESULT 95
US-08-403-888A-35
; Sequence 35, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard

```

; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-403-888A:35

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Query Match	1.1%;	Score 19.2;	DB 1;	Length 24;
Best Local Similarity	87.5%;	Pred. No. 1.2e+02;		
Matches 21;	Conservative	0;	Mismatches 3;	Indels 0;
	Gaps	0;		

Qy 1019 TTGGGATGGGCTGGGTTGTGG 1042
|||
pb 1 TTGGGGTTGGGGTTGGGGTTGGGG 24

RESULT 96
US-08-403-888A-43
; Sequence 43, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor

Query Match	1.1%	Score 19.2;	DB 1;	Length 24;
Best Local Similarity	87.5%	Pred. NO. 1.2e+02;		
Matches vs. 21: Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 1019 TTGGGATGGGGCTGGGTGTGG 1042
|||||
pB 1 TTGGGTTGGGGTGGGGTGGGG 24
|||||

RESULT 97
US-08-403-888A-109
; Sequence 109, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-888A-109
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGATGGGGTGGGTGGG 1042
Db 1 TTGGGTTGGGGTTGGGTGGGG 24
RESULT 98
US-08-403-888A-116
; Sequence 116, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,888A
FILING DATE: 12-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/954,185
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1229
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-403-888A-116
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGATGGGGTGGGTGGG 1042
Db 1 TTGGGTTGGGGTTGGGTGGGG 24
RESULT 99
US-08-729-598-3
; Sequence 3, Application US/08729598
; Patent No. 6001657
; GENERAL INFORMATION:
; APPLICANT: Hardin, Charles C.
; APPLICANT: Brown II, Bernard A.
; APPLICANT: Roberts, John J.
; APPLICANT: Pelsue, Stephen A.
; TITLE OF INVENTION: Antibodies That Selectively Bind
; TITLE OF INVENTION: Quadruplex Nucleic Acids
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sorojini J. Biswas
; STREET: P.O. Box 37428
; CITY: Raleigh
; STATE: No. 6001657th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,598
; FILING DATE: 11-OCT-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Biswas, Sorojini J.
; REGISTRATION NUMBER: 39,111
; REFERENCE/DOCKET NUMBER: 5051-301A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 854-1400
; TELEFAX: (919) 854-1401
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant


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; MOLECULE TYPE: DNA (genomic)
US-08-729-598-3

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGATGGGCTGGGTTGTGG 1042
Db 1 TTGGGTTGGGTTGGGTTGGG 24

RESULT 100
US-08-819-867-29/c
; Sequence 29, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,867
; FILING DATE: March 14, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989ember 12, 1993
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-819-867-29

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGATGGGCTGGGTTGTGG 1042
Db 1 TTGGGTTGGGTTGGGTTGGG 24

RESULT 101
US-08-819-867-32
; Sequence 32, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,867
; FILING DATE: March 14, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989ember 12, 1993
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-819-867-32

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGATGGGCTGGGTTGTGG 1042
Db 1 TTGGGTTGGGTTGGGTTGGG 24
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Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGATGGGCTGGGTTGTGG 1042
Db 24 TTGGGTTGGGTTGGGTTGGG 1

RESULT 101
US-08-819-867-32
; Sequence 32, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,867
; FILING DATE: March 14, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989ember 12, 1993
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-819-867-32

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGATGGGCTGGGTTGTGG 1042
Db 1 TTGGGTTGGGTTGGGTTGGG 24
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RESULT 102
US-08-819-867-34
; Sequence 34, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TEOLOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,867
; FILING DATE: March 14, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989ember 12, 1993
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-819-867-34
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGGGCTGGGTTGTGG 1042
Db 1 TTGGGGTTGGGGTTGGGGTTGGG 24
RESULT 103
US-09-378-535-29/c
; Sequence 29, Application US/09378535

; Patent No. 6551774
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TEOLOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,535
; FILING DATE: 20-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/819,867
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-378-535-29
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGGGCTGGGTTGTGG 1042
Db 24 TTGGGGTTGGGGTTGGGGTTGGG 1
RESULT 104
US-09-378-535-32
; Sequence 32, Application US/09378535
; Patent No. 6551774
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl

Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-378-535-32
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24
RESULT 105
US-09-378-535-34
Sequence 34, Application US/09378535
Patent No. 6551774
GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-378-535-34
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24
RESULT 106
PCT-US94-02471-52
Sequence 52, Application PC/TUS9402471
GENERAL INFORMATION:
APPLICANT: Draper et al.
TITLE OF INVENTION: Oligonucleotide Therapies for
Modulating the Effects of Herpesviruses
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02471
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 485,297
; FILING DATE: February 26, 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,132
; FILING DATE: April 28, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 954,185
; FILING DATE: September 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISIS-0469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; PCT-US94-02471-52

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGTTGTGG 1042
Db 1 TTGGGGTTGGGTTGGGTTGGG 24

RESULT 107
US-08-403-888A-33
; Sequence 33, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-403-888A-34

Query Match 1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGTTGTGG 1042
Db 1 TTGGGGTTGGGTTGGGTTGGG 24

RESULT 109
US-08-403-888A-33
; Sequence 33, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
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;
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-403-888A-33

Query Match 1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGTTGTGG 1042
Db 1 TTGGGGTTGGGTTGGGTTGGG 24

RESULT 108
US-08-403-888A-34
; Sequence 34, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-403-888A-34

Query Match 1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGTTGTGG 1042
Db 1 TTGGGGTTGGGTTGGGTTGGG 24

RESULT 109
US-08-756-728A-1/c
; Sequence 1, Application US/08756728A
; Patent No. 5821354
```

GENERAL INFORMATION:
APPLICANT: Leclerc, Guy
APPLICANT: Martel, Remi
TITLE OF INVENTION: RADIOLABELED DNA OLIGONUCLEOTIDE, METHOD
TITLE OF INVENTION: OF PREPARATION AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,728A
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1398-1-001
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PRIMER"
HYPOTHETICAL: NO
US-08-756-728A-1

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 110
US-08-469-852A-2/c
Sequence 2, Application US/08469852A
Patent No. 5874213
GENERAL INFORMATION:
APPLICANT: Cummins, Lendell L.
APPLICANT: Freier, Susan M.
APPLICANT: Griffey, Richard
APPLICANT: Srivatsa, Susan G.
TITLE OF INVENTION: Capillary Electrophoretic Detection of
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5874213ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,852A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,509
FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2015
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-852A-2

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 111
US-08-271-882B-16/c
Sequence 16, Application US/08271882B
Patent No. 6017696
GENERAL INFORMATION:
APPLICANT: Michael J. Heller
APPLICANT: Eugene Tu
APPLICANT: Glen A. Evans
APPLICANT: Ronald G. Sosnowski
TITLE OF INVENTION: SELF-ADDRESSABLE
TITLE OF INVENTION: SELF-ASSEMBLING
TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND
TITLE OF INVENTION: DEVICES FOR
TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS
TITLE OF INVENTION: AND DIAGNOSTICS
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,882B
FILING DATE: July 7, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146,504
FILING DATE: No. 6017696ember 1, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, David B.
REGISTRATION NUMBER: 31,125
REFERENCE/DOCKET NUMBER: 207/263
TELECOMMUNICATION INFORMATION:

```
;
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic
; TYPE: acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-271-882B-16

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
| | | | | | | | | | | | | | | | |
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 112
US-08-295-509B-2/c
; Sequence 2, Application US/08295509B
; Patent No. 6045995
; GENERAL INFORMATION:
; APPLICANT: Cummins, Lendell L.
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard
; APPLICANT: Srivatsa, Susan G.
; TITLE OF INVENTION: Capillary Electrophoretic Detection of
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6045995ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,509B
; FILING DATE: 24-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-1395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-295-509B-2

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
| | | | | | | | | | | | | | | | |
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

;
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic
; TYPE: acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-271-882B-16

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
| | | | | | | | | | | | | | | | |
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 113
US-09-234-237-1/c
; Sequence 1, Application US/09234237
; Patent No. 6127124
; GENERAL INFORMATION:
; APPLICANT: Leeds, Janet M
; APPLICANT: Cummins, Lendell L
; TITLE OF INVENTION: Fluorescence Based Nuclease Assay
; FILE REFERENCE: ISIS3308
; CURRENT APPLICATION NUMBER: US/09/234,237
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6127124el
; OTHER INFORMATION: Sequence
; US-09-234-237-1

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
| | | | | | | | | | | | | | | | |
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 114
US-09-016-520-20/c
; Sequence 20, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-aminoxyethoxy
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; US-09-016-520-20

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
| | | | | | | | | | | | | | | | |
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 115
US-09-016-520-21/c
; Sequence 21, Application US/09016520A
; Patent No. 6127533
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; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminooxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-016-520-21

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 116

US-09-016-520-22/c
; Sequence 22, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminooxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-methoxyethoxy
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-016-520-22

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 117

US-09-016-520-23/c
; Sequence 23, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminooxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-016-520-23

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 118

US-09-016-520-24/c
; Sequence 24, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminooxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-016-520-24

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 123
US-09-016-520-33/c
; Sequence 33, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-33

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 124
US-09-016-520-34/c
; Sequence 34, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy

US-09-016-520-34

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 125
US-09-016-520-44/c
; Sequence 44, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-methyleneiminoxyethoxy
US-09-016-520-44

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 126
US-09-378-568-4/c
; Sequence 4, Application US/09378568
; Patent No. 6147200
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Fraser, Allister S
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: 2'-O-acetamido Modified Monomers and Oligomers
; FILE REFERENCE: ISIS4071
; CURRENT APPLICATION NUMBER: US/09/378,568
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-378-568-4

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 127

US-09-130-973-20/c
; Sequence 20, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5 methyl, 2'-aminoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
US-09-130-973-20

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 128

US-09-130-973-21/c
; Sequence 21, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5 methyl, 2'-dimethylaminoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
US-09-130-973-21

US-09-130-973-21

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 129

US-09-130-973-22/c
; Sequence 22, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-O-methoxyethyl (MOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
US-09-130-973-22

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 130

US-09-130-973-23/c
; Sequence 23, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-O-dimethylaminoxyethyl
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
US-09-130-973-23

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; OTHER INFORMATION: Sequence
US-09-130-973-23

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 131
US-09-130-973-24/c
; Sequence 24, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-O-methoxyethyl
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-24

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 132
US-09-130-973-25/c
; Sequence 25, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-O-propyl
; OTHER INFORMATION: Sequence
US-09-130-973-25

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 133
US-09-130-973-26/c
; Sequence 26, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)
; OTHER INFORMATION: 5 methyl, 2'-dimethylaminoxyethyl
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-26

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 134
US-09-130-973-27/c
; Sequence 27, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)
; OTHER INFORMATION: Sequence
US-09-130-973-27
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; OTHER INFORMATION: 5 methyl, 2'-O-methoxyethyl
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-27

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 135

US-09-130-973-31/c
; Sequence 31, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-31

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 136

US-09-130-973-33/c
; Sequence 33, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-33

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 137

US-09-130-973-34/c
; Sequence 34, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209el
; OTHER INFORMATION: Sequence
US-09-130-973-34

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 138

US-09-130-973-44/c
; Sequence 44, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
 |||||
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
 |||||

RESULT 142
 US-09-477-902-23/c
 ; Sequence 23, Application US/09477902
 ; Patent No. 6194598
 ; GENERAL INFORMATION:
 ; APPLICANT: Cook, Phillip D
 ; APPLICANT: Manoharan, Muthiah
 ; APPLICANT: Kawasaki, Andrew
 ; TITLE OF INVENTION: Aminooxy-Modified Oligonucleotides
 ; FILE REFERENCE: ISIS2824
 ; CURRENT APPLICATION NUMBER: US/09/477,902
 ; CURRENT FILING DATE: 2000-01-05
 ; PRIOR APPLICATION NUMBER: 09/016,520

```
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-477-902-23

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 143
US-09-477-902-24/c
; Sequence 24, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-477-902-24

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 144
US-09-477-902-25/c
; Sequence 25, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
```

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; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-O-propyl
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-477-902-25

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 145
US-09-477-902-26/c
; Sequence 26, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-477-902-26

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 146
US-09-477-902-27/c
; Sequence 27, Application US/09477902
```

Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-477-902-27

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 147
US-09-477-902-31/c
; Sequence 31, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: misc_feature
; LOCATION: (15)..
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-477-902-31

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 148
US-09-477-902-33/c
; Sequence 33, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: misc_feature
; LOCATION: (16)..
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-477-902-33

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 149
US-09-477-902-34/c
; Sequence 34, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: misc_feature
; LOCATION: (16)..
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-477-902-34

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;

Matches	19;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy 1736 AAAAAAAAAAAAAAAAAA 1754
19 AAAAAAAAAAAAAAAAAA 1

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 150

```

US-09-477-902-44/c
; Sequence 44, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Mancharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Sequence
; NAME/KEY: misc.feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-methyleiminoxyethoxy
US-09-477-902-44

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels

	1736	1754
Qy	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA
Dp	19 AAAAAAAAAAAAAAAAAA	1 AAAAAAAAAAAAAAAAAA

D^b 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 151

```

US-08-726-278-16/c
; Sequence 16, Application US/08726278
; Patent No. 6238624
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Evans, Glen A.
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC TRANSPORT IN MOLECULAR
; TITLE OF INVENTION: BIOLOGICAL ANALYSIS AND DIAGNOSTICS
; FILE REFERENCE: DAVID B. MURPHY/NANOGEN: 222-210
; CURRENT APPLICATION NUMBER: US/08/726,278
; CURRENT FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: 08/271,882
; PRIOR FILING DATE: 1994-07-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequences for
; OTHER INFORMATION: Labeling
US-08-726-278-16

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 152

```

US-09-338-907-515/c
; Sequence 515, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 515
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..19
; OTHER INFORMATION: potential microsequen
US-09-338-907-515

```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels
```

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 153

```

US-09-123-108-6/c
; Sequence 6, Application US/09123108
; Patent No. 6271358
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venkatraman
; APPLICANT: Boswell, Herb
; TITLE OF INVENTION: RNA TARGETED 2'-MODIFIED OLIGONUCLEOTIDES THAT ARE
; TITLE OF INVENTION: CONFORMATIONALLY PREORGANIZED
; FILE REFERENCE: ISIS-3147 sequence listing
; CURRENT APPLICATION NUMBER: US/09/123,108
; CURRENT FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6271358el
US-09-123-108-6

```

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 154
US-09-378-665A-5/c
; Sequence 5, Application US/09378665A
; Patent No. 6277982
; GENERAL INFORMATION:
; APPLICANT: Fraser, Allister S.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Jung, Michael E.
; APPLICANT: Kawasaki, Andrew M.
; TITLE OF INVENTION: Alkylation of Alcohols, Amines, Thiols and Their
; TITLE OF INVENTION: Derivatives by Cyclic Sulfate Intermediates
; FILE REFERENCE: ISIS4072
; CURRENT APPLICATION NUMBER: US/09/378,665A
; CURRENT FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-modified T
US-09-378-665A-5

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 155
US-09-202-294-4/c
; Sequence 4, Application US/09202294
; Patent No. 6329519
; GENERAL INFORMATION:
; APPLICANT: Collingwood, Stephen P.
; APPLICANT: Moser, Heinz E.
; APPLICANT: Altmann, Karl-Heinz
; APPLICANT: Douglas, Mark E.
; TITLE OF INVENTION: Intermediates for oligonucleotides
; FILE REFERENCE: 4-20900/A/MA2134/PCT
; CURRENT APPLICATION NUMBER: US/09/202,294
; CURRENT FILING DATE: 1999-03-15
; EARLIER APPLICATION NUMBER: PCT/GB97/01490
; EARLIER FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-202-294-4

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 156
US-09-218-207-515/c
; Sequence 515, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 515
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..19
; OTHER INFORMATION: potential microsequencing oligo for 4-4-187.mis2
US-09-218-207-515

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 157
US-09-303-586-15/c
; Sequence 15, Application US/09303586
; Patent No. 6369209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Oligonucleotides Having A DNA Form And B-DNA Form Confirmation C
; FILE REFERENCE: ISIS3310
; CURRENT APPLICATION NUMBER: US/09/303,586
; CURRENT FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (16)..(17)
; OTHER INFORMATION: 3' - O-MOE linkage
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 3' - O-MOE linkage
; NAME/KEY: misc_feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 3' - O-MOE linkage
US-09-303-586-15/c

US-09-303-586-15

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 158

US-09-303-586-16/c
; Sequence 16, Application US/09303586
; Patent No. 6369209

```

;
; GENERAL INFORMATION:
;
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Oligonucleotides Having A DNA Form And B-DNA Form Confirmational
; FILE REFERENCE: ISIS3310
; CURRENT APPLICATION NUMBER: US/09/303,586
; CURRENT FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
;

```

```

; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (16)..(17)
; OTHER INFORMATION: 2' - O-MOE linkage
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2' - O-MOE linkage
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2' - O-MOE linkage

```

```
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAAAAAAA 1754
D6 19 AAAAAAAAAAAAAAAAAA 1

RESULT 159

US-09-303-586-17/c
; Sequence 17, Application US/09303586
; Patent No. 6369209

```

; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Oligonucleotides Having A DNA Form And B-DNA Form Confirmational
; FILE REFERENCE: ISIS3310
; CURRENT APPLICATION NUMBER: US/09/303,586
; CURRENT FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 17
;
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (15)..(16)

```


RESULT 165
US-09-227-782-4/c
; Sequence 4, Application US/09227782
; Patent No. 6403779
; GENERAL INFORMATION:
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Fraser, Allister S
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip D
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS3315
; CURRENT APPLICATION NUMBER: US/09/227,782
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5- methyl- 2'- dimethylaminooxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403779el Sequence
US-09-227-782-4

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 166
US-09-227-782-5/c
; Sequence 5, Application US/09227782
; Patent No. 6403779
; GENERAL INFORMATION:
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Fraser, Allister S
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip D
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS3315
; CURRENT APPLICATION NUMBER: US/09/227,782
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5- methyl- 2'-methoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403779el Sequence
US-09-227-782-5

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 167
US-09-227-782-6/c
; Sequence 6, Application US/09227782
; Patent No. 6403779
; GENERAL INFORMATION:
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Fraser, Allister S
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip D
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS3315
; CURRENT APPLICATION NUMBER: US/09/227,782
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5- methyl- 2'-O-propyl
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403779el Sequence
US-09-227-782-6

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 168
US-09-227-782-7/c
; Sequence 7, Application US/09227782
; Patent No. 6403779
; GENERAL INFORMATION:
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Fraser, Allister S
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip D
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS3315
; CURRENT APPLICATION NUMBER: US/09/227,782
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)
; OTHER INFORMATION: 5- methyl- 2'- dimethylaminooxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403779el Sequence
US-09-227-782-7

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 169

US-09-227-782-8/c
; Sequence 8, Application US/09227782
; Patent No. 6403779
; GENERAL INFORMATION:
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Fraser, Allister S
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip D
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS3315
; CURRENT APPLICATION NUMBER: US/09/227,782
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403779el Sequence
US-09-227-782-8

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 170

US-09-227-782-12/c
; Sequence 12, Application US/09227782
; Patent No. 6403779
; GENERAL INFORMATION:
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Fraser, Allister S
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip D
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS3315
; CURRENT APPLICATION NUMBER: US/09/227,782
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403779el Sequence
US-09-227-782-12

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 171

US-09-227-782-12/c

RESULT 173

US-09-227-782-25/c

RESULT 172

US-09-227-782-14/c
; Sequence 14, Application US/09227782
; Patent No. 6403779
; GENERAL INFORMATION:
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Fraser, Allister S
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip D
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS3315
; CURRENT APPLICATION NUMBER: US/09/227,782
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403779el Sequence
US-09-227-782-14

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 173

US-09-227-782-15/c
; Sequence 15, Application US/09227782
; Patent No. 6403779
; GENERAL INFORMATION:
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Fraser, Allister S
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip D
; APPLICANT: Prakash, Thazha P
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS3315
; CURRENT APPLICATION NUMBER: US/09/227,782
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403779el Sequence
US-09-227-782-15

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

; Sequence 25, Application US/09227782
; Patent No. 6403779
; GENERAL INFORMATION:

; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Fraser, Allister S
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip D
; APPLICANT: Prakash, Thazha P

; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides

; FILE REFERENCE: ISIS3315

; CURRENT APPLICATION NUMBER: US/09/227,782

; CURRENT FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (15)..(18)

; OTHER INFORMATION: 2'-methyleneiminoxyethoxy

; Description of Artificial Sequence: No. 6403779el Sequence

US-09-227-782-25

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 174

US-09-619-103-25

; Sequence 25, Application US/09619103

; Patent No. 6429300

; GENERAL INFORMATION:

; APPLICANT: Kurz, Markus

; APPLICANT: Lohse, Peter

; APPLICANT: Wagner, Richard

; TITLE OF INVENTION: Peptide Acceptor Ligation Methods

; FILE REFERENCE: 50036/031002

; CURRENT APPLICATION NUMBER: US/09/619,103

; CURRENT FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 60/145,834

; PRIOR FILING DATE: 1999-07-27

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: designed sequence for nucleic acid purification

US-09-619-103-25

Query Match

Best Local Similarity 1.1%; Score 19; DB 1; Length 19;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 175

US-09-288-679-1/c

; Sequence 1, Application US/09288679

; Patent No. 6465628

; GENERAL INFORMATION:

; APPLICANT: Ravikumar, Vasulinga

; APPLICANT: Manoharan, Muthia

; APPLICANT: Capaldi, Daniel

; APPLICANT: Krotz, Achim

; APPLICANT: Cole, Douglas

; APPLICANT: Guzaev, Andrei

; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric Compounds

; FILE REFERENCE: ISIS3380

; CURRENT APPLICATION NUMBER: US/09/288,679

; CURRENT FILING DATE: 1999-04-09

; PRIOR APPLICATION NUMBER: 60/118,564

; PRIOR FILING DATE: 1999-02-04

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: No. 6465628el Sequence

US-09-288-679-1

Query Match

Best Local Similarity 1.1%; Score 19; DB 1; Length 19;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 176

US-09-612-531-3/c

; Sequence 3, Application US/09612531

; Patent No. 6534639

; GENERAL INFORMATION:

; APPLICANT: Manoharan, Muthiah

; APPLICANT: Cook, Philip Dan

; APPLICANT: Prakash, Thazha P.

; APPLICANT: Mohan, Venkatraman

; TITLE OF INVENTION: Guanidinium Functionalized Oligomers And Methods

; FILE REFERENCE: Isis-4406

; CURRENT APPLICATION NUMBER: US/09/612,531

; CURRENT FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: 09/349,040

; PRIOR FILING DATE: 1999-07-07

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide

; NAME/KEY: misc_feature

; LOCATION: (16)..(19)

; OTHER INFORMATION: T*=2'-O-[2-(guanidinium)ethyl]

US-09-612-531-3

Query Match

Best Local Similarity 1.1%; Score 19; DB 1; Length 19;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 177

US-09-612-531-7/c

; Sequence 7, Application US/09612531

; Patent No. 6534639

; GENERAL INFORMATION:

; APPLICANT: Manoharan, Muthiah

; APPLICANT: Cook, Philip Dan
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Guanidinium Functionalized Oligomers And Methods
; FILE REFERENCE: Isis-4406
; CURRENT APPLICATION NUMBER: US/09/612,531
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/349,040
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: T*=2'-O-[2-(guanidinium)ethyl]
US-09-612-531-7

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 178

US-09-612-531-13/c
; Sequence 13, Application US/09612531
; Patent No. 6534639
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Philip Dan
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Guanidinium Functionalized Oligomers And Methods
; FILE REFERENCE: Isis-4406
; CURRENT APPLICATION NUMBER: US/09/612,531
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/349,040
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: T*=2'-O-[2-(guanidinium)ethyl]
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: T*=2'-O-[2-(guanidinium)ethyl]
US-09-612-531-13

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 179

US-10-121-135-5/c

; Sequence 5, Application US/10121135
; Patent No. 6552178
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; TITLE OF INVENTION: 2'-O-Aminoethyloxethyl-Modified Oligonucleotides
; FILE REFERENCE: ISIS-5036
; CURRENT APPLICATION NUMBER: US/10/121,135
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/370,625
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 09/130,566
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-modified T
US-10-121-135-5

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 180

US-10-121-135-5/c
; Sequence 5, Application US/10121135
; Patent No. 6673912
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; TITLE OF INVENTION: 2'-O-Aminoethyloxethyl-Modified Oligonucleotides
; FILE REFERENCE: ISIS-5036
; CURRENT APPLICATION NUMBER: US/10/121,135
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/370,625
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 09/130,566
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-modified T
US-10-121-135-5

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 181
US-10-121-135-26/c
; Sequence 26, Application US/10121135
; Patent No. 6552178
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; TITLE OF INVENTION: 2'-O-Aminoethyloxyethyl-Modified Oligonucleotides
; FILE REFERENCE: ISIS-5036
; CURRENT APPLICATION NUMBER: US/10/121,135
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/370,625
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 09/130,566
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: (16)..(19)
; OTHER INFORMATION: -sub-T)
US-10-121-135-26

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 182
US-09-142-212A-10/c
; Sequence 10, Application US/09142212A
; Patent No. 6562960
; GENERAL INFORMATION:
; APPLICANT: Baxter, Anthony David
; APPLICANT: Collingwood, Stephen Paul
; APPLICANT: Douglas, Mark Edward
; APPLICANT: Taylor, Roger John
; TITLE OF INVENTION: Oligonucleotide Analogues
; FILE REFERENCE: ISIS4385
; CURRENT APPLICATION NUMBER: US/09/142,212A
; CURRENT FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: 97/00499
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (16)..(18)
; OTHER INFORMATION: Modified internucleoside linkage
US-09-142-212A-10

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 183
US-09-349-040A-3/c
; Sequence 3, Application US/09349040A
; Patent No. 6593466
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Functionalized Oligomers
; FILE REFERENCE: ISIS-3811
; CURRENT APPLICATION NUMBER: US/09/349,040A
; CURRENT FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6593466el Sequence
US-09-349-040A-3

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 184
US-09-349-040A-4/c
; Sequence 4, Application US/09349040A
; Patent No. 6593466
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Functionalized Oligomers
; FILE REFERENCE: ISIS-3811
; CURRENT APPLICATION NUMBER: US/09/349,040A
; CURRENT FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6593466el Sequence
US-09-349-040A-4

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 185
US-09-349-040A-5/c

; Sequence 5, Application US/09349040A
; Patent No. 6593466
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Functionalized Oligomers
; FILE REFERENCE: ISIS-3811
; CURRENT APPLICATION NUMBER: US/09/349,040A
; CURRENT FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6593466el Sequence
US-09-349-040A-5

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 186

US-09-409-926-17/c
; Sequence 17, Application US/09409926
; Patent No. 6617442
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Lima, Walter F.
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Human Rnase H1 and Oligonucleotide Compositions Thereof
; FILE REFERENCE: ISIS4186
; CURRENT APPLICATION NUMBER: US/09/409,926
; CURRENT FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6617442el Sequence
US-09-409-926-17

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 187

US-09-409-926-18/c
; Sequence 18, Application US/09409926
; Patent No. 6617442
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Lima, Walter F.
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Human Rnase H1 and Oligonucleotide Compositions Thereof
; FILE REFERENCE: ISIS4186
; CURRENT APPLICATION NUMBER: US/09/409,926

; CURRENT FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: No. 6617442el Sequence
US-09-409-926-18

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 188

US-10-123-597-1/c
; Sequence 1, Application US/10123597
; Patent No. 6624294
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-aminoxyethoxy
US-10-123-597-1

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 189

US-10-123-597-2/c
; Sequence 2, Application US/10123597
; Patent No. 6624294
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597

```
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-10-123-597-2
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 190
US-10-123-597-3/c
; Sequence 3, Application US/10123597
; Patent No. 6624294
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-methoxyethoxy
US-10-123-597-3
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 191
US-10-123-597-4/c
; Sequence 4, Application US/10123597
; Patent No. 6624294
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
```

```
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-10-123-597-4
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 192
US-10-123-597-5/c
; Sequence 5, Application US/10123597
; Patent No. 6624294
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
US-10-123-597-5
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 193
US-10-123-597-6/c
; Sequence 6, Application US/10123597
; Patent No. 6624294
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
```

```
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc:feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-O-propyl
US-10-123-597-6

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 194
US-10-123-597-7/c
; Sequence 7, Application US/10123597
; Patent No. 6624294
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc:feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
US-10-123-597-7

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 195
US-10-123-597-8/c
; Sequence 8, Application US/10123597
; Patent No. 6624294
```

```
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc:feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
US-10-123-597-8

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 196
US-10-123-597-12/c
; Sequence 12, Application US/10123597
; Patent No. 6624294
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc:feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
US-10-123-597-12

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 197
```

US-10-123-597-14/c
; Sequence 14, Application US/10123597
; Patent No. 6624294
; GENERAL INFORMATION:

; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040

; CURRENT APPLICATION NUMBER: US/10/123,597

; CURRENT FILING DATE: 2002-07-10

; PRIOR APPLICATION NUMBER: 09/227,782

; PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct

; NAME/KEY: misc feature

; LOCATION: (16)..(19)

; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy

US-10-123-597-14

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 198

US-10-123-597-15/c

; Sequence 15, Application US/10123597

; Patent No. 6624294

; GENERAL INFORMATION:

; APPLICANT: Cook, Phillip D

; APPLICANT: Kawasaki, Andrew M

; APPLICANT: Manoharan, Muthiah

; APPLICANT: Prakash, Thazha P

; APPLICANT: Fraser, Allister S

; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides

; FILE REFERENCE: ISIS5040

; CURRENT APPLICATION NUMBER: US/10/123,597

; CURRENT FILING DATE: 2002-07-10

; PRIOR APPLICATION NUMBER: 09/227,782

; PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 15

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct

; NAME/KEY: misc feature

; LOCATION: (16)..(19)

; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy

US-10-123-597-15

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 199

US-10-123-597-25/c

; Sequence 25, Application US/10123597

; Patent No. 6624294

; GENERAL INFORMATION:

; APPLICANT: Cook, Phillip D

; APPLICANT: Kawasaki, Andrew M

; APPLICANT: Manoharan, Muthiah

; APPLICANT: Prakash, Thazha P

; APPLICANT: Fraser, Allister S

; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides

; FILE REFERENCE: ISIS5040

; CURRENT APPLICATION NUMBER: US/10/123,597

; CURRENT FILING DATE: 2002-07-10

; PRIOR APPLICATION NUMBER: 09/227,782

; PRIOR FILING DATE: 1999-01-08

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct

; NAME/KEY: misc feature

; LOCATION: (15)..(18)

; OTHER INFORMATION: 2'-methyleneiminoxyethoxy

US-10-123-597-25

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 200

US-09-349-033A-1/c

; Sequence 1, Application US/09349033A

; Patent No. 6639061

; GENERAL INFORMATION:

; APPLICANT: Cook, Phillip Dan

; APPLICANT: Manoharan, Muthiah

; APPLICANT: Maier, Martin

; APPLICANT: An, Haoyun

; TITLE OF INVENTION: C3'-Methylene Hydrogen Phosphonate Oligomers and Related Compounds

; FILE REFERENCE: ISIS-3312

; CURRENT APPLICATION NUMBER: US/09/349,033A

; CURRENT FILING DATE: 1999-07-07

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide Sequence

US-09-349-033A-1

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 201

```
US-09-435-806-6/c
; Sequence 6, Application US/09435806
; Patent No. 6653458
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Guinosa, Charles J.
; TITLE OF INVENTION: MODIFIED OLIGONUCLEOTIDES
; FILE REFERENCE: ISIS-4289
; CURRENT APPLICATION NUMBER: US/09/435,806
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: US 09/115,043
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 08/602,862
; PRIOR FILING DATE: 1996-02-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-435-806-6
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
Db      19 AAAAAAAAAAAAAAAAAA 1

RESULT 202
US-08-482-918-32/c
; Sequence 32, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid

US-09-435-806-6/c
; Sequence 6, Application US/09435806
; Patent No. 6653458
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Guinosa, Charles J.
; TITLE OF INVENTION: MODIFIED OLIGONUCLEOTIDES
; FILE REFERENCE: ISIS-4289
; CURRENT APPLICATION NUMBER: US/09/435,806
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: US 09/115,043
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 08/602,862
; PRIOR FILING DATE: 1996-02-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-435-806-6
Query Match          1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAAAAAAAAAAAAAA 1753
Db      19 CAAAAAAAAAAAAAAAAA 1

RESULT 203
US-09-224-681-32/c
; Sequence 32, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX:
```

; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-224-681-32

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
|||||
Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 204

US-08-336-728A-32/c
; Sequence 32, Application US/08336728A
; Patent No. 6207802

; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989

; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-336-728A-32

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
|||||
Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 205

US-08-359-295C-23/c
; Sequence 23, Application US/08359295C
; Patent No. 5695934

; GENERAL INFORMATION:

; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: Massively Parallel Sequencing of Sorted Polynucleotides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/359,295C
; FILING DATE: 19-DEC-94
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/322,348
; FILING DATE: 13-OCT-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: mps1

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-359-295C-23

Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 206

US-08-485-105A-23/c
; Sequence 23, Application US/08485105A
; Patent No. 5863722

; GENERAL INFORMATION:

; APPLICANT: Sydney Brenner
; TITLE OF INVENTION: Massively Parallel Sequencing of Sorted Polynucleotides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,105A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/359,295
FILING DATE: 19-DEC-94
APPLICATION NUMBER: 08/322,348
FILING DATE: 13-OCT-94
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: mps1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-485-105A-23

Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 207
US-09-183-650-23/c
Sequence 23, Application US/09183650B
Patent No. 6140489
GENERAL INFORMATION:
APPLICANT: Brenner, Sydney
TITLE OF INVENTION: Improved compositions for sorting polynucleotides
FILE REFERENCE: 803-03
CURRENT APPLICATION NUMBER: US/09/183,650B
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: US 08/485,105
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: US 08/359,295
EARLIER FILING DATE: 1994-12-19
EARLIER APPLICATION NUMBER: US 08/322,348
EARLIER FILING DATE: 1994-10-13
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Word97
SEQ ID NO 23
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: No. 6140489special biological significance.
NAME/KEY: Primer.
LOCATION: N.a.
OTHER INFORMATION: Primer for synthesis of first strand of cDNA.
US-09-183-650-23

Query Match 1.1%; Score 19; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3
RESULT 208
PCT-US94-05407-7
Sequence 7, Application PC/TUS9405407
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05407
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/061,694
FILING DATE: 13-MAY-1993
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
PCT-US94-05407-7

Query Match 1.1%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
Db 5 CAAAAAAAAAAAAAAAAAAAAA 23

RESULT 209
PCT-US94-05407-8/c
Sequence 8, Application PC/TUS9405407
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05407
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/061,694

```
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 23 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-05407-8

Query Match      1.1%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAAAAAA 1753
Db 19 CAAAAAATAAAAAAAAAA 1

RESULT 210
US-09-721-154-6/c
; Sequence 6, Application US/09721154
; Patent No. 6651008
; GENERAL INFORMATION:
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Adams, Cynthia
; APPLICANT: Sabry, James
; APPLICANT: Crompton, Anne
; TITLE OF INVENTION: Database system including computer code
; TITLE OF INVENTION: for predictive cellular bioinformatics
; FILE REFERENCE: CytoP007C2
; CURRENT APPLICATION NUMBER: US/09/721,154
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/311,996
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Psuedo-sequence
US-09-721-154-6

Query Match      1.1%; Score 19; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAATAAAAAAAAAA 1752
Db 20 ACAAATAAAAAAAAAA 2

RESULT 211
US-09-721-154-2/c
; Sequence 2, Application US/09721154
; Patent No. 6651008
; GENERAL INFORMATION:
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Adams, Cynthia
; APPLICANT: Sabry, James
; APPLICANT: Crompton, Anne
; TITLE OF INVENTION: Database system including computer code
; TITLE OF INVENTION: for predictive cellular bioinformatics
; FILE REFERENCE: CytoP007C2
; CURRENT APPLICATION NUMBER: US/09/721,154
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/311,996
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
```

```
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Psuedo-sequence
US-09-721-154-2

Query Match      1.1%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACAAATAAAAAAAAAA 1755
Db 24 ACAAATAAAAAAAAAA 3

RESULT 212
US-08-482-918-33/c
; Sequence 33, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
US-08-482-918-33

Query Match      1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAAAAAA 1754
Db 20 CAAAAAATAAAAAAAAAA 1

RESULT 213
US-08-482-918-34/c
; Sequence 34, Application US/08482918
; Patent No. 6207417
```


; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-224-681-34

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA-33/c 1754
Db 20 CGAAAAA-33/c 1

RESULT 216
US-08-336-728A-33/c
; Sequence 33, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-336-728A-33

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA-33/c 1754
Db 20 CTAAAAA-33/c 1

RESULT 217
US-08-336-728A-34/c
; Sequence 34, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-336-728A-34

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1754
Db 20 CGAAAAAATAAAAAA 1

RESULT 218
US-09-588-950A-5/c
; Sequence 5, Application US/09588950A
; Patent No. 6399305
; GENERAL INFORMATION:
; APPLICANT: Makino, Yoshihiko
; APPLICANT: Abe, Yoshihiko
; APPLICANT: Ogawa, Masashi
; APPLICANT: Takagi, Makoto
; APPLICANT: Takenaka, Shigeori
; APPLICANT: Yamashita, Kenichi
; TITLE OF INVENTION: Protection of Partial Complementary Nucleic Acid Fragment Using a
; TITLE OF INVENTION: Electroconductive Chip and Intercalator
; FILE REFERENCE: JG-YY-4980/500569.20039
; CURRENT APPLICATION NUMBER: US/09/588,950A
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: Japan 11-159339
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
```

```
US-09-588-950A-5
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAATAAAAAA 1755
Db 20 AAAAAAATAAAAAA 1

RESULT 219
US-09-475-947A-119/c
; Sequence 119, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS00667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-119

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAATAAAAAA 1755
Db 21 AAAAAAATAAAAAA 2

RESULT 220
US-08-881-784-18/c
; Sequence 18, Application US/08881784
; Patent No. 6083731
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Lupien, Shari L.
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE PRODUCTION OF LIMONENE HYDROXYLASES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; ADDRESSEE: PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,784
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: WSUR19777
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (206) 224-0718
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..19
; OTHER INFORMATION: /product= "Primer 3.B (Table 1)"
US-08-881-784-18

Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 DAAAAAAAAAAAAAAAAAAAAA 1

RESULT 221
US-09-292-768-18/c
; Sequence 18, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Kaip, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; TITLE OF INVENTION: LIMONENE HYDROXYLASES
; FILE REFERENCE: wsur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer 3.B
; NAME/KEY: misc_feature
; LOCATION: (1)-(19)
; OTHER INFORMATION: Oligonucleotide primer that primes the polyA tail
; OTHER INFORMATION: on cDNA molecules
US-09-292-768-18

Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 DAAAAAAAAAAAAAAAAAAAAA 1

RESULT 222
US-08-621-914A-16/c
; Sequence 16, Application US/08621914A
; Patent No. 5707807
; GENERAL INFORMATION:
; APPLICANT: KATO, KIKUYA
; TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
; TITLE OF INVENTION: ANALYSIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,914A
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAWRENCE III, STANTON T.
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
US-08-621-914A-16

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 223
US-08-346-429-3
; Sequence 3, Application US/08346429
; Patent No. 5837820
; GENERAL INFORMATION:
; APPLICANT: DeRose, Richard
; APPLICANT: Douce, Roland
; APPLICANT: Duval, Manuel
; APPLICANT: Job, Claudette
; APPLICANT: Job, Dominique
; TITLE OF INVENTION: PROTEIN CAPABLE OF BEING BIOTINYLATED WHICH CAN
; TITLE OF INVENTION: BE USED FOR DETERMINING THE GERMINATION STAGE OF
; TITLE OF INVENTION: A SEED
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,429
; FILING DATE: 29-NOV-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
```



```

; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9507
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-346-429-3

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 224
US-08-358-556A-12/c
; Sequence 12, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..18
US-08-346-429-3
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; LOCATION: 1..18
US-08-358-556A-12
; Query Match 1.0%; Score 18; DB 1; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 225
US-08-358-556A-18
; Sequence 18, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..18
US-08-358-556A-18

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18
```

RESULT 226

US-08-469-852A-4/c
; Sequence 4, Application US/08469852A
; Patent No. 5874213
; GENERAL INFORMATION:
; APPLICANT: Cummins, Lendell L.
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard
; APPLICANT: Srivatsa, Susan G.
; TITLE OF INVENTION: Capillary Electrophoretic Detection of
; Nucleic Acids
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5874213ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,852A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,509
; FILING DATE: 24-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher

REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-469-852A-4

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 227

US-08-295-509B-4/c
; Sequence 4, Application US/082955509B
; Patent No. 6045995
; GENERAL INFORMATION:
; APPLICANT: Cummins, Lendell L.
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard
; APPLICANT: Srivatsa, Susan G.
; TITLE OF INVENTION: Capillary Electrophoretic Detection of
; Nucleic Acids
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6045995ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.

ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,509B
; FILING DATE: 24-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-1395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-295-509B-4

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 228

US-08-884-029-9/c
; Sequence 9, Application US/08884029
; Patent No. 6071745
; GENERAL INFORMATION:
; APPLICANT: Lin, Ching-I Patsy
; APPLICANT: Wallace, Robert Bruce
; APPLICANT: Cossman, Jeffrey
; APPLICANT: French, Cynthia
; TITLE OF INVENTION: Lyophilization of Cultured Human Cells
; TITLE OF INVENTION: to Preserve RNA and DNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

US-08-884-029-9/c

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,029
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 02558B-059100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 13..18
OTHER INFORMATION: /mod base= OTHER
OTHER INFORMATION: /note= "t at positions 13-18 may be present or absent"
US-08-884-029-9

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 229

US-08-941-445A-30
Sequence 30, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO

US-08-941-445A-30
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 230
US-09-637-751A-6/c
Sequence 6, Application US/09637751A
Patent No. 6383754
GENERAL INFORMATION:
APPLICANT: Kaufman, Joseph C.
APPLICANT: Roth, Matthew E.
APPLICANT: Lizardi, Paul M.
APPLICANT: Feng, Li
APPLICANT: Latimer, Darin R.
TITLE OF INVENTION: Binary Encoded Sequence Tags
Patent No. 6383754
FILE REFERENCE: AGL 100
CURRENT APPLICATION NUMBER: US/09/637,751A
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-6

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAAAAAA 1751
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 231

US-09-545-225-9/c
Sequence 9, Application US/09545225
Patent No. 6410321
GENERAL INFORMATION:
APPLICANT: Lin, Ching-I Patsy
Wallace, Robert Bruce
Cossman, Jeffrey
French, Cynthia
TITLE OF INVENTION: Lyophilization of Cultured Human Cells
to Preserve RNA and DNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/545,225
FILING DATE: 07-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/884,029
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 02558B-059100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

```
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 18 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: 13..18
;   OTHER INFORMATION: /mod_base= OTHER
; /note= "t at positions 13-18 may be
; present or absent"
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-545-225-9

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 232
US-09-619-103-24
; Sequence 24, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-24

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 233
US-09-370-541-14/c
; Sequence 14, Application US/09370541
; Patent No. 6639062
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Nucleosidic Compounds And Oligomeric
; FILE REFERENCE: ISIS3993
; CURRENT APPLICATION NUMBER: US/09/370,541
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: 09/130,973
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; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 09/016,520
; EARLIER FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 09/344,260
; EARLIER FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-370-541-14

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 234
US-10-125-295-9/c
; Sequence 9, Application US/10125295
; Patent No. 6686460
; GENERAL INFORMATION:
; APPLICANT: Lin, Ching-I Patsy
; APPLICANT: Wallace, Robert Bruce
; APPLICANT: Cossman, Jeffrey
; APPLICANT: French, Cynthia
; TITLE OF INVENTION: Lyophilization of Cultured Human Cells
; to Preserve RNA and DNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/125,295
; FILING DATE: 17-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/545,225
; FILING DATE: 07-Apr-2000
; APPLICATION NUMBER: US 08/884,029
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 02558B-059100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: DNA
; FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: 13..18
;   OTHER INFORMATION: /mod_base= OTHER
;   /note= "t at positions 13-18 may be
;   present or absent"
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-125-295-9

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 235
PCT-US94-05407-4/c
; Sequence 4, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-05407-4

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 236
US-09-435-806-7/c
; Sequence 7, Application US/09435806
; Patent No. 6653458
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Guinosa, Charles J.
; TITLE OF INVENTION: MODIFIED OLIGONUCLEOTIDES
; FILE REFERENCE: ISIS-4289
; CURRENT APPLICATION NUMBER: US/09/435,806
; CURRENT FILING DATE: 1999-11-08
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; PRIOR APPLICATION NUMBER: US 09/115,043
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 08/602,862
; PRIOR FILING DATE: 1996-02-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n = uracil
; US-09-435-806-7

Query Match      1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 237
US-08-123-449A-1/c
; Sequence 1, Application US/08123449A
; Patent No. 5583032
; GENERAL INFORMATION:
; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRYSTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,449A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-123-449A-1

Query Match          1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 238
US-08-123-449A-2/c
; Sequence 2, Application US/08123449A
; Patent No. 5583032
; GENERAL INFORMATION:
; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,449A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-123-449A-2
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```
Query Match          1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 239
```

```
US-08-458-050-1/c
; Sequence 1, Application US/08458050
; Patent No. 5677289
; GENERAL INFORMATION:
; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,050
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,449
; FILING DATE: 17-SEP-1993
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-458-050-1

Query Match          1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 240
US-08-458-050-2/c
; Sequence 2, Application US/08458050
; Patent No. 5677289
; GENERAL INFORMATION:
; APPLICANT: TORRENCE, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRISTYNA, LESIAK
; TITLE OF INVENTION: METHOD OF CLEAVING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
```


; REFERENCE/DOCKET NUMBER: NIH034.001QPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-950-196-2

Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 243

US-08-906-156A-82/c
; Sequence 82, Application US/08906156A
; Patent No. 6287854
; GENERAL INFORMATION:
; APPLICANT: SPURR, NIGEL K
; APPLICANT: GRAY, IAN C
; APPLICANT: STEWART, LORNA M
; TITLE OF INVENTION: DIAGNOSIS OF SUSCEPTIBILITY TO CANCER
; TITLE OF INVENTION: AND TREATMENT THEREOF
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,156A
; FILING DATE: 05-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/042,655
; FILING DATE: 02-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,147
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,840
; FILING DATE: 23-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/96GB/02588
; FILING DATE: 22-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1090-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 82:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC OLIGO"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-906-156A-82

Query Match 1.0%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 24 AAAAAAAAAAAAAAAAAA 7

RESULT 244

US-07-912-900-20/c
; Sequence 20, Application US/07912900
; Patent No. 5349125
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Kovacic, Filippa
; APPLICANT: Tanaka, Yoshikazu
; APPLICANT: Lester, Diane R.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/912,900
; FILING DATE: 19920713
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELETYPE: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-912-900-20

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAA 1


```

; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/285,309
; FILING DATE: 03-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8633Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-502-046-20

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAGAAAAA 1753
Db 19 CTAAAAAAGAAAAA 1

RESULT 248
US-08-108-591B-4
; Sequence 4, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-4

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAGAAAAA 1754
Db 1 AAAAAAGAAAAA 19

RESULT 249
US-08-704-966-7/c
; Sequence 7, Application US/08704966
; Patent No. 6013523
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J.
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein

```

```

; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA
; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,966
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,839
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,191
; FILING DATE: 03-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,844
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 07/242,482
; FILING DATE: 09-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MPS 8-88AFD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 407-426-7500
; TELEFAX: 407-839-8589
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-704-966-7

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAAAGAAAAA 1751
Db 19 TGAAGAAAAAAGAAAAA 1

RESULT 250
US-08-705-438-7/c
; Sequence 7, Application US/08705438
; Patent No. 6015891
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J.
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Merlo, Donald
; APPLICANT: Murray, Elizabeth E.
; TITLE OF INVENTION: Synthetic Insecticidal Crystal Protein
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 1000 Legion Place, Suite 1750
; CITY: Orlando
; STATE: Florida
; COUNTRY: USA

```

; ZIP: 32801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,438
; FILING DATE: 29-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/369,839
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,191
; FILING DATE: 03-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,844
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/242,482
; FILING DATE: 09-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: NPS 8-88AFD4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 407-426-7500
; TELEFAX: 407-839-8589
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-705-438-7

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1751
Db 19 TGCAAAAA 1

RESULT 251
US-09-130-079-1
; Sequence 1, Application US/09130079
; Patent No. 6270966
; GENERAL INFORMATION:
; APPLICANT: The United States of America, as represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: RESTRICTION DISPLAY (RD-PCR) OF DIFFERENTIALLY EXPRESS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,079
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/011/379
; FILING DATE: 09-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirkpatrick, Anita M
; REGISTRATION NUMBER: 32,617
; REFERENCE/DOCKET NUMBER: NIH108.001VPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
US-09-130-079-1

Query Match 1.0%; Score 17.2; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA 1752
Db 2 BAAAAA 19

RESULT 252
US-08-403-888A-36
; Sequence 36, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-888A-36

Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2e+02;

```
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1015 GTGGTTGGGATGGGCTGGG 1036
Db 1 GGGGTTGGGTTGGGTTGGG 22

RESULT 253
US-08-403-888A-44
; Sequence 44, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Leggaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-403-888A-44

Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1015 GTGGTTGGGATGGGCTGGG 1036
Db 1 GGGGTTGGGTTGGGTTGGG 22

RESULT 254
US-08-403-888A-110
; Sequence 110, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
```

```
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Leggaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-403-888A-110

Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1015 GTGGTTGGGATGGGCTGGG 1036
Db 1 GGGGTTGGGTTGGGTTGGG 22

RESULT 255
US-08-403-888A-117
; Sequence 117, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Leggaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
```


INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:
LENGTH: 22
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-403-888A-117

Query Match 1.0%; Score 17.2; DB 1; Length 22;

Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGGCTGGGG 1036
Db 1 GGGTTGGGGTTGGGGTTGGGG 22

RESULT 256

US-08-851-843A-132/c
Sequence 132, Application US/08851843A

Patent No. 6093809

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/851,843A

FILING DATE: 06-MAY-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-851-843A-132

Query Match 1.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 257

US-09-250-075-5/c

Sequence 5, Application US/09250075

Patent No. 6207819

GENERAL INFORMATION:

APPLICANT: Manoharan, Muthiah

APPLICANT: Maier, Martin A

TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of

TITLE OF INVENTION: Mixed Backbone Oligomeric Compounds

FILE REFERENCE: ISIS3299

CURRENT APPLICATION NUMBER: US/09/250,075

CURRENT FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5

LENGTH: 17

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)-(17)

OTHER INFORMATION: 2'-methoxyethoxy (MOE); modified linkage

OTHER INFORMATION: Description of Artificial Sequence: No. 6207819el

OTHER INFORMATION: Sequence

Query Match 1.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 258

US-08-854-050-132/c

Sequence 132, Application US/08854050

Patent No. 6261836

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin

APPLICANT: Andrews, William H.

TITLE OF INVENTION: No. 6261836el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050

; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-854-050-132

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
|||||
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 259
US-09-430-323-132/c
; Sequence 132, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-430-323-132

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
|||||
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 260
US-09-619-103-23
; Sequence 23, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-23

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
|||||
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 261
US-09-726-096A-5/c
; Sequence 5, Application US/09726096A
; Patent No. 6462184
; GENERAL INFORMATION:

```
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Martin A.
; TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of Mixed Back
; TITLE OF INVENTION: Oligomeric Compounds
; FILE REFERENCE: ISIS4528
; CURRENT APPLICATION NUMBER: US/09/726,096A
; CURRENT FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)-(19)
; OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate
; OTHER INFORMATION: internucleoside linkage
US-09-726-096A-5

Query Match          1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 262
US-09-637-751A-5/c
; Sequence 5, Application US/09637751A
; Patent No. 6383754
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Feng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6383754
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/09/637,751A
; CURRENT FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-5

Query Match          1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1751
Db 17 CAAAAAAAAAAAAAAAAA 1

RESULT 263
US-08-973-857-6/c
; Sequence 6, Application US/08973857
; Patent No. 6221584
; GENERAL INFORMATION:
; APPLICANT: EMRICH, Thomas
; APPLICANT: LEYING, Hermann
; APPLICANT: HINZPETER, Matthias
```

```
; APPLICANT: KARL, Gerlinde
; TITLE OF INVENTION: METHOD FOR THE DETECTION OF
; TITLE OF INVENTION: POLYMERASE ACTIVITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth St., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,857
; FILING DATE: 29-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/05245
; FILING DATE: 11-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19544317.9
; FILING DATE: 28-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19644302.4
; FILING DATE: 24-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Berman, Richard J.
; REGISTRATION NUMBER: 39,107
; REFERENCE/DOCKET NUMBER: P564-7031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-973-857-6

Query Match          1.0%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 264
US-08-031-147A-55
; Sequence 55, Application US/08031147A
; Patent No. 5514577
; GENERAL INFORMATION:
; APPLICANT: Draper et al.
; TITLE OF INVENTION: Oligonucleotide Therapies for
; TITLE OF INVENTION: Modulating the Effects of Herpesviruses
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5514577ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
```

; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,147A
; FILING DATE: March 12, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 485,297
; FILING DATE: February 26, 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,132
; FILING DATE: April 28, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 954,185
; FILING DATE: September 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISIS-0469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
US-08-031-147A-55

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGGTT 1038
||||| ||||| ||||| |||||
Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 265
US-08-403-888A-37
; Sequence 37, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-888A-37

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGGTT 1038
||||| ||||| ||||| |||||
Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 266
US-08-403-888A-45
; Sequence 45, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-888A-45

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGGTT 1038
||||| ||||| ||||| |||||
Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 267
US-08-403-888A-114

; Sequence 114, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-403-888A-114

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGCTGGGTT 1038
Db 1 TTGGGGTTGGGTTGGGTT 20

RESULT 268
US-08-403-888A-118
; Sequence 118, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A

; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-403-888A-118

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGCTGGGTT 1038
Db 1 TTGGGGTTGGGTTGGGTT 20

RESULT 269
US-09-490-692-68/c
; Sequence 68, Application US/09490692
; Patent No. 6180353
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RTS-0120
; CURRENT APPLICATION NUMBER: US/09/490,692
; CURRENT FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-490-692-68

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 859 GCAGGAAGAGGAGGAGG 878
Db 20 GGAGGAAGAAGAGAGGAGG 1

RESULT 270
US-09-228-942-7
; Sequence 7, Application US/09228942
; Patent No. 6203988
; GENERAL INFORMATION:
; APPLICANT: Kambara, Hideki
; APPLICANT: Uematsu, Chihiro
; TITLE OF INVENTION: DNA FRAGMENT ANALYSIS METHOD AND REAGENT KIT
; FILE REFERENCE: ASA-757
; CURRENT APPLICATION NUMBER: US/09/228,942
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 20

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide ligated to 3' end of DNA fragment
US-09-228-942-7

Query Match          1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1750
Db 1 TCTCCAAAAA 20

RESULT 271
PCT-US94-02471-55
; Sequence 55, Application PC/TUS9402471
; GENERAL INFORMATION:
; APPLICANT: Draper et al.
; TITLE OF INVENTION: Oligonucleotide Therapies for
; TITLE OF INVENTION: Modulating the Effects of Herpesviruses
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02471
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 485,297
; FILING DATE: February 26, 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,132
; FILING DATE: April 28, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 954,185
; FILING DATE: September 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISIS-0469
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
PCT-US94-02471-55

Query Match          1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGTGGGTT 1038
Db 1 TTGGGGTGGGGTTGGGGTT 20
```

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RESULT 272
US-09-198-452A-2140/c
; Sequence 2140, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2140
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2140

Query Match          0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 137 TCTGGAGTCCCTTTCC 154
Db 18 TCTGGAGTCCCTTTCC 1

RESULT 273
US-07-971-978-36/c
; Sequence 36, Application US/07971978
; Patent No. 5614617
; GENERAL INFORMATION:
; APPLICANT: Cook and Sanghvi
; TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
; TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate
; TITLE OF INVENTION: Gene Expression
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5614617ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,978
; FILING DATE: February 18, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/558,806
; FILING DATE: July 27, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```


MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site

LOCATION: 15
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
US-07-971-978-36
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAA 1
RESULT 274
US-07-971-978-42/c
Sequence 42, Application US/07971978
Patent No. 5614617
GENERAL INFORMATION:
APPLICANT: Cook and Sanghvi
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate
TITLE OF INVENTION: Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5614617ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: July 27, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-0333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution

FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
US-07-971-978-42

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
| | | | | | | | | | | | | | | |
Db 16 AAAAAAAAAAAAAA 1

RESULT 275
US-07-971-978-60/c

; Sequence 60, Application US/07971978
; Patent No. 5614617
; GENERAL INFORMATION:
; APPLICANT: Cook and Sanghvi
; TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
; TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate
; TITLE OF INVENTION: Gene Expression
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5614617ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,978
; FILING DATE: February 18, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/558,806
; FILING DATE: July 27, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:

; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: 5-iodo-2'-deoxyuridine
; OTHER INFORMATION: substitution
; US-07-971-978-60

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 276
US-08-415-370-2/c
; Sequence 2, Application US/08415370
; Patent No. 5801155
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Meyer, Jr., Rich B.
; TITLE OF INVENTION: COVALENTLY LINKED OLIGONUCLEOTIDE MINOR
; TITLE OF INVENTION: GROOVE BINDER CONJUGATES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLEIN & SZEKERES
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: USA

; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,370
; FILING DATE: 03-APR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-09-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-854-5502
; TELEFAX: 714-854-4897
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-415-370-2

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 277
US-08-687-551-15/c
; Sequence 15, Application US/08687551
; Patent No. 5856435
; GENERAL INFORMATION:
; APPLICANT: BAZILE, Didier
; APPLICANT: EMILE, Carole
; APPLICANT: HELENE, Claude
; APPLICANT: SPENLEHAUER, Gilles
; TITLE OF INVENTION: NUCLEIC ACID-CONTAINING COMPOSITION, ITS
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,551
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/01381
; FILING DATE: 08-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00098
; FILING DATE: 27-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST94007-US
; TELECOMMUNICATION INFORMATION:

```
/ TELEPHONE: (610)454-3839
/ TELEFAX: (610)454-3808
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "oligonucleotide"
US-08-687-551-15

Query Match          0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAA 1

RESULT 278
US-09-141-764-2/c
; Sequence 2, Application US/09141764
; Patent No. 6084102
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Meyer, Jr., Rich B.
; TITLE OF INVENTION: COVALENTLY LINKED OLIGONUCLEOTIDE
; TITLE OF INVENTION: MINOR
; TITLE OF INVENTION: GROOVE BINDER CONJUGATES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLEIN & SZEKERES
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: USA
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/141,764
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-09-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-854-5502
; TELEFAX: 714-854-4897
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-141-764-2

Query Match          0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
```

```
Db 16 AAAAAAAAAAAAAA 1

RESULT 279
US-08-851-843A-131
; Sequence 131, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-851-843A-131

Query Match          0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAA 16

RESULT 280
US-08-854-050-131
; Sequence 131, Application US/08854050
```

; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-854-050-131

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAA 16

RESULT 281
US-09-430-323-131
; Sequence 131, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.

; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-430-323-131

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAA 16

RESULT 282
US-09-507-345A-2/c
; Sequence 2, Application US/09507345A
; Patent No. 6426408
; GENERAL INFORMATION:
; APPLICANT: Kutuyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamber, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/507,345A
FILING DATE: 18-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
APPLICATION NUMBER: US 09/141,764
FILING DATE: 27-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-507-345A-2

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 283
US-09-619-103-22
; Sequence 22, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-22

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 284

US-09-739-928-2/c
; Sequence 2, Application US/09739928
; Patent No. 6486308
; GENERAL INFORMATION:
; APPLICANT: Kutuyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamper, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-928-2

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 285
US-08-821-827C-30/c
; Sequence 30, Application US/08821827C
; Patent No. 6297425
; GENERAL INFORMATION:
; APPLICANT: Scelonge, Christopher J.

APPLICANT: Bidney, Dennis L.
TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM
TITLE OF INVENTION: ASPERGILLUS PHOENICES
FILE REFERENCE: 0561A
CURRENT APPLICATION NUMBER: US/08/821,827C
CURRENT FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
NAME/KEY: misc_feature
LOCATION: (1)...(17)
OTHER INFORMATION: n = A,T,C or G
US-08-821-827C-30

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751
|||||
Db 17 AAAAAAAAAAAAAA 2

RESULT 286
US-09-290-202B-30/c
Sequence 30, Application US/09290202B
Patent No. 6303846
GENERAL INFORMATION:
APPLICANT: Scelonge, Christopher J.
APPLICANT: Bidney, Dennis L.
TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM
TITLE OF INVENTION: ASPERGILLUS PHOENICES
FILE REFERENCE: 0561D
CURRENT APPLICATION NUMBER: US/09/290,202B
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 08/821,827
PRIOR FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
NAME/KEY: misc_feature
LOCATION: (1)...(17)
OTHER INFORMATION: n = A,T,C or G
US-09-290-202B-30

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751
|||||
Db 17 AAAAAAAAAAAAAA 2

RESULT 287
US-08-584-040-2550/c
Sequence 2550, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2550:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-2550

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751
|||||
Db 17 AAAAAAAAAAAAAA 2

RESULT 288
US-08-584-040-2551/c
Sequence 2551, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California

; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2551:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2551

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 289

US-09-788-338-3/c
; Sequence 3, Application US/09788338
; Patent No. 6485916
; GENERAL INFORMATION:
; APPLICANT: MURAMATSU, TAKAMICHI
; APPLICANT: FUJITA, TAKESHI
; APPLICANT: KIYAMA, MASAHARU
; APPLICANT: IRIE, TAKASHI
; TITLE OF INVENTION: PREPARATION METHOD OF NUCLEIC ACID SAMPLE FOR RARE
; TITLE OF INVENTION: EXPRESSED GENES AND ANALYZING METHOD USING THE PREPARED
; TITLE OF INVENTION: NUCLEIC ACID SAMPLES THEREBY
; FILE REFERENCE: NIT-129-02
; CURRENT APPLICATION NUMBER: US/09/788,338
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 09/313,637
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: JP 10-153651
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; US-09-788-338-3

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2
RESULT 290
US-09-300-958A-64/c
; Sequence 64, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; US-09-300-958A-64

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2

RESULT 291

US-09-371-772B-1074/c
; Sequence 1074, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-371-772B-1074

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ADDRESSEE: Woodland Falls Corporate Park
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/063,167A
FILING DATE: 19930517
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 939,855
FILING DATE: September 2, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05209
FILING DATE: July 23, 1991
APPLICATION NUMBER: 567,286
FILING DATE: August 14, 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-063-167A-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGGTCTCTGGCCC 857
||| |||||
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 297
US-08-007-997A-57/c
Sequence 57, Application US/08007997A
Patent No. 5591623
GENERAL INFORMATION:
APPLICANT: Bennett and Mirabelli
TITLE OF INVENTION: Oligonucleotide Modulation
TITLE OF INVENTION: of Cell Adhesion
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5591623ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,997A
FILING DATE: 19930121
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 939,855
FILING DATE: September 2, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05209
FILING DATE: July 23, 1991
APPLICATION NUMBER: 567,286
FILING DATE: August 14, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISIS-0709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-007-997A-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGGTCTCTGGCCC 857
||| |||||
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 298
US-08-440-740A-57/c
Sequence 57, Application US/08440740A
Patent No. 5843738
GENERAL INFORMATION:
APPLICANT: Bennett and Mirabelli
TITLE OF INVENTION: Oligonucleotide Modulation
TITLE OF INVENTION: of Cell Adhesion
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,740A
FILING DATE: May 12, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 063,167
FILING DATE: May 17, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 969,151
FILING DATE: February 10, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 007,997
FILING DATE: January 20, 1993

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 939,855
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 567,286
; FILING DATE: August 14, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-440-740A-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGTCTCTGGCCC 857
Db 19 CTCCTCGGTCTCTGGCCC 1

RESULT 299
US-08-344-155C-57/c
; Sequence 57, Application US/08344155C
; Patent No. 583082
; GENERAL INFORMATION:
; APPLICANT: Bennett and Stepkowski
; TITLE OF INVENTION: Compositions and Methods for Preventing
; TITLE OF INVENTION: and Treating Allograft Rejection
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodland Falls Corporate Park
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,155C
; FILING DATE: No. 5883082ember 23, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 939,855
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05209
; FILING DATE: July 23, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063,167
; FILING DATE: 5/17/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/007,997
; FILING DATE: 1/21/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,855
; FILING DATE: 9/2/92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,286

```

```

; FILING DATE: 8/14/90
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0098
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-344-155C-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGTCTCTGGCCC 857
Db 19 CTCCTCGGTCTCTGGCCC 1

RESULT 300
US-08-982-845B-57/c
; Sequence 57, Application US/08982845B
; Patent No. 6015894
; GENERAL INFORMATION:
; APPLICANT: Bennett and Mirabelli
; TITLE OF INVENTION: Oligonucleotide Modulation
; TITLE OF INVENTION: of Cell Adhesion
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,845B
; FILING DATE: December 2, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/440,740
; FILING DATE: May 12, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 063,167
; FILING DATE: May 17, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 969,151
; FILING DATE: February 10, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 007,997
; FILING DATE: January 21, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 939,855
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 567,286
; FILING DATE: August 14, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0243

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-982-845B-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 301

US-09-344-001-12/c
; Sequence 12, Application US/09344001
; Patent No. 6054440
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF JUN N-TERMINAL KINASE-2 EXPRESSION
; FILE REFERENCE: RTS-0067
; CURRENT APPLICATION NUMBER: US/09/344,001
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-001-12

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 997 GGTGGCTCGGAGAGATG 1015
Db 19 GGTGGCGCGGGGAGATG 1

RESULT 302

US-08-991-525B-57/c
; Sequence 57, Application US/08991525B
; Patent No. 6093811
; GENERAL INFORMATION:
; APPLICANT: Bennett and Mirabelli
; TITLE OF INVENTION: Oligonucleotide Modulation
; TITLE OF INVENTION: of Cell Adhesion
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,525B

; FILING DATE: December 16, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,740
; FILING DATE: May 12, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 063,167
; FILING DATE: May 17, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 969,151
; FILING DATE: February 10, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 007,997
; FILING DATE: January 21, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 939,855
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 567,286
; FILING DATE: August 14, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-991-525B-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 303

US-09-085-759-57/c
; Sequence 57, Application US/09085759
; Patent No. 6096722
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Christopher Mirabelli,
; APPLICANT: Brenda Baker
; TITLE OF INVENTION: Antisense Modulation of Cell Adhesion
; TITLE OF INVENTION: Molecule Expression and Treatment of Cell Adhesion
; TITLE OF INVENTION: Molecule-Associated Diseases
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,759
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/440,740
FILING DATE: May 12, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 063,167
FILING DATE: May 17, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 969,151
FILING DATE: February 10, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 007,997
FILING DATE: January 20, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 939,855
FILING DATE: September 2, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 567,286
FILING DATE: August 14, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-09-085-759-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 304

US-09-128-496-57/c
Sequence 57, Application US/09128496
Patent No. 6169079
GENERAL INFORMATION:
APPLICANT: Bennett and Mirabelli
TITLE OF INVENTION: Oligonucleotide Modulation
TITLE OF INVENTION: of Cell Adhesion
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,496
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/440,740
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 969,151
FILING DATE: February 10, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 007,997
FILING DATE: January 20, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 939,855
FILING DATE: September 2, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 567,286
FILING DATE: August 14, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-09-128-496-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 305

US-09-009-490A-57/c
Sequence 57, Application US/09009490A
Patent No. 6300491
GENERAL INFORMATION:
APPLICANT: Bennett and Mirabelli
TITLE OF INVENTION: Oligonucleotide Modulation
TITLE OF INVENTION: of Cell Adhesion
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: Windows 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,490A
FILING DATE: January 20, 1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,740
FILING DATE: May 12, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 063,167
FILING DATE: May 17, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 969,151
FILING DATE: February 10, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 007,997
FILING DATE: January 20, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 939,855

```
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 567,286
; FILING DATE: August 14, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-009-490A-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 306
PCT-US93-08101-57/c
; Sequence 57, Application PC/TUS9308101
; GENERAL INFORMATION:
; APPLICANT: Bennett and Mirabelli
; TITLE OF INVENTION: Oligonucleotide Modulation
; TITLE OF INVENTION: of Cell Adhesion
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodland Falls Corporate Park
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08101
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 939,855
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05209
; FILING DATE: July 23, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 567,286
; FILING DATE: August 14, 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 57:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
PCT-US93-08101-57

Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 307
US-09-422-978-10471/c
; Sequence 10471, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10471
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-12181 for SEQ 2606, in complete
US-09-422-978-10471

Query Match 0.9%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 289 GTCAATTTTGGCCCCCTTC 307
Db 19 GTCAATTTTGGCCTCTTTC 1

RESULT 308
US-08-937-067-17/c
; Sequence 17, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
```

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-937-067-17

Query Match 0.9%; Score 15.6; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAATAAAAAAAAAA 1751
Db 17 SNAATAAAAAAAAAAAAAA 1

RESULT 309
US-08-715-202A-7
; Sequence 7, Application US/08715202A
; Patent No. 5965403
; GENERAL INFORMATION:
; APPLICANT: CELESTE, ANTHONY J.
; APPLICANT: MURRAY, BETH L.
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-16 (BMP-16)
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,202A
; FILING DATE: September 18, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, STEVEN R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8260
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;

```

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US-08-715-202A-7

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1479 CTCTGAGGGCGAGTGTC 1495
Db 1 CTGTGAGGGCGAGTGTC 17

RESULT 310
US-09-328-775-7
; Sequence 7, Application US/09328775
; Patent No. 6331612
; GENERAL INFORMATION:
; APPLICANT: CELESTE, ANTHONY J.
; APPLICANT: MURRAY, BETH L.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN-16
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,775
; FILING DATE: June 9, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, STEVEN R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5275-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 665-8260
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-09-328-775-7

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1479 CTCTGAGGGCGAGTGTC 1495
Db 1 CTGTGAGGGCGAGTGTC 17

RESULT 311
US-09-994-177-7
; Sequence 7, Application US/09994177
; Patent No. 6623934
; GENERAL INFORMATION:
; APPLICANT: CELESTE, ANTHONY J.
; APPLICANT: MURRAY, BETH L.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN-16
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
;

```

```
;
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/994,177
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/328,775
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, STEVEN R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5275-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 665-8260
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-09-994-177-7
;
; Query Match 0.9%; Score 15.4; DB 1; Length 18;
; Best Local Similarity 94.1%; Pred. No. 2.7e+02;
; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 1479 CTCTGAGGGCGAGTGTC 1495
;
Db 1 CTGTGAGGGCGAGTGTC 17
;
;
; RESULT 312
; PCT-US91-03680-73/c
; Sequence 73, Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
; TITLE OF INVENTION: DUPLEX DNA
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03680
; FILING DATE: 19910524
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4610-0011.40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
;
;
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/994,177
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/328,775
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, STEVEN R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5275-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 665-8260
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-09-994-177-7
;
; Query Match 0.9%; Score 15.4; DB 1; Length 18;
; Best Local Similarity 94.1%; Pred. No. 2.7e+02;
; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 1736 AAAAAAAAAAAAAA 1752
;
Db 17 AAAAAAAAAAAAAAGAAA 1
;
;
; RESULT 313
; PCT-US91-03680-74/c
; Sequence 74, Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; APPLICANT: Krawczyk, Steven
; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
; TITLE OF INVENTION: DUPLEX DNA
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03680
; FILING DATE: 19910524
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4610-0011.40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
;
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 5
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 18
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N4,N4-ethanocytosine"
;
PCT-US91-03680-73
;
; Query Match 0.9%; Score 15.4; DB 1; Length 18;
; Best Local Similarity 94.1%; Pred. No. 2.7e+02;
; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 1736 AAAAAAAAAAAAAA 1752
;
Db 17 AAAAAAAAAAAAAAGAAA 1
;
;
; RESULT 313
; PCT-US91-03680-74/c
; Sequence 74, Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; APPLICANT: Krawczyk, Steven
; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
; TITLE OF INVENTION: DUPLEX DNA
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03680
; FILING DATE: 19910524
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4610-0011.40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
;
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
;
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 5
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 18
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N4,N4-ethanocytosine"
;
PCT-US91-03680-73
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/ LOCATION: 5
/ OTHER INFORMATION: /mod_base= OTHER
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: 18
/ OTHER INFORMATION: /mod_base= OTHER
/ OTHER INFORMATION: /note= "N4,N4-ethanocytosine"
PCT-US91-03680-74

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 314
US-08-715-461-3/c
; Sequence 3, Application US/08715461
; Patent No. 5985556
; GENERAL INFORMATION:
; APPLICANT: KAMBARA, Hideki
; APPLICANT: OKANO, Kazunori
; TITLE OF INVENTION: DNA SEQUENCING METHOD AND DNA SAMPLE
; TITLE OF INVENTION: PREPARATION METHOD
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY STOUT & KRAUS
; STREET: 1300 No. 5985556th Seventeenth Street, Suite 1800
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,461
; FILING DATE: 18-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TERRY, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 500.34872X00
; TELEPHONE: 703-312-6600
; TELEFAX: 703-312-6666
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-715-461-3

Query Match          0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAAAAAA 1749
Db 17 TGCAAAAAAAAAAAAAAAAA 1

RESULT 315
US-08-715-461-3/c
; Sequence 5, Application US/08715461
; Patent No. 5985556
; GENERAL INFORMATION:
; APPLICANT: KAMBARA, Hideki
; APPLICANT: OKANO, Kazunori
; TITLE OF INVENTION: DNA SEQUENCING METHOD AND DNA SAMPLE
; TITLE OF INVENTION: PREPARATION METHOD
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY STOUT & KRAUS
; STREET: 1300 No. 5985556th Seventeenth Street, Suite 1800
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,461
; FILING DATE: 18-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TERRY, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 500.34872X00
; TELEPHONE: 703-312-6600
; TELEFAX: 703-312-6666
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-715-461-3
```

```
US-08-715-461-4/c
; Sequence 4, Application US/08715461
; Patent No. 5985556
; GENERAL INFORMATION:
; APPLICANT: KAMBARA, Hideki
; APPLICANT: OKANO, Kazunori
; TITLE OF INVENTION: DNA SEQUENCING METHOD AND DNA SAMPLE
; TITLE OF INVENTION: PREPARATION METHOD
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY STOUT & KRAUS
; STREET: 1300 No. 5985556th Seventeenth Street, Suite 1800
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,461
; FILING DATE: 18-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TERRY, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 500.34872X00
; TELEPHONE: 703-312-6600
; TELEFAX: 703-312-6666
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-715-461-4

Query Match          0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAAAAAA 1749
Db 17 TGCAAAAAAAAAAAAAAAAA 1

RESULT 316
US-08-715-461-5/c
; Sequence 5, Application US/08715461
; Patent No. 5985556
; GENERAL INFORMATION:
; APPLICANT: KAMBARA, Hideki
; APPLICANT: OKANO, Kazunori
; TITLE OF INVENTION: DNA SEQUENCING METHOD AND DNA SAMPLE
; TITLE OF INVENTION: PREPARATION METHOD
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY STOUT & KRAUS
; STREET: 1300 No. 5985556th Seventeenth Street, Suite 1800
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-715-461-5
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; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(17)
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: "V=A,C,G; N=A,C,G,T"
US-10-015-593-2

Query Match 0.9%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA 1750
Db 16 BAAAAA 1

RESULT 320

US-08-117-952-253/c
; Sequence 253, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392

; INFORMATION FOR SEQ ID NO: 253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-117-952-253

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 914 CAGAGGATGAGCTGGATAGG 933
Db 20 CAGAAGGTGAGCTGGAAGG 1

RESULT 321

US-08-767-979-22/c
; Sequence 22, Application US/08767979
; Patent No. 5945283
; GENERAL INFORMATION:
; APPLICANT: Kwok, Pui-Yan
; APPLICANT: Chen, Xiangning
; TITLE OF INVENTION: Method for Nucleic Acid Analysis Using
; TITLE OF INVENTION: Fluorescence Resonance Energy Transfer
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Boulevard, Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,979
; FILING DATE: 17-DEC-1996
; CLASSIFICATION: 455
; ATTORNEY/AGENT INFORMATION:
; NAME: Holland, Donald R
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 96-5219
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DONOR SEQ; SYNTHETIC
; DESCRIPTION: NUCLEOTIDE SEQUENCE COMPLEMENTARY TO NUCLEOTIDES 1-20 IN SEQ ID
; DESCRIPTION: NO:1, SEQ ID NO:2, SEQ ID NO:3, AND SEQ ID NO:4;"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-767-979-22

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1729 AGTTTACAAAAA 1748
Db 20 ATTTTACAAAAA 1

RESULT 322

US-09-357-071-12
; Sequence 12, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-357-071-12

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1176 TGCCACGTGCTCCAGCCCA 1195
|||||
Db 1 TGCCACGTTCTCCAGCCCA 20

RESULT 323

US-08-954-536-3
; Sequence 3, Application US/08954536
; Patent No. 6100445
; GENERAL INFORMATION:
; APPLICANT: Seshadri, Tara
; APPLICANT: Li, Ping
; APPLICANT: Allen, Hamish
; APPLICANT: Banerjee, Subhashis
; APPLICANT: Paskind, Michael
; TITLE OF INVENTION: Transgenic No. 6100445human Animal Having Functionally
; Disrupted Interleukin-1b Converting Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,536
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,490
FILING DATE: 14-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, GIULIO, A. JR.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-019
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
US-08-954-536-3

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 820 CCAGGGGCCAAAGAGGAGC 839
|||
Db 1 CCTGAGGGCAAGAGGAGC 20

RESULT 324

US-08-765-340-10
; Sequence 10, Application US/08765340
; Patent No. 6150092
; GENERAL INFORMATION:

APPLICANT: UCHIDA, K.,
APPLICANT: UCHIDA, T.,
APPLICANT: TANAKA, Y.,
APPLICANT: MATSUDA, Y.,
APPLICANT: KONDO, S.,
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
COMPOUND
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 145146/94
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 311130/94
FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE

REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-765-340-10

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAACAAACACAAA 20

RESULT 325

US-09-407-675-2
; Sequence 2, Application US/09407675
; Patent No. 6169176
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas C.
; APPLICANT: Arya, Dev P.

TITLE OF INVENTION: DEOXYNUCLEIC ALKYL THIOUREA COMPOUNDS AND USES THEREOF
FILE REFERENCE: 30448.65US02
CURRENT APPLICATION NUMBER: US/09/407,675
CURRENT FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 09/347,443
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/091,481
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/111,800
PRIOR FILING DATE: 1998-12-11

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligo 2
US-09-407-675-2

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAACAAAAA 1754
Db 1 CAAAAAATAAAACAAAAA 20

RESULT 326
US-09-295-026-22/c
; Sequence 22, Application US/09295026
; Patent No. 6177249
; GENERAL INFORMATION:
; APPLICANT: Kwok, Pui-Yan
; Chen, Xiangning
; TITLE OF INVENTION: Method for Nucleic Acid Analysis Using
; Fluorescence Resonance Energy Transfer
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Boulevard, Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/295,026
; FILING DATE: 20-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/767,979
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Holland, Donald R
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 96-5219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DONOR SEQ; SYNTHETIC
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-295-026-22

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 20 ATTTTACAAAATAAAACAA 1

RESULT 327
US-09-780-173A-93
; Sequence 93, Application US/09780173A
; Patent No. 6455307
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION
; FILE REFERENCE: RTS-0165
; CURRENT APPLICATION NUMBER: US/09/780,173A
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 93
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-173A-93

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 857 CTGCAGGAAGAGGAGGAGGA 876
Db 1 CTGCAGGAAGAGGAGGAGGAGGA 20

RESULT 328
US-09-422-978-6563
; Sequence 6563, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6563
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-12356 for SEQ 2629,
US-09-422-978-6563

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1014 TGTGGTTGGGATGGGGCTG 1033
Db 1 TCTGATTTGGGATGGGGCTG 20

RESULT 329
US-09-422-978-6563

US-09-422-978-10187/c
; Sequence 10187, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10187
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-10438 for SEQ 2322, in complement
US-09-422-978-10187

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 564 CCTGAAGCCAAATCCAGCCT 583
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CCTGAAGCCAAACACACCCT 1

RESULT 330
US-09-823-634A-18
; Sequence 18, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: MISMATCHES USING RNASE H
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02025
US-09-823-634A-18

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAATTATAAAAAA 20

RESULT 331
US-09-823-647B-18
; Sequence 18, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:

; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02025
US-09-823-647B-18

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAATTATAAAAAA 20

RESULT 332
US-09-112-580-72
; Sequence 72, Application US/09112580
; Patent No. 6610539
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping
; APPLICANT: DUGOURD, Dominique
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF
; TITLE OF INVENTION: MICROORGANISMS
; FILE REFERENCE: 032396-016
; CURRENT APPLICATION NUMBER: US/09/112,580
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: US 60/052,160
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 265
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 72
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-112-580-72

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1204 CGGATCCTGCGGCTATGGG 1223
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CGGATCAACCGGCTATGGG 20

RESULT 333
US-08-452-196A-6
; Sequence 6, Application US/08452196A
; Patent No. 5576427
; GENERAL INFORMATION:
; APPLICANT: Cook, Philip D.
; APPLICANT: Delecki, Daniel J.
; APPLICANT: Guinasso, Charles
; TITLE OF INVENTION: ACYCLIC NUCLEOSIDE
; TITLE OF INVENTION: ANALOGS AND
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; TITLE OF INVENTION: CONTAINING THEM

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Department
STREET: 9 Great Valley Parkway
CITY: Malvern
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19355
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.4 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.0B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,196A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,326
FILING DATE: 30 March 1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul E. Dupont
REGISTRATION NUMBER: 27,438
REFERENCE/DOCKET NUMBER: 2525
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)889-6338
TELEFAX: (215)889-8800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: Nucleic Acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Nucleic Acid
DESCRIPTION:
ANTI-SENSE: no
ORIGINAL SOURCE: synthesized
US-08-452-196A-6

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 334
US-07-971-978-1/c
Sequence 1, Application US/07971978
Patent No. 5614617
GENERAL INFORMATION:
APPLICANT: Cook and Sanghvi
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate
TITLE OF INVENTION: Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5614617ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: July 27, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-0333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:

```
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: 6-aza-thymidine substitution
US-07-971-978-1

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 335
US-08-756-728A-2
; Sequence 2, Application US/08756728A
; Patent No. 5821354
; GENERAL INFORMATION:
; APPLICANT: Leclerc, Guy
; APPLICANT: Martel, Remi
; TITLE OF INVENTION: RADIOLABELED DNA OLIGONUCLEOTIDE, METHOD
; TITLE OF INVENTION: OF PREPARATION AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,728A
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1398-1-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PRIMER"
; HYPOTHETICAL: NO
US-08-756-728A-2

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 336
US-08-663-918-3/c
; Sequence 3, Application US/08663918
; Patent No. 5824793
; GENERAL INFORMATION:
```

```
; APPLICANT: Bernard Hirschbein, Karen Fearon, Sergei Gryaznov, Sarah McCurdy, Jeffrey
; TITLE OF INVENTION: Solid Phase Synthesis of Oligonucleotide N3 {symbol 174 \f "Syn
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,918
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/603,566
; FILING DATE: 21-FEB-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: LYNX-035/01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-663-918-3

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 337
US-08-663-918-4
; Sequence 4, Application US/08663918
; Patent No. 5824793
; GENERAL INFORMATION:
; APPLICANT: Bernard Hirschbein, Karen Fearon, Sergei Gryaznov, Sarah McCurdy, Jeffrey
; TITLE OF INVENTION: Solid Phase Synthesis of Oligonucleotide N3 {symbol 174 \f "Syn
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,918
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/603,566
; FILING DATE: 21-FEB-96
```



```
Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 340
US-08-771-789-3/c
; Sequence 3, Application US/08771789
; Patent No. 5859233
; GENERAL INFORMATION:
; APPLICANT: Bernard Hirschbein
; APPLICANT: Karen Fearon
; APPLICANT: Sergei Gryaznov
; APPLICANT: Sarah McCurdy
; APPLICANT: Jeffery Nelson
; APPLICANT: Ronald G. Schultz
; TITLE OF INVENTION: Solid Phase Synthesis of Oligonucleotide
; TITLE OF INVENTION: N3 {symbol 174 \f "Symbol" \s 12}}P5 Phosphoramidates
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,789
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,918
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/603,566
; FILING DATE: 21-FEB-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: LYNX-035/01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-771-789-3

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 341
US-08-771-789-4
; Sequence 4, Application US/08771789
; Patent No. 5859233
```

```
; GENERAL INFORMATION:
; APPLICANT: Bernard Hirschbein
; APPLICANT: Karen Fearon
; APPLICANT: Sergei Gryaznov
; APPLICANT: Sarah McCurdy
; APPLICANT: Jeffery Nelson
; APPLICANT: Ronald G. Schultz
; TITLE OF INVENTION: Solid Phase Synthesis of Oligonucleotide
; TITLE OF INVENTION: N3 {symbol 174 \f "Symbol" \s 12}}P5 Phosphoramidates
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
; STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
; ZIP: 94545
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: Microsoft Word for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,789
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,918
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/603,566
; FILING DATE: 21-FEB-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: LYNX-035/01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 670-9365
; TELEFAX: (510) 670-9302
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-771-789-4

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 342
US-08-358-556A-10/c
; Sequence 10, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; US-08-358-556A-10

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 343
US-08-358-556A-16
; Sequence 16, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; US-08-358-556A-16

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 344
US-08-922-170B-5/c
; Sequence 5, Application US/08922170B
; Patent No. 5968822
; GENERAL INFORMATION:
; APPLICANT: Iris Pecker, Israel Vlodavsky and Elena
; APPLICANT: Feinstein
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
; TITLE OF INVENTION: HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
; TITLE OF INVENTION: SAME IN TRANSFUSED CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
; STREET: 2940 Birchtree lane
; CITY: Silver Spring
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 20906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,170B
; FILING DATE: 2 SEP 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 910/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

```
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-922-170B-5

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 345
US-08-663-639A-5
; Sequence 5, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-663-639A-5

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 346
US-08-663-639A-7
; Sequence 7, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
```

```
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-7

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 15

RESULT 347
US-08-863-639A-9/c
; Sequence 9, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-9

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 348
US-08-693-831-1/c
; Sequence 1, Application US/08693831
; Patent No. 6017700
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Balasubramanian, Tanjore N.
; TITLE OF INVENTION: CATIONIC OLIGONUCLEOTIDES, AND RELATED METHODS OF
; TITLE OF INVENTION: SYNTHESIS AND USE
; FILE REFERENCE: 1117.002
; CURRENT APPLICATION NUMBER: US/08/693,831
; CURRENT FILING DATE: 1996-07-31
; EARLIER APPLICATION NUMBER: US 08/693,831
; EARLIER FILING DATE: 1996-07-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Description of Artificial Sequence: poly-T
US-08-693-831-1

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 349
US-08-832-021-61/c
; Sequence 61, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinias, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
```

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; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-61

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAA 1747
Db 15 TACAAAAAAAAAAAAA 1

RESULT 350
US-09-183-619-4/c
; Sequence 4, Application US/09183619
; Patent No. 6103474
; GENERAL INFORMATION:
; APPLICANT: DELLINGER, DOUGLAS J.
; APPLICANT: DAHM, SUEANN C.
; APPLICANT: ILSLEY, DIANE D.
; APPLICANT: ACH, ROBERT A.
; APPLICANT: TROLL, MARK A.
; TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
; FILE REFERENCE: 10981619-1
; CURRENT APPLICATION NUMBER: US/09/183,619
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 08/735,381
; EARLIER FILING DATE: 1996-10-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Reporter probe
US-09-183-619-4

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 351
US-09-071-845-361/c
; Sequence 361, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
```

STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
MEDIUM TYPE: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 361:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-361
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 352
US-09-071-845-362/c
Sequence 362, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-362
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 353
US-09-167-375-1
Sequence 1, Application US/09167375B
Patent No. 6291438
GENERAL INFORMATION:
APPLICANT: Jui H. Wang
TITLE OF INVENTION: Antiviral anticancer poly-substituted phenyl derivatized oligoribonucleotides
TITLE OF INVENTION: methods for their use.
FILE REFERENCE: WNGJ 2002 (CIP-1)
CURRENT APPLICATION NUMBER: US/09/167,375B
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 1
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Retroviral reverse transcriptase inhibitor
US-09-167-375-1
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 354
US-08-150-156A-19/c
Sequence 19, Application US/08150156A
Patent No. 6357163

;
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150,156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
; US-08-150-156A-19

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 355
US-08-150-156A-20
; Sequence 20, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150,156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
; US-08-150-156A-20

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 356
US-08-108-591B-17/c
; Sequence 17, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
; US-08-108-591B-17

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 357
US-08-108-591B-18
; Sequence 18, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-18

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 15

RESULT 358

US-09-619-103-21
; Sequence 21, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-21

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 15

RESULT 359

US-09-300-958A-68/c
; Sequence 68, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-68

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | | | |
Db 15 AAAAAAAAAAAAAA 1

RESULT 360

US-08-988-024C-9/c
; Sequence 9, Application US/08988024C
; Patent No. 6635452
; GENERAL INFORMATION:
; APPLICANT: Monforte, Joseph A.
; APPLICANT: Becker, Christopher H.
; APPLICANT: Pollart, Daniel J.
; APPLICANT: Shaler, Thomas A.
; TITLE OF INVENTION: Releasable No. 6635452volatile Mass-Label Molecules
; FILE REFERENCE: 24736-2057
; CURRENT APPLICATION NUMBER: US/08/988,024C
; CURRENT FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: US 60/033,037
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: US 60/046,719
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-08-988-024C-9

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | | | |
Db 15 AAAAAAAAAAAAAA 1

RESULT 361

US-09-435-739-5/c
; Sequence 5, Application US/09435739
; Patent No. 6664105
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 00/20454
; CURRENT APPLICATION NUMBER: US/09/435,739
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-435-739-5

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 362

US-10-091-231-2/c
; Sequence 2, Application US/10091231
; Patent No. 6664388
; GENERAL INFORMATION:
; APPLICANT: NELSON, Jeffrey S.
; TITLE OF INVENTION: REAGENTS FOR OLIGONUCLEOTIDE CLEAVAGE AND DEPROTECTION
; FILE REFERENCE: 4688US
; CURRENT APPLICATION NUMBER: US/10/091,231
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/274,309
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-10-091-231-2

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 363

US-09-930-218-5/c
; Sequence 5, Application US/09930218
; Patent No. 6677137
; GENERAL INFORMATION:
; APPLICANT: goldshmidt, orit
; APPLICANT: pecker, iris
; APPLICANT: vlodavsky, israel
; APPLICANT: israel, michael
; TITLE OF INVENTION: AVIAN AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE H
; FILE REFERENCE: 01/22335
; CURRENT APPLICATION NUMBER: US/09/930,218
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/666,390
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide
US-09-930-218-5

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 364

US-09-507-345A-3/c

; Sequence 3, Application US/09507345A
; Patent No. 6426408
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamper, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,345A
; FILING DATE: 18-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003500US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod_base= OTHER
; /note= "N = thymidine modified by 6-aminohexanoic acid
; (-NH(CH₂)-6COOH)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-507-345A-3

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 365

US-09-507-345A-4/c
; Sequence 4, Application US/09507345A
; Patent No. 6426408
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamper, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor

; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,345A
; FILING DATE: 18-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003500US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod base= OTHER
; /note= "N = thymidine modified by minor groove binder moiety
; represented by X, where m = one
; 4-amino-N-methylpyrrol-2-carboxylic acid residue"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-507-345A-4

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 366
US-09-507-345A-5/C
; Sequence 5, Application US/09507345A
; Patent No. 6426408
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamper, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,345A
; FILING DATE: 18-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003500US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod base= OTHER
; /note= "N = thymidine modified by minor groove binder moiety
; represented by X, where m = two
; 4-amino-N-methylpyrrol-2-carboxylic acid residues"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-507-345A-5

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 367
US-09-507-345A-6/c
; Sequence 6, Application US/09507345A
; Patent No. 6426408
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamper, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/507,345A
FILING DATE: 18-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
APPLICATION NUMBER: US 09/141,764
FILING DATE: 27-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: /mod base= OTHER
/note= "N = thymidine modified by minor groove binder moiety represented by X, where m = three
4-amino-N-methylpyrrol-2-carboxylic acid residues"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-507-345A-6
Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 368
US-09-507-345A-7/c
Sequence 7, Application US/09507345A
Patent No. 6426408
GENERAL INFORMATION:
APPLICANT: Kutvavin, Igor V.
Lukhtanov, Eugeny A.
Gamper, Howard B.
Meyer Jr., Rich B.
TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor Groove Binder Conjugates
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/507,345A
FILING DATE: 18-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995

APPLICATION NUMBER: US 09/141,764
FILING DATE: 27-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: /mod base= OTHER
/note= "N = thymidine modified by minor groove binder moiety represented by X, where m = four
4-amino-N-methylpyrrol-2-carboxylic acid residues"
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-507-345A-7
Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 369
US-09-507-345A-8/c
Sequence 8, Application US/09507345A
Patent No. 6426408
GENERAL INFORMATION:
APPLICANT: Kutvavin, Igor V.
Lukhtanov, Eugeny A.
Gamper, Howard B.
Meyer Jr., Rich B.
TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor Groove Binder Conjugates
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/507,345A
FILING DATE: 18-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
APPLICATION NUMBER: US 09/141,764
FILING DATE: 27-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003500US
TELECOMMUNICATION INFORMATION:

```
;
;
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   FEATURE:
;     NAME/KEY: modified_base
;     LOCATION: 16
;     OTHER INFORMATION: /mod_base= OTHER
;   /note= "N" = thymidine modified by minor groove binder moiety
;   represented by X, where m = five
;   4-amino-N-methylpyrrol-2-carboxylic acid residues"
;   SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-507-345A-8

Query Match      0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 370
US-09-739-928-3/c
; Sequence 3, Application US/09739928
; Patent No. 6486308
; GENERAL INFORMATION:
;   APPLICANT: Kutyavin, Igor V.
;               Lukhtanov, Eugeny A.
;               Gamber, Howard B.
;               Meyer Jr., Rich B.
;   TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                       Groove Binder Conjugates
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     STREET: Two Embarcadero Center, Eighth Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/739,928
;     FILING DATE: 11-May-2001
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/415,370
;     FILING DATE: 03-APR-1995
;     APPLICATION NUMBER: US 09/141,764
;     FILING DATE: 27-AUG-1998
;     APPLICATION NUMBER: US 09/507,345
;     FILING DATE: 18-FEB-2000
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Kezer, William B.
;     REGISTRATION NUMBER: 37,369
;     REFERENCE/DOCKET NUMBER: 17682A-003510US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 576-0200
;     TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 16 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;         NAME/KEY: modified_base
```

```
;
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: 16
;   OTHER INFORMATION: /mod_base= OTHER
;   /note= "N" = thymidine modified by 6-aminohexanoic acid
;   (-NH(CH2)-6COOH)"
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-739-928-3

Query Match      0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 371
US-09-739-928-4/c
; Sequence 4, Application US/09739928
; Patent No. 6486308
; GENERAL INFORMATION:
;   APPLICANT: Kutyavin, Igor V.
;               Lukhtanov, Eugeny A.
;               Gamber, Howard B.
;               Meyer Jr., Rich B.
;   TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;                       Groove Binder Conjugates
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     STREET: Two Embarcadero Center, Eighth Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/739,928
;     FILING DATE: 11-May-2001
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/415,370
;     FILING DATE: 03-APR-1995
;     APPLICATION NUMBER: US 09/141,764
;     FILING DATE: 27-AUG-1998
;     APPLICATION NUMBER: US 09/507,345
;     FILING DATE: 18-FEB-2000
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Kezer, William B.
;     REGISTRATION NUMBER: 37,369
;     REFERENCE/DOCKET NUMBER: 17682A-003510US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 576-0200
;     TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 16 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;         NAME/KEY: modified_base
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; LOCATION: 16
; OTHER INFORMATION: /mod_base= OTHER
; /note= "N = thymidine modified by minor groove binder moiety
; represented by X, where m = one
; 4-amino-N-methylpyrrol-2-carboxylic acid residue"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-739-928-4

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 372

US-09-739-928-5/c
; Sequence 5, Application US/09739928
; Patent No. 6486308

GENERAL INFORMATION:

APPLICANT: Kutyavin, Igor V.
Lukhtanov, Eugeny A.
Gamber, Howard B.
Meyer Jr., Rich B.

TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
Groove Binder Conjugates

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/739,928
FILING DATE: 11-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
APPLICATION NUMBER: US 09/141,764
FILING DATE: 27-AUG-1998
APPLICATION NUMBER: US 09/507,345
FILING DATE: 18-FEB-2000

ATTORNEY/AGENT INFORMATION:

NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003510US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: modified_base
LOCATION: 16

OTHER INFORMATION: /mod_base= OTHER

/note= "N = thymidine modified by minor groove binder moiety
represented by X, where m = two
4-amino-N-methylpyrrol-2-carboxylic acid residues"

US-09-739-928-5
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 373

US-09-739-928-6/c
; Sequence 6, Application US/09739928
; Patent No. 6486308

GENERAL INFORMATION:

APPLICANT: Kutyavin, Igor V.
Lukhtanov, Eugeny A.
Gamber, Howard B.
Meyer Jr., Rich B.

TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
Groove Binder Conjugates

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/739,928
FILING DATE: 11-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
APPLICATION NUMBER: US 09/141,764
FILING DATE: 27-AUG-1998
APPLICATION NUMBER: US 09/507,345
FILING DATE: 18-FEB-2000

ATTORNEY/AGENT INFORMATION:

NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003510US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: modified_base

LOCATION: 16

OTHER INFORMATION: /mod_base= OTHER

/note= "N = thymidine modified by minor groove binder moiety
represented by X, where m = three
4-amino-N-methylpyrrol-2-carboxylic acid residues"

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-739-928-6

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;


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; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1682:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-1682
;
; Query Match 0.9%; Score 15; DB 1; Length 17;
; Best Local Similarity 100.0%; Pred. No. 2.8e+02;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 257 CCCACGGAGCAGCAC 271
; DB 15 CCCACGGAGCAGCAC 1
;
; RESULT 377
; US-08-985-162-35
; Sequence 35, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
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two

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; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-35
;
; Query Match 0.9%; Score 15; DB 1; Length 17;
; Best Local Similarity 86.7%; Pred. No. 2.8e+02;
; Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
; QY 907 CAGCCTCCAGAGGAT 921
; DB 3 CAGCCUCCAGAGGAU 17
;
; RESULT 378
; US-09-071-845-1682/c
; Sequence 1682, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
```

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1682:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1682

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 CCCACGGAGCAGCAC 271
Db 15 CCCACGGAGCAGCAC 1

RESULT 379
US-08-584-040-2549/c
Sequence 2549, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2549:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-2549

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAAAAAA 3

RESULT 380
US-08-584-040-2552/c
Sequence 2552, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

```
;
;   TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 2552:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 17 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;
US-08-584-040-2552

Query Match          0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 381
US-09-475-947A-118/c
; Sequence 118, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
; LENGTH: 17
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-118

Query Match          0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 382
US-09-300-958A-63/c
; Sequence 63, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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;
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-63

Query Match          0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 383
US-09-371-772B-1073/c
; Sequence 1073, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1073

Query Match          0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAAAAAA 3

RESULT 384
US-09-371-772B-1076/c
; Sequence 1076, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
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US-09-371-772B-1076

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 385

US-09-401-063-35
; Sequence 35, Application US/09401063
; Patent No. 6623962

GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:

CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-401-063-35

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 907 CAGCCTCCAGAGGAT 921
Db 3 CAGCCUCCAGAGGAU 17

RESULT 386

US-09-437-076-1

; Sequence 1, Application US/09437076
; Patent No. 6261779
; GENERAL INFORMATION:
; APPLICANT: Barber-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form c
; CURRENT APPLICATION NUMBER: US/09/437,076
; CURRENT FILING DATE: 1999-11-09
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Word for Windows
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized

US-09-437-076-1

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 4 AAAAAAAAAAAAAA 18

RESULT 387

US-09-437-076-2/c
; Sequence 2, Application US/09437076
; Patent No. 6261779
; GENERAL INFORMATION:
; APPLICANT: Barber-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form c
; CURRENT APPLICATION NUMBER: US/09/437,076
; CURRENT FILING DATE: 1999-11-09
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Word for Windows
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized

US-09-437-076-2

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 18 AAAAAAAAAAAAAA 4

RESULT 388

US-09-349-035-2/c
; Sequence 2, Application US/09349035
; Patent No. 6414135
; GENERAL INFORMATION:
; APPLICANT: Cook, Philip Dan


```
; APPLICANT: Wang, Tingmin
; APPLICANT: Manoharan, Muthiah
; APPLICANT: An, Haoyun
; TITLE OF INVENTION: C3'-Methylene Hydrogen Phosphonate Monomers and Related Compounds
; FILE REFERENCE: IS18-3311
; CURRENT APPLICATION NUMBER: US/09/349,035
; CURRENT FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: M=2'-O-methyl nucleotide; *=3'-methylenephosphonate linkage
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: n=5-methyluridine
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: M=2'-O-methyl nucleotide
; US-09-349-035-2

Query Match          0.9%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAA 1

RESULT 389
US-08-534-479-1/c
; Sequence 1, Application US/08534479
; Patent No. 5851769
; GENERAL INFORMATION:
; APPLICANT: GRAY, JOE W.
; APPLICANT: WEIER, HEINZ-ULRICH G.
; TITLE OF INVENTION: QUANTITATIVE FIBER MAPPING
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,479
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MACKNIGHT, KAMRIN T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: LBL-01754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

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; MOLECULE TYPE: DNA (genomic)
US-08-534-479-1

Query Match          0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      857 CTGCAGGAAGAGGAA 871
Db      15 CTGCAGGAAGAGGAA 1

RESULT 390
US-09-676-610B-116/c
; Sequence 116, Application US/09676610B
; Patent No. 6444465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-676-610B-116

Query Match          0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      907 CAGCCTCCAGAGGAT 921
Db      15 CAGCCTCCAGAGGAT 1

RESULT 391
US-09-965-599-4/c
; Sequence 4, Application US/099655599
; Patent No. 6555670
; GENERAL INFORMATION:
; APPLICANT: Aizawa, Akira
; APPLICANT: Kawakami, Akiko
; APPLICANT: Kondo, Toshihiko
; TITLE OF INVENTION: Testis-Specific Gene
; FILE REFERENCE: 6920/0J871
; CURRENT APPLICATION NUMBER: US/09/965,599
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer HT15-C
; US-09-965-599-4

Query Match          0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1750
Db      19 AAAAAAAAAAAAAA 5
```

```
RESULT 392
US-08-031-147A-57
; Sequence 57, Application US/08031147A
; Patent No. 5514577
; GENERAL INFORMATION:
; APPLICANT: Draper et al.
; TITLE OF INVENTION: Oligonucleotide Therapies for
; TITLE OF INVENTION: Modulating the Effects of Herpesviruses
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5514577ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,147A
; FILING DATE: March 12, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 485,297
; FILING DATE: February 26, 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,132
; FILING DATE: April 28, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 954,185
; FILING DATE: September 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISIS-0469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
US-08-031-147A-57

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGGG 1036
Db 1 TTGGGGTTGGGGTTGGGG 18

RESULT 393
US-08-482-115B-36/c
; Sequence 36, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115B-36

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGGG 1036
Db 18 TTGGGGTTGGGGTTGGGG 1

RESULT 394
US-08-482-115B-37/c
; Sequence 37, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
```

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115B-37

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1017 GGTGGGATGGGGCTGG 1034
Db 18 GGTGGGGTGGGGTTGG 1

RESULT 395
US-08-403-888A-38
; Sequence 38, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

US-08-403-888A-38
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGG 1036
Db 1 TTGGGGTGGGGTTGGG 18

RESULT 396
US-08-403-888A-54
; Sequence 54, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/954,185
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-888A-54

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGG 1036
Db 1 TTGGGGTGGGGTTGGG 18

RESULT 397
US-08-403-888A-111
; Sequence 111, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,888A
FILING DATE: 12-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/954,185
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1229
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-403-888A-111

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGG 1036
||||| ||||| |||||
Db 1 TTGGGGTTGGGGTTGGGG 18

RESULT 398
US-08-472-802C-35/c
Sequence 35, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-35

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGG 1036
||||| ||||| |||||
Db 18 TTGGGGTTGGGGTTGGGG 1

RESULT 399
US-08-472-802C-36/c
Sequence 36, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-36

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1017 GGTGGGATGGGGCTGG 1034
Db 18 GGTGGGTTGGGGTTGG 1

RESULT 400
US-09-161-015-26
; Sequence 26, Application US/09161015A
; Patent No. 5965370
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF RHO G EXPRESSION
; FILE REFERENCE: RTS-0015
; CURRENT APPLICATION NUMBER: US/09/161,015A
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-161-015-26

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1507 CCGCTGGATGGGCACATC 1524
Db 1 CAGCAGGATGGGCACATC 18

RESULT 401
US-09-214-178-9
; Sequence 9, Application US/09214178
; Patent No. 6294332
; GENERAL INFORMATION:
; APPLICANT: CHABOT, Benoit
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR MODULATING THE LENGTH OF
; TITLE OF INVENTION: TELOMERES
; FILE REFERENCE: 13024.2
; CURRENT APPLICATION NUMBER: US/09/214,178
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/CA97/00471
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/020,956
; PRIOR FILING DATE: 1996-07-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-214-178-9

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGG 1036
Db 1 TTGGGGTTGGGGTTGGG 18

RESULT 402
US-08-584-040-3043/c
; Sequence 3043, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3043:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-3043

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 773 GAGGTGAAGTCTGGGGC 790
Db 18 GAGTTGTAGTCTGGGGC 1

RESULT 403
US-09-387-341-169
; Sequence 169, Application US/09387341
; Patent No. 6410323
; GENERAL INFORMATION:
; APPLICANT: Roberts, M. Luisa
; APPLICANT: Cowser, Lex M.
; TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0404
; CURRENT APPLICATION NUMBER: US/09/387,341
; CURRENT FILING DATE: 1999-08-31

EARLIER APPLICATION NUMBER: 09/156,424
EARLIER FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 09/156,979
EARLIER FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 09/156,807
EARLIER FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 09/161,015
EARLIER FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 169
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-387-341-169

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1507 CCGTGGATGGGCACATC 1524
| | | | | | | | | | | | | | | | | |
Db 1 CAGCAGGATGGGCACATC 18

RESULT 404
US-08-275-951-32/c
Sequence 32, Application US/08275951
Patent No. 6451968
GENERAL INFORMATION:
APPLICANT: Egholm, Michael
APPLICANT: Kiely, John
APPLICANT: Griffin, Michael
APPLICANT: Coull, James M.
APPLICANT: Neilsen, Peter
APPLICANT: Buchardt, Ole
APPLICANT: Dueholm, Kim L.
APPLICANT: Christensen, Leif
TITLE OF INVENTION: Linked Peptide Nucleic Acids
FILE REFERENCE: ISIS1577
CURRENT APPLICATION NUMBER: US/08/275,951
CURRENT FILING DATE: 1994-07-15
PRIOR APPLICATION NUMBER: 08/108,591
PRIOR FILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: 08/088,658
PRIOR FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/088,661
PRIOR FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: PCT/EP92/01219
PRIOR FILING DATE: 1992-05-22
PRIOR APPLICATION NUMBER: 986/91
PRIOR FILING DATE: 1991-05-22
PRIOR APPLICATION NUMBER: 987/91
PRIOR FILING DATE: 1991-05-24
PRIOR APPLICATION NUMBER: 510/92
PRIOR FILING DATE: 1991-04-15
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence
NAME/KEY: misc feature
LOCATION: (9)..(10)
OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine, Amino
OTHER INFORMATION: Hexanoic Acid, Lysine Linkage
US-08-275-951-32

Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAGAGAAAAAAAAACAAA 1
RESULT 405
US-08-275-951-33/c
Sequence 33, Application US/08275951
Patent No. 6451968
GENERAL INFORMATION:
APPLICANT: Egholm, Michael
APPLICANT: Kiely, John
APPLICANT: Griffin, Michael
APPLICANT: Coull, James M.
APPLICANT: Neilsen, Peter
APPLICANT: Buchardt, Ole
APPLICANT: Dueholm, Kim L.
APPLICANT: Christensen, Leif
TITLE OF INVENTION: Linked Peptide Nucleic Acids
FILE REFERENCE: ISIS1577
CURRENT APPLICATION NUMBER: US/08/275,951
CURRENT FILING DATE: 1994-07-15
PRIOR APPLICATION NUMBER: 08/108,591
PRIOR FILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: 08/088,658
PRIOR FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/088,661
PRIOR FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: PCT/EP92/01219
PRIOR FILING DATE: 1992-05-22
PRIOR APPLICATION NUMBER: 986/91
PRIOR FILING DATE: 1991-05-22
PRIOR APPLICATION NUMBER: 987/91
PRIOR FILING DATE: 1991-05-24
PRIOR APPLICATION NUMBER: 510/92
PRIOR FILING DATE: 1991-04-15
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence
NAME/KEY: misc feature
LOCATION: (9)..(10)
OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine, Amino
OTHER INFORMATION: Hexanoic Acid, Lysine Linkage
US-08-275-951-33

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAGAGAAAAAAAAACAAA 1

RESULT 406
US-09-057-351-35/c
Sequence 35, Application US/09057351
Patent No. 6548298
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/057,351
;; FILING DATE: 08-APR-1994
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/272,102
;; FILING DATE: 07-JUL-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/330,123
;; FILING DATE: 27-OCT-1994
;;
;; APPLICATION NUMBER: US 08/472,802
;; FILING DATE: 07-JUN-1995
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Storella, John R.
;; REGISTRATION NUMBER: 32,944
;; REFERENCE/DOCKET NUMBER: 015389-000821US
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 35:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;;
US-09-057-351-35
;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1019 TTGGGGATGGGCTGGG 1036
Db 18 TTGGGGTTGGGTTGGG 1
;
RESULT 407
US-09-057-351-36/c
; Sequence 36, Application US/09057351
; Patent No. 6548298
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
;
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/057,351
;; FILING DATE: 08-APR-1994
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/272,102
;; FILING DATE: 07-JUL-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/330,123
;; FILING DATE: 27-OCT-1994
;;
;; APPLICATION NUMBER: US 08/472,802
;; FILING DATE: 07-JUN-1995
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Storella, John R.
;; REGISTRATION NUMBER: 32,944
;; REFERENCE/DOCKET NUMBER: 015389-000821US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 36:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;;
US-09-057-351-36
;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1017 GGTGGGATGGGCTGG 1034
Db 18 GGTGGGTTGGGTTGG 1
;
RESULT 408
US-09-371-772B-1471/c
; Sequence 1471, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1471
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-09-371-772B-1471
;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 773 GAGGTGAGTCTGGGGC 790
Db 18 GAGTTGTAGTCTGGGGC 1

RESULT 409
PCT-US94-02471-57
; Sequence 57, Application PC/TUS9402471
; GENERAL INFORMATION:
; APPLICANT: Draper et al.
; TITLE OF INVENTION: Oligonucleotide Therapies for
; TITLE OF INVENTION: Modulating the Effects of Herpesviruses
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02471
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 485,297
; FILING DATE: February 26, 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,132
; FILING DATE: April 28, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 954,185
; FILING DATE: September 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISIS-0469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
PCT-US94-02471-57

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGG 1036
Db 1 TTGGGGTTGGGGTTGGG 18

RESULT 410
US-09-672-717-2/c
; Sequence 2, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001

; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-09-672-717-2

Query Match 0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 900 CCTGAGCCAGCCTCCAGA 917
Db 18 CCTGAGCCACCCTCTAGA 1

RESULT 411
US-09-050-159-12/c
; Sequence 12, Application US/09050159A
; Patent No. 6197505
; GENERAL INFORMATION:
; APPLICANT: No. 6197505berg, Leif T
; APPLICANT: Andersson, Maria K
; APPLICANT: Linstrom, Per H
; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
; FILE REFERENCE: 1248/1D042
; CURRENT APPLICATION NUMBER: US/09/050,159A
; CURRENT FILING DATE: 1998-03-27
; EARLIER APPLICATION NUMBER: 60/042,930
; EARLIER FILING DATE: 1987-04-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-09-050-159-12

Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1385 AGCCAGGTCAGGAGGA 1400
Db 16 AGCCAGGTCAGGGGA 1

RESULT 412
US-09-866-108A-7877
; Sequence 7877, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7877
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7877

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 834 GGAAGCTGCTGGGGTC 849
Db 2 GGGAGCTGCTGGGGTC 17

RESULT 413
US-09-866-108A-7878
; Sequence 7878, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7878
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7878

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 834 GGAAGCTGCTGGGGTC 849
Db 1 GGGAGCTGCTGGGGTC 16

RESULT 414
US-09-161-244-71
; Sequence 71, Application US/09161244
; Patent No. 6004814
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowser, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD71 EXPRESSION
; FILE REFERENCE: RTS-0007
; CURRENT APPLICATION NUMBER: US/09/161,244
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 71
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-161-244-71

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 GGCTTCTGGGCCCTC 744
Db 3 GGCTTCTGGTCCCTC 18

RESULT 415
US-09-920-760-49/c
; Sequence 49, Application US/09920760
; Patent No. 6492173
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION
; FILE REFERENCE: RTS-0275
; CURRENT APPLICATION NUMBER: US/09/920,760
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 49
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-760-49

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1518 GCACATCTGTGCAAG 1533

Db 17 GCACATCTTGGCGAAG 2

RESULT 416

US-09-077-619-6

; Sequence 6, Application US/09077619

; Patent No. 6500614

; GENERAL INFORMATION:

; APPLICANT: ARGUELLO, Rafael

; APPLICANT: AVAKIAN, Hovanes

; APPLICANT: MADRIGAL, Alejandro

; TITLE OF INVENTION: METHOD FOR IDENTIFYING AN UNKNOWN ALLELE

; FILE REFERENCE: 028979/0104

; CURRENT APPLICATION NUMBER: US/09/077,619

; CURRENT FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: PCT/GB96/02959

; PRIOR FILING DATE: 1996-11-29

; PRIOR APPLICATION NUMBER: GB 9524381.2

; PRIOR FILING DATE: 1995-11-29

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-077-619-6

Query Match 0.8%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 CAGCCTCCAGAGGATG 922

Db 2 CACCCTCCAGAGGATG 17

RESULT 417

US-09-663-834A-35/c

; Sequence 35, Application US/09663834A

; Patent No. 6613567

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION

; FILE REFERENCE: RTS-0033

; CURRENT APPLICATION NUMBER: US/09/663,834A

; CURRENT FILING DATE: 2000-09-15

; NUMBER OF SEQ ID NOS: 48

; SEQ ID NO 35

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-663-834A-35

Query Match 0.8%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1650 TCTCCCTGACATCCAC 1665

Db 16 TCTGCCTGACATCCAC 1

RESULT 418

US-09-053-293-4

; Sequence 4, Application US/09053293

; Patent No. 6218597

; GENERAL INFORMATION:

; APPLICANT: PORT, J. D.

; APPLICANT: BRISTOW, MICHAEL R.

; TITLE OF INVENTION: "TRANSGENIC MODEL AND TREATMENT FOR

; TITLE OF INVENTION: HEART DISEASE"

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SHERIDAN ROSS P.C.

; STREET: 1700 LINCOLN ST., SUITE 3500

; CITY: DENVER

; STATE: COLORADO

; COUNTRY: USA

; ZIP: 80203

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/053,293

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/041,966

; FILING DATE: 03-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: CROOK, WANNELL M.

; REGISTRATION NUMBER: 31,071

; REFERENCE/DOCKET NUMBER: 3595-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 863-9700

; TELEFAX: (303) 863-0223

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "primer"

US-09-053-293-4

Query Match 0.8%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 3.9e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 CAGAGGCTCGGGCTT 125

Db 2 CAGCGGCTCGGGCTT 17

RESULT 419

US-09-422-375-42/c

; Sequence 42, Application US/09422375

; Patent No. 6534633

; GENERAL INFORMATION:

; APPLICANT: Weidanz, Jon A.

; APPLICANT: Card, Kimberly F.

; APPLICANT: Sherman, Linda A.

; APPLICANT: Klinman, No. 6534633man

; APPLICANT: Wong, Hing C.

; TITLE OF INVENTION: POLYSPECIFIC BINDING MOLECULES AND USES THEREOF

; FILE REFERENCE: 48531

; CURRENT APPLICATION NUMBER: US/09/422,375

; CURRENT FILING DATE: 1999-10-21

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 42

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-422-375-42

Query Match 0.8%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 3.9e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 527 ATGAGCCCCGCCACC 542
Db 19 ATGAGCCCCCTCCACC 4

RESULT 420
US-09-526-193A-148
; Sequence 148, Application US/09526193A
; Patent No. 6617122
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Pimstone, Simon N.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: CHOLESTEROL LEVELS
; FILE REFERENCE: 50110/002005
; CURRENT APPLICATION NUMBER: US/09/526,193A
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-193A-148

Query Match 0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1184 GCTCCCGAGCCCATCCT 1199
Db 4 GCTACCAGCCCATCCT 19

RESULT 421
US-08-882-649A-7
; Sequence 7, Application US/08882649A
; Patent No. 6344316
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; APPLICANT: Chee, Mark
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chaoqiang, Lai
; APPLICANT: Wodicka, Lisa
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Lee, Danny
; APPLICANT: Tran, Huu M.
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: McGall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joe Liebeschuetz
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/882,649A
; FILING DATE: 25-Jun-1997
; CLASSIFICATION: 435-006.000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,471
; FILING DATE: 23-JAN-1996
; APPLICATION NUMBER: US 60/035,170
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: PCT/US97/01603
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-019410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; FEATURES:
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-882-649A-7

Query Match 0.8%; Score 14.2; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAIAAAAAAAAA 1749
Db 1 CVAIAAAAAAAAAAAAA 15

RESULT 422
US-08-173-489C-75
; Sequence 75, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880

; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; DESCRIPTION: esterase D gene (Accession # M13450)
; DESCRIPTION: nucleotides 962 to 975
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: chromosome 13
; MAP POSITION: 13q14.1-q14.2
; PUBLICATION INFORMATION:
; AUTHORS: Lee, E Y H P, Lee, W H.
; TITLE: Molecular cloning of the
; TITLE: human esterase D gene, a genetic marker of
; TITLE: retinoblastoma
; JOURNAL: Proceedings of the National Academy of
; JOURNAL: Sciences, USA
; VOLUME: 83
; PAGES: 6337-6341
; DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO: 75 :FROM 1 TO 14
US-08-173-489C-75

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 423
US-08-173-489C-76/c
; Sequence 76, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173.489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from esterase D
; DESCRIPTION: sequence region in Seq ID No. 586124475
; HYPOTHETICAL: Yes
; ANTI-SENSE: No
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 76 :FROM 1 TO 14
US-08-173-489C-76

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 424
US-08-832-021-16/c
; Sequence 16, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-16

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAA 1747
Db 14 AAAAAAAAAAAAAA 1

RESULT 425
US-08-724-466B-14/c
; Sequence 14, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9

COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-724-466B-14

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAA 1747
Db 14 ACAAAAAAAAAAAAA 1

RESULT 426

US-09-019-095A-26/c
Sequence 26, Application US/09019095A
Patent No. 6287858
GENERAL INFORMATION:
APPLICANT: D'Andrea, Alan D.
TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
TITLE OF INVENTION: Cell Growth
FILE REFERENCE: DFCI-435p2A2
CURRENT APPLICATION NUMBER: US/09/019,095A
CURRENT FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: PCT/US96/12884
PRIOR FILING DATE: 1996-08-07
PRIOR APPLICATION NUMBER: US 60/002,066
PRIOR FILING DATE: 1995-08-09
PRIOR APPLICATION NUMBER: US 60/019,787
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 14
TYPE: DNA
ORGANISM: murine
US-09-019-095A-26

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAA 1747
Db 14 ACAAAAAAAAAAAAA 1

RESULT 427

US-08-882-164D-14/c

Sequence 14, Application US/08882164D
Patent No. 6306624
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,164D
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-882-164D-14

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAA 1747
Db 14 ACAAAAAAAAAAAAA 1

RESULT 428

US-09-462-569B-1/c
Sequence 1, Application US/09462569B
Patent No. 6392124
GENERAL INFORMATION:
APPLICANT: PONZ ASCASO, Fernando
APPLICANT: TORRES PASCUAL, Vicente
APPLICANT: SANCHEZ SANCHEZ, Florentina
APPLICANT: MARTINEZ HERRERA, David
TITLE OF INVENTION: INFECTIOUS VECTORS AND CLONES OF PLANTS DERIVED FROM
TITLE OF INVENTION: THE TURNIP MOSAIC VIRUS (TMV)
FILE REFERENCE: P/613-110
CURRENT APPLICATION NUMBER: US/09/462,569B
CURRENT FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: PCT/ES98/00200
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: ES P 9701522
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 14

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 427

US-08-882-164D-14/c

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-462-569B-1

```

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

```

RESULT 429
US-09-619-103-20
; Sequence 20, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-20

```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1736	AAAAAAAAAAAAAA	1749
Db	1	AAAAAAAAAAAAAA	14

RESULT 430
5453496-4/c
; Patent No. 5453496
; APPLICANT: CARUTHERS, MARVIN H.; MARSHALL, WILLIAM S.; BRILL,
; WOLFGANG; NIELSEN, JOHN
; TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,140
; FILING DATE: 15-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 793,171
; FILING DATE: 18-NOV-1991
; APPLICATION NUMBER: 545,238
; FILING DATE: 27-JUN-1990
; APPLICATION NUMBER: 332,247
; FILING DATE: 31-MAR-1989
; APPLICATION NUMBER: 198,886
; FILING DATE: 26-MAY-1988
; SEQ ID NO:4:
; LENGTH: 14
5453496-4

Query Match 0.8%; Score 14; DB 1; Length 14;

```

Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
    |||||
Db 14 AAAAAAAAAAAAAA 1

```

RESULT 431
5453496-5
; Patent No. 5453496
; APPLICANT: CARUTHERS, MARVIN H.; MARSHALL, WILLIAM S.; BRILL,
; WOLFGANG; NIELSEN, JOHN
; TITLE OF INVENTION: POLYNUCLEOTIDE PHOSPHORODITHIOATE
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,140
; FILING DATE: 15-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 793,171
; FILING DATE: 18-NOV-1991
; APPLICATION NUMBER: 545,238
; FILING DATE: 27-JUN-1990
; APPLICATION NUMBER: 332,247
; FILING DATE: 31-MAR-1989
; APPLICATION NUMBER: 198,886
; FILING DATE: 26-MAY-1988
; SEQ ID NO:5:
; LENGTH: 14
5453496-5

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 432
US-08-452-196A-3
; Sequence 3, Application US/08452196A
; Patent No. 5576427
; GENERAL INFORMATION:
; APPLICANT: Cook, Philip D.
; APPLICANT: Delecki, Daniel J.
; APPLICANT: Guinasso, Charles
; TITLE OF INVENTION: ACYCLIC NUCLEOSIDE
; TITLE OF INVENTION: ANALOGS AND
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; TITLE OF INVENTION: CONTAINING THEM
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Department
; STREET: 9 Great Valley Parkway
; CITY: Malvern
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19355
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.4 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.0B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,196A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/040,326

APPLICATION NUMBER: 08/040,326

; FILING DATE: 30 March 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul E. Dupont
; REGISTRATION NUMBER: 27,438
; REFERENCE/DOCKET NUMBER: 2525
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)889-6338
; TELEFAX: (215)889-8800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: Nucleic Acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Nucleic Acid
; DESCRIPTION:
; ANTI-SENSE: yes
; ORIGINAL SOURCE: synthesized
; FEATURE:
; LOCATION: 14
; OTHER INFORMATION: 8-[2,2-bis
; OTHER INFORMATION: (methoxymethyl)
; OTHER INFORMATION: propoxy]-9-
; OTHER INFORMATION: methyladenosine
US-08-452-196A-3

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred.No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 433
US-08-452-196A-4
; Sequence 4, Application US/08452196A
; Patent No. 5576427
; GENERAL INFORMATION:
; APPLICANT: Cook, Philip D.
; APPLICANT: Delecki, Daniel J.
; APPLICANT: Guinasso, Charles
; TITLE OF INVENTION: ACYCLIC NUCLEOSIDE
; TITLE OF INVENTION: ANALOGS AND
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES
; TITLE OF INVENTION: CONTAINING THEM
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Department
; STREET: 9 Great Valley Parkway
; CITY: Malvern
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19355
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.4 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.0B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,196A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/040,326
; FILING DATE: 30 March 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul E. Dupont
; REGISTRATION NUMBER: 27,438
; REFERENCE/DOCKET NUMBER: 2525

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)889-6338
; TELEFAX: (215)889-8800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: Nucleic Acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Nucleic Acid
; DESCRIPTION:
; ANTI-SENSE: yes
; ORIGINAL SOURCE: synthesized
; FEATURE:
; LOCATION: 13
; OTHER INFORMATION: 8-[2,2-bis
; OTHER INFORMATION: (methoxymethyl)
; OTHER INFORMATION: propoxy]-9-
; OTHER INFORMATION: methyladenosine
US-08-452-196A-4

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred.No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 434
US-08-291-932A-16
; Sequence 16, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-291-932A-16

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 3.3e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 727 CAGGCTTCTGGGCC 740
|||||:|:|||||
Db 1 CAGGCUUCUGGGCC 14

RESULT 435
US-08-292-620A-56/c
; Sequence 56, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid

two

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-56

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 CCCACGGAGCAGCA 270
|||||:|:|||||
Db 14 CCCACGGAGCAGCA 1

RESULT 436
US-08-292-620A-360/c
; Sequence 360, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-360

two

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 15 AAAAAAAAAAAAAA 2

RESULT 437

US-08-292-620A-363/c
; Sequence 363, Application US/08292620A
; Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 363:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-363

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 438

US-08-292-620A-597/c
; Sequence 597, Application US/08292620A
; Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 597:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-597

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 257 CCCACGGAGCAGCA 270
Db 14 CCCACGGAGCAGCA 1

RESULT 439

US-08-832-021-62/c
; Sequence 62, Application US/08832021
; Patent No. 6045998

GENERAL INFORMATION:

APPLICANT: Combates, N.
APPLICANT: Pardini, J.
APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-62

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1747
|||||
Db 14 ACAAAAAAAAAAAAAA 1

RESULT 440
US-08-832-021-63/c
; Sequence 63, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-63

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1747
|||||
Db 14 ACAAAAAAAAAAAAAA 1

RESULT 441
US-08-832-021-64/c
; Sequence 64, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-64

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1747
|||||
Db 14 ACAAAAAAAAAAAAAA 1

RESULT 442
US-09-071-845-56/c
; Sequence 56, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-071-845-56

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 257 CCCACGGAGCAGCA 270
Db 14 CCCACGGAGCAGCA 1

RESULT 443

US-09-071-845-360/c
; Sequence 360, Application US/09071845
; Patent No. 6132967

; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-071-845-360

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749

Db 15 AAAAAAAAAAAAAA 2

RESULT 444

US-09-071-845-363/c
; Sequence 363, Application US/09071845
; Patent No. 6132967

; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 363:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-363

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 445

US-09-071-845-597/c
; Sequence 597, Application US/09071845

; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 597:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-071-845-597

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 CCCACGGAGCAGCA 270
Db 14 CCCACGGAGCAGCA 1

RESULT 446
US-09-475-947A-158/c
; Sequence 158, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667

; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 15
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: n signifies a, t, c or g.
US-09-475-947A-158

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 447

US-08-087-387-6/c
; Sequence 6, Application US/08087387
; Patent No. 5473060
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic and therapeutic applica
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,387
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-087-387-6

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3

RESULT 448

US-08-455-627-6/c
; Sequence 6, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-627-6

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3

RESULT 449
US-08-461-271-6/c
; Sequence 6, Application US/08461271
; Patent No. 5741643
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-461-271-6

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3

RESULT 450
US-08-713-685A-6/c
; Sequence 6, Application US/08713685A
; Patent No. 5817795
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,685A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,271
; FILING DATE:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-713-685A-6

```
Query Match      0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3

RESULT 451
US-08-689-856-6/c
; Sequence 6, Application US/08689856
; Patent No. 5830658.
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-689-856-6

Query Match      0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3

RESULT 452
US-08-822-028-23
; Sequence 23, Application US/08822028
; Patent No. 5993813
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHOLOM, JEFFREY
; APPLICANT: SCHOLOM, JEFFREY
```

```
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUANE C ULMER
; STREET: P.O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,028
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-37,075C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-822-028-23

Query Match      0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16

RESULT 453
US-08-822-028-39
; Sequence 39, Application US/08822028
; Patent No. 5993813
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHOLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUANE C ULMER
; STREET: P.O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,028
```

```
;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-37,075C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-822-028-39
;
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16

RESULT 454
US-09-070-477-6/c
; Sequence 6, Application US/09070477
; Patent No. 6048974
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,685
; FILING DATE:
; APPLICATION NUMBER: 08/461,271
; FILING DATE:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-09-070-477-6
;
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3

RESULT 455
US-08-479-285-23
; Sequence 23, Application US/08479285
; Patent No. 6207815
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHOLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUANE C ULMER
; STREET: P.O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,285
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040687
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-37,075C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-479-285-23
;
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16

RESULT 456..
US-08-479-285-39
; Sequence 39, Application US/08479285
; Patent No. 6207815
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
```

APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, WH KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P.O. BOX 1967
CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,285
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040687
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-479-285-39
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16
RESULT 457
US-08-882-649A-8/c
Sequence 8, Application US/08882649A
Patent No. 6344316
GENERAL INFORMATION:
APPLICANT: Lockhart, David J.
Chee, Mark
Gunderson, Kevin
Chaoqiang, Lai
Wodicka, Lisa
Cronin, Maureen T.
Lee, Danny
Tran, Huu M.
Matsuzaki, Hajime
McGall, Glenn H.
TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joe Liebeschuetz
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,649A
FILING DATE: 25-Jun-1997
CLASSIFICATION: 435-006.000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,471
FILING DATE: 23-JAN-1996
APPLICATION NUMBER: US 60/035,170
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: PCT/US97/01603
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-019410US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-882-649A-8
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3
RESULT 458
US-09-503-653A-23
Sequence 23, Application US/09503653A
Patent No. 6641999
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S
APPLICANT: Gourlie, Brian B
APPLICANT: Rixon, Mark W
APPLICANT: Anderson, WH Kerr
APPLICANT: Kaplan, Donald A
APPLICANT: Schlom, Jeffrey
TITLE OF INVENTION: Probing Method for Identifying Antibodies
TITLE OF INVENTION: Specific for Selected Antigens
FILE REFERENCE: 37075H-CIP1
CURRENT APPLICATION NUMBER: US/09/503,653A
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 08/040,687
PRIOR FILING DATE: 1993-03-31
PRIOR APPLICATION NUMBER: US 07/424,362
PRIOR FILING DATE: 1989-10-19
PRIOR APPLICATION NUMBER: US 07/261,942
PRIOR FILING DATE: 1988-10-24
PRIOR APPLICATION NUMBER: US 07/259,943
PRIOR FILING DATE: 1988-10-19
NUMBER OF SEQ ID NOS: 74
SOFTWARE: MICROSOFT Word 97 SR-2
SEQ ID NO 23
LENGTH: 16


```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..16
; OTHER INFORMATION: Oligo JH2(-)
US-09-503-653A-23

Query Match      0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1396 GAGGAGACTGTGAG 1409
Db      3 GAGGAGACTGTGAG 16

RESULT 459
US-09-503-653A-39
; Sequence 39, Application US/09503653A
; Patent No. 6641999
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S
; APPLICANT: Gourlie, Brian B
; APPLICANT: Rixon, Mark W
; APPLICANT: Anderson, WH Kerr
; APPLICANT: Kaplan, Donald A
; APPLICANT: Schlom, Jeffrey
; TITLE OF INVENTION: Probing Method for Identifying Antibodies
; TITLE OF INVENTION: Specific for Selected Antigens
; FILE REFERENCE: 37075H-CIP1
; CURRENT APPLICATION NUMBER: US/09/503,653A
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 08/040,687
; PRIOR FILING DATE: 1993-03-31
; PRIOR APPLICATION NUMBER: US 07/424,362
; PRIOR FILING DATE: 1989-10-19
; PRIOR APPLICATION NUMBER: US 07/261,942
; PRIOR FILING DATE: 1988-10-24
; PRIOR APPLICATION NUMBER: US 07/259,943
; PRIOR FILING DATE: 1988-10-19
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: MICROSOFT Word 97 SR-2
; SEQ ID NO 39
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..16
; OTHER INFORMATION: Oligo JH2(-)
US-09-503-653A-39

Query Match      0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1396 GAGGAGACTGTGAG 1409
Db      3 GAGGAGACTGTGAG 16

RESULT 460
US-08-584-040-2548/c
; Sequence 2548, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
```

```
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2548:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2548

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      17 AAAAAAAAAAAAAA 4

RESULT 461
US-08-584-040-2553/c
; Sequence 2553, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
```

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2553:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-2553

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 462
US-09-371-772B-1072/c
Sequence 1072, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1072
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-1072

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 17 AAAAAAAAAAAAAA 4

RESULT 463
US-09-371-772B-1077/c
Sequence 1077, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1077
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-1077

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 464
US-08-373-124A-196/c
Sequence 196, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132

;
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 196:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-373-124A-196
;
; Query Match 0.8%; Score 13.8; DB 1; Length 17;
; Best Local Similarity 88.2%; Pred. No. 4.1e+02;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
Qy 861 AGGAAGAGGAGGAG 877
Db 17 AGAAAGAGGAGGAG 1
;
RESULT 465
US-08-435-628-196/c
; Sequence 196, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327

;
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 196:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-196
;
; Query Match 0.8%; Score 13.8; DB 1; Length 17;
; Best Local Similarity 88.2%; Pred. No. 4.1e+02;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
Qy 861 AGGAAGAGGAGGAG 877
Db 17 AGAAAGAGGAGGAG 1
;
RESULT 466
US-09-317-350-3/c
; Sequence 3, Application US/09317350
; Patent No. 6277607
; GENERAL INFORMATION:
; APPLICANT: Tyagi, Sanjay
; APPLICANT: Kramer, Fred R.
; APPLICANT: Vartikian, Robert
; TITLE OF INVENTION: HIGH SPECIFICITY PRIMERS, AMPLIFICATION
; TITLE OF INVENTION: METHODS AND KITS
; FILE REFERENCE: 07763-036001
; CURRENT APPLICATION NUMBER: US/09/317,350
; CURRENT FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
; US-09-317-350-3
;
; Query Match 0.8%; Score 13.8; DB 1; Length 17;
; Best Local Similarity 88.2%; Pred. No. 4.1e+02;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
Qy 242 CGGGGCCACCACCGGCC 258
Db 17 CGCGCGCACCACCGGCC 1
;
RESULT 467
US-09-334-938-3/c
; Sequence 3, Application US/09334938
; Patent No. 6331140
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle
; TITLE OF INVENTION: Mobile Genetic Elements as tools for
; TITLE OF INVENTION: genetic modification of L. Debrueckii and L. Helveticus
; FILE REFERENCE: 8265-261-999
; CURRENT APPLICATION NUMBER: US/09/334,938
; CURRENT FILING DATE: 1999-06-17
; EARLIER APPLICATION NUMBER: EP 9820228.1
; EARLIER FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence

;
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-334-938-3

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1672 GACTTGTGCACCAATG 1688
||| |||||
Db 17 GACATTGTCACCAAGG 1

RESULT 468
US-08-584-040-2130/c
; Sequence 2130, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-584-040-2130
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 771 CCGAGGTGAAGTCTGGG 787
||| |||||
Db 17 CCGAGTTGTAGTCTGGG 1

RESULT 469
US-08-584-040-2554/c
; Sequence 2554, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2554:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-584-040-2554
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1748
||| |||||
Db 17 TTGAAAAA 1

RESULT 470
US-08-584-040-2555/c
; Sequence 2555, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2554:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-584-040-2554
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1748
||| |||||
Db 17 TTGAAAAA 1

RESULT 470
US-08-584-040-2555/c
; Sequence 2555, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-584-040-2130
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 771 CCGAGGTGAAGTCTGGG 787
||| |||||
Db 17 CCGAGTTGTAGTCTGGG 1

;; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
;; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
;; TITLE OF INVENTION: GROWTH FACTOR
;; NUMBER OF SEQUENCES: 8502
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; STREET: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 2555:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-584-040-2555

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1747
Db 17 TTTGAAAAA 1

RESULT 471
US-08-584-040-7818/c
; Sequence 7818, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 7818:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-584-040-7818

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAA 1752
Db 17 AAACAAAAA 1

RESULT 472
US-08-584-040-7819/c
; Sequence 7819, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974

```
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7819:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7819

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAACAAAAA 1

RESULT 473
US-08-584-040-7820/c
; Sequence 7820, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7821:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7821

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAACAAAAA 1

RESULT 474
US-08-584-040-7821/c
; Sequence 7821, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7821:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7821

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAACAAAAA 1
```


RESULT 475

US-08-584-040-7823/c

; Sequence 7823, Application US/08584040

; Patent No. 6346398

; GENERAL INFORMATION:

; APPLICANT: Pavco, Pamela

; APPLICANT: McSwiggen, James

; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: METHOD AND REAGENT FOR THE

; TITLE OF INVENTION: TREATMENT OF DISEASES OR

; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

; TITLE OF INVENTION: GROWTH FACTOR

; NUMBER OF SEQUENCES: 8502

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/584,040

; FILING DATE: January 11, 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/005,974

; FILING DATE: October 26, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 218/064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 7823:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-584-040-7823

Query Match

Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1734 ACAAAAAAAAAAAAAA 1750

|||||

17 ACAACAACAAACAAAAA 1

Db

RESULT 476

US-08-679-645-881/c

; Sequence 881, Application US/08679645

; Patent No. 6350934

; GENERAL INFORMATION:

; APPLICANT: Zwick, Michael G.

; APPLICANT: Edington, Brent E.

; APPLICANT: McSwiggen, James A.

; APPLICANT: Merlo, Patricia Ann Owens

; APPLICANT: Guo, Lining

```
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
US-09-903-915-3

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 242 CGGGCCACCACCGGCC 258
Db 17 CGCGCGACCAACCGGCC 1

RESULT 478
US-09-474-432B-467
; Sequence 467, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 467
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-467

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 4.1e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1151 GCTACGTGGCCACCTG 1167
Db 1 GCUACGUUGCCCCCUG 17

RESULT 479
US-09-474-432B-564/c
; Sequence 564, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
```

```
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 564
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-564

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 232 CGCGGCACCCCGGGGCC 248
Db 17 CGCGGCTGCCCGGGGCC 1

RESULT 480
US-09-371-772B-675/c
; Sequence 675, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 675
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-675

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 771 CCGAGGTGAAGTCTGGG 787
Db 17 CCGAGTTGTAGTCTGGG 1

RESULT 481
US-09-371-772B-1078/c
; Sequence 1078, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
```

```
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1078
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1078

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1732 TTACAAAAA 1748
Db      17 TTGGA 1

RESULT 482
US-09-371-772B-1079/c
; Sequence 1079, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1079

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1731 TTTACAAAA 1747
Db      17 TTTGGA 1

RESULT 483
US-09-371-772B-3602/c
; Sequence 3602, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
```

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; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3602

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1736 AAAAAA 1752
Db      17 AAACA 1

RESULT 484
US-09-371-772B-3603/c
; Sequence 3603, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3603
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3603

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1736 AAAAAA 1752
Db      17 AAACA 1

RESULT 485
US-09-371-772B-3604/c
; Sequence 3604, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
```

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3604
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3604

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1735 CAAAAA... 1751
Db 17 CAAAAA... 1

RESULT 486
US-09-371-772B-3605/c
; Sequence 3605, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3605
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3605

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 AC... 1750
Db 17 AC... 1

RESULT 487
US-09-371-772B-3607/c
; Sequence 3607, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3607
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3607

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 AC... 1750
Db 17 AC... 1

RESULT 488
US-09-371-772B-5015/c
; Sequence 5015, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5015
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5015

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 772 CGAGGTGAAGTCTGGGG 788
Db 17 CGAGTTGTAGTCTGGGG 1

RESULT 489
US-09-476-387-466
; Sequence 466, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot

FILE REFERENCE: MBHB00-831-C (249/073)
CURRENT APPLICATION NUMBER: US/09/476,387
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/301,511
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 60/083,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 466
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-476-387-466

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 4.1e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1151 GCTACGTGGCCACCCTG 1167
||:||||:||||:|
Db 1 GCUACGUUGCCCCCUG 17

RESULT 490
US-09-476-387-563/c
Sequence 563, Application US/09476387
Patent No. 6617438
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
FILE REFERENCE: MBHB00-831-C (249/073)
CURRENT APPLICATION NUMBER: US/09/476,387
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/301,511
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 60/083,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 563
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-476-387-563

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 232 CGCGGACCCCGGGGCC 248
||||| |||||
Db 17 CGCGGCTGCCCGGGGCC 1

RESULT 491
US-09-827-998-484
Sequence 484, Application US/09827998
Patent No. 6656700
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDHMORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6656700
SEQ ID NO 484
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-827-998-484

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 37 AAAAAAAAAAGCCAGAAA 53
||||||| |||||
Db 1 AAAAAAAAAAGAAAGAAA 17

RESULT 492
US-09-866-108A-896
Sequence 896, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188

```
; SEQ ID NO 896
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-896

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1020 TGGGGATGGGGCTGGG 1036
      ||||| ||||| |||
Db 1 TGGGAAGGGGCTTGGG 17

RESULT 493
US-09-866-108A-7879
; Sequence 7879, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10022
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10022

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 132 CGCTGTCTGGAGTCCCC 148
      ||||| ||||| |||
Db 1 CGGTGTCTGGAGTCCCTC 17

RESULT 495
US-09-866-108A-10502
; Sequence 10502, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7879
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7879

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 835 GAAGCTGCTGGGGTCTC 851
      ||||| ||||| |||
Db 1 GGAGCTGCTGGGGTCTC 17

RESULT 494
US-09-866-108A-10022
; Sequence 10022, Application US/09866108A
```

```
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10022
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10022

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 132 CGCTGTCTGGAGTCCCC 148
      ||||| ||||| |||
Db 1 CGGTGTCTGGAGTCCCTC 17

RESULT 495
US-09-866-108A-10502
; Sequence 10502, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10022
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7879

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 835 GAAGCTGCTGGGGTCTC 851
      ||||| ||||| |||
Db 1 GGAGCTGCTGGGGTCTC 17

RESULT 494
US-09-866-108A-10022
; Sequence 10022, Application US/09866108A
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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10502
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10502

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 805 CAGAGAGCCAGGGCC 821
| | | | | | | | | |
Db 1 CGGAGAGAGCCAGGGAC 17

RESULT 496
US-09-866-108A-10504
; Sequence 10504, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188
; SEQ ID NO 10504
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10504

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 807 GAGAGAGCCAGGGCCAG 823
| | | | | | | | | |
Db 1 GAGAGAGCCAGGGACGG 17

RESULT 497
US-09-866-108A-10505
; Sequence 10505, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10505
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10505

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 808 AGAGAGCCAGGGCCAGG 824
| | | | | | | | | |
Db 1 AGAGAGCCAGGGACGGG 17

RESULT 498
US-09-866-108A-10506

```
; Sequence 10506, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10506
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10506

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      809 GAGAGCCAGGGCCAGGG 825
Db      1 GAGAGCCAGGGACGGG 17
      |||||
      |||||

RESULT 499
US-08-632-673B-9/c
; Sequence 9, Application US/08632673B
; Patent No. 5712098
; GENERAL INFORMATION:
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Gnirke, Andreas
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Ruddy, David
; APPLICANT: Wolff, Roger K.
; APPLICANT: Feder, John N.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS
; TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
```

```
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,673B
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 017957-000410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-632-673B-9

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1237 CCTGGTGCTTCACCTG 1253
Db      18 CCTGGTGCTCCACCTG 2
      |||||
      |||||

RESULT 500
US-08-752-844-52/c
; Sequence 52, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
```

```
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 18 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-752-844-52

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 297 TTGCCCCCTTCCATCTG 313
Db 17 TTGGGCCCTTCCATCTG 1

RESULT 501
US-08-591-196-52/c
; Sequence 52, Application US/08591196
; Patent No. 5977316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,196
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 18 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-591-196-52

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 297 TTGCCCCCTTCCATCTG 313
Db 17 TTGGGCCCTTCCATCTG 1

RESULT 502
US-09-280-409-13
; Sequence 13, Application US/09280409
; Patent No. 6107092
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: C. Frank Bennett
; APPLICANT: Bert W. O'Malley
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRA EXPRESSION
; FILE REFERENCE: RTS-0048
; CURRENT APPLICATION NUMBER: US/09/280,409
; CURRENT FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 13
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-280-409-13

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 768 AGCCCGAGGTGAAGTCT 784
Db 2 AGCCCGAGGAGAGTCT 18

RESULT 503
US-09-280-409-92
; Sequence 92, Application US/09280409
; Patent No. 6107092
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: C. Frank Bennett
; APPLICANT: Bert W. O'Malley
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRA EXPRESSION
; FILE REFERENCE: RTS-0048
; CURRENT APPLICATION NUMBER: US/09/280,409
; CURRENT FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 92
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-280-409-92

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 768 AGCCCGAGGTGAAGTCT 784
Db 1 AGCCCGAGGAGAGTCT 17

RESULT 504
US-09-306-595C-30
; Sequence 30, Application US/09306595C
; Patent No. 6284506
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOL PRODUCTION
; FILE REFERENCE: ISOPRENOL PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/306,595C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 98108210
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
```

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; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of 5'-adjacent region of MVK gene
US-09-306-595C-30

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 28 GGAAGAGGAAAAAAA 44
Db 1 GGAAGAGGAGAGAAAA 17

RESULT 505
US-08-584-040-8372/c
; Sequence 8372, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8372:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-8372

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of 5'-adjacent region of MVK gene
US-09-306-595C-30

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 28 GGAAGAGGAAAAAAA 44
Db 1 GGAAGAGGAGAGAAAA 17

RESULT 505
US-08-584-040-8372/c
; Sequence 8372, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8372:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-8372
```

```

QY 773 GAGGTGAAGTCTGGGG 789
Db 18 GAGTTGTAGTCTGGGG 2

RESULT 506
US-09-686-179A-2
; Sequence 2, Application US/09686179A
; Patent No. 6350580
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph
; TITLE OF INVENTION: Methods for Detection of a Target Nucleic Acid Using a
; TITLE OF INVENTION: Probe Comprising Secondary Structure
; FILE REFERENCE: 25436/1140
; CURRENT APPLICATION NUMBER: US/09/686,179A
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: synthetic oligonucleotide fragment of cleaved template
US-09-686-179A-2

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAATAAATAAAAAAAAA 17

RESULT 507
US-09-194-842A-48
; Sequence 48, Application US/09194842A
; Patent No. 6416948
; GENERAL INFORMATION:
; APPLICANT: Pilarski, Linda M.
; APPLICANT: Belch, Andrew R.
; APPLICANT: Szczepek, Agnieszka J.
; TITLE OF INVENTION: METHODS FOR DETECTION OF REARRANGED DNA
; FILE REFERENCE: STI-008USCPA
; CURRENT APPLICATION NUMBER: US/09/194,842A
; PRIOR FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: US 60/019,106
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: PCT/US97/09534
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-194-842A-48

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 982 TACTTTGGCCAGTGTGG 998
Db 1 TACTTTGACCAGTGGGG 17

RESULT 508
US-09-360-545-60
; Sequence 60, Application US/09360545
; Patent No. 6429014
```

; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wsur13885
; CURRENT APPLICATION NUMBER: US/09/360,545
; CURRENT FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide that corresponds to amino acid
; OTHER INFORMATION: sequence set forth in SEQ ID NO:49
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(18)
; OTHER INFORMATION: Oligonucleotide that corresponds to conserved
; OTHER INFORMATION: amino acid sequence set forth in SEQ ID NO:49
US-09-360-545-60

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 749 GCCCCCACCTTCTCTC 765
Db 1 GCCACCACCTTCTCTC 17

RESULT 509
US-09-293-533-52/c
; Sequence 52, Application US/09293533
; Patent No. 6509016
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,533
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-293-533-52

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 297 TTGCCCCCTTCCATCTG 313
Db 17 TTGGGCCCTTCCATCTG 1

RESULT 510
US-09-371-772B-4028/c
; Sequence 4028, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4028
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-4028

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 773 GAGGTGAAGTCTGGGG 789
Db 18 GAGTTGTAGTCTGGGG 2

RESULT 511
US-09-925-388-30
; Sequence 30, Application US/09925388
; Patent No. 6586202
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/925,388
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/306,595
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1

```
; SEQ ID NO 30
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of 5'-adjacent region of MVK gene
US-09-925-388-30

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 28 GGAAGAGGAAAAA 44
Db 1 GGAAGAGGAGAGAGAA 17

RESULT 512
US-09-981-621-2
; Sequence 2, Application US/09981621
; Patent No. 6589743
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph
; TITLE OF INVENTION: Methods for Detection of a Target Nucleic Acid Using a
; TITLE OF INVENTION: Probe Comprising Secondary Structure
; FILE REFERENCE: 25436/1140
; CURRENT APPLICATION NUMBER: US/09/981,621
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US/09/686,179
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: synthetic oligonucleotide fragment of cleaved template
US-09-981-621-2

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 513
5182262-6
; Patent No. 5182262
; APPLICANT: LETO, THOMAS
; TITLE OF INVENTION: CALMODULIN BINDING PEPTIDE DERIVATIVES
; OF NON-ERYTHROID ALPHA SPECTRIN
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,172
; FILING DATE: 02-MAR-1989
; SEQ ID NO: 6
; LENGTH: 18
5182262-6

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1156 GTGGCCACCTGGAGAA 1172
Db 1 GTGGCCACCTGGCCAA 17
```

```
RESULT 514
US-08-242-664-19
; Sequence 19, Application US/08242664
; Patent No. 5571937
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,664
; FILING DATE: May 12, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-242-664-19

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAAGAGGAGG 878
Db 1 AAGAGGAGGAGGAGG 15

RESULT 515
US-08-484-138-19
; Sequence 19, Application US/08484138
; Patent No. 5652350
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-138-19

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 864 AAGAGGAAGAGGAGG 878
Db 1 AAGAGGAGGAGGAGG 15

RESULT 516
US-08-854-041-4/c
Sequence 4, Application US/08854041
Patent No. 5916779
GENERAL INFORMATION:
APPLICANT: Pearson, Robert E.
APPLICANT: Dickson, Julie A.
APPLICANT: Mehropuyan, Majid
TITLE OF INVENTION: STRAND DISPLACEMENT AMPLIFICATION OF RNA
TITLE OF INVENTION: TARGETS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: R. J. Rodrick, Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,041
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3853
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-854-041-4

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 828 CAAAGAGGAAGCTGC 842
Db 15 CAATGAGGAAGCTGC 1

RESULT 517
US-08-863-639A-8
Sequence 8, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-8

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1745
Db 1 TTTAAAAA 15

RESULT 518
US-08-893-204C-2/c
Sequence 2, Application US/08893204C
Patent No. 6043044
GENERAL INFORMATION:
APPLICANT: Hudson, Perry B.
APPLICANT: Hakky, Said I.
APPLICANT: Meyer-Siegler, Katherine
APPLICANT: Hakki, A-Hamid
TITLE OF INVENTION: DIAGNOSTIC AND PROGNOSTIC MARKER
TITLE OF INVENTION: FOR METASTATIC ADEMOCARCINOMA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rosenberg, Klein & Bilker
STREET: 3444 Ellicott Center Drive, Suite 105
CITY: Ellicott City

```
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 21043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inches,
; MEDIUM TYPE: 1.44Mb storage
; COMPUTER: IBM
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,204C
; FILING DATE: 7/15/97
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenberg, Morton
; REGISTRATION NUMBER: 26,049
; REFERENCE/DOCKET NUMBER: MR2493-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (410) 465-6678
; TELEFAX: (410) 461-3067
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHEetical: yes
; ANTI-SENSE: no
; ORIGINAL SOURCE: synthetic
; PUBLICATION INFORMATION:
; AUTHORS: Katherine Meyer-Siegler
; AUTHORS: Perry Hudson
; TITLE: Enhanced Expression of Macrophage Migration
; TITLE: Inhibitory Factor in Prostatic Adenocarcinoma Metastases
; JOURNAL: Urology
; VOLUME: 48
; ISSUE: 3
; PAGES: 448-452
; DATE: 1996
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 15
; US-08-893-204C-2
;
; Query Match 0.8%; Score 13.4; DB 1; Length 15;
; Best Local Similarity 93.3%; Pred. No. 4e+02;
; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 1734 ACAAAAAAAAAAAAAA 1748
Db 15 AGAAAAAAAAAAAAAAAA 1
;
RESULT 519
; US-08-832-021-17/c
; Sequence 17, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-37
```

```
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-17
;
; Query Match 0.8%; Score 13.4; DB 1; Length 15;
; Best Local Similarity 93.3%; Pred. No. 4e+02;
; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 1731 TTACAAAAAAAAAAAA 1745
Db 15 TTTAAAAAAAAAAAAAAAA 1
;
RESULT 520
; US-08-832-021-25/c
; Sequence 25, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-25
;
; Query Match 0.8%; Score 13.4; DB 1; Length 15;
; Best Local Similarity 93.3%; Pred. No. 4e+02;
; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 1733 TACAAAAAAAAAAAAA 1747
Db 15 TTCAAAAAAAAAAAAAAA 1
;
RESULT 521
; US-08-832-021-37/c
; Sequence 37, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-37
;
; Query Match 0.8%; Score 13.4; DB 1; Length 15;
; Best Local Similarity 93.3%; Pred. No. 4e+02;
; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1733 TACAAAAA 1747
| | | | | | | | | |
Db 15 TCGAAAAA 1

RESULT 522

US-08-832-021-44/c

; Sequence 44, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 44

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-44

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAA 1748
| | | | | | | | | |
Db 15 ACTAAAAA 1

RESULT 523

US-08-832-021-48/c

; Sequence 48, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 48

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-48

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAA 1748
| | | | | | | | | |
Db 15 ACGAAAAA 1

RESULT 524

US-08-832-021-49/c

; Sequence 49, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 49

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-49

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1747
| | | | | | | | | |
Db 15 TCCAAAAA 1

RESULT 525

US-08-832-021-52/c

; Sequence 52, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 52

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-52

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAA 1748
| | | | | | | | | |
Db 15 ACCAAAAA 1

RESULT 526

US-08-832-021-53/c

; Sequence 53, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 53

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-53

```
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-53
```

```
Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1733 TACAAAAA 1747
Db 15 TATAAAAA 1
```

```
RESULT 527
US-08-832-021-55/c
; Sequence 55, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-55
```

```
Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1735 CAAAAA 1749
Db 15 CATAAAAA 1
```

```
RESULT 528
US-08-832-021-56/c
; Sequence 56, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 56
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-56
```

```
Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAA 1750
Db 15 AATAAAAA 1
```

```
RESULT 529
US-08-832-021-57/c
; Sequence 57, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-57
```

```
Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1733 TACAAAAA 1747
Db 15 TAGAAAAA 1
```

```
RESULT 530
US-08-832-021-59/c
; Sequence 59, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-59
```

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1749
Db 15 CAGAAAAAATAAAAAA 1

RESULT 531

US-08-832-021-60/c
; Sequence 60, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 60

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-60

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAATAAAAAA 1750
Db 15 AAGAAAAAATAAAAAA 1

RESULT 532

US-09-475-947A-164/c

; Sequence 164, Application US/09475947A

; Patent No. 6472154

; GENERAL INFORMATION:

; APPLICANT: Garner, Harold R.

; APPLICANT: Wren, Jonathan D.

; APPLICANT: Minna, John D.

; TITLE OF INVENTION: Polymorphic Repeats in Human Genes

; FILE REFERENCE: UTSD0667

; CURRENT APPLICATION NUMBER: US/09/475,947A

; CURRENT FILING DATE: 1999-12-31

; NUMBER OF SEQ ID NOS: 346

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 164

; LENGTH: 15

; TYPE: DNA

; ORGANISM: human

US-09-475-947A-164

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAATAAAAAA 1750
Db 15 AAAAAAATAAAAAA 1

RESULT 533

US-09-335-629-7
; Sequence 7, Application US/09335629
; Patent No. 6664045
; GENERAL INFORMATION:

; APPLICANT: Hyldig-Nielsen, Jens J.

; APPLICANT: Coull, James M.

; TITLE OF INVENTION: PNA Probes, Probe Sets, Methods and Kits Pertaining To

; TITLE OF INVENTION: The Detection Of Microorganisms

; FILE REFERENCE: BP9804US

; CURRENT APPLICATION NUMBER: US/09/335,629

; CURRENT FILING DATE: 1999-06-19

; EARLIER APPLICATION NUMBER: 60/089,737

; EARLIER FILING DATE: 1998-06-18

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:PNA

; OTHER INFORMATION: Probing Nucleobase Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:PNA Probing

; OTHER INFORMATION: Nucleobase Sequence

US-09-335-629-7

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 649 GCTGGCCAGCCTTC 663
Db 1 GCTGGCCTAGCCTTC 15

RESULT 534

PCT-US91-03680-19

; Sequence 19, Application PC/TUS9103680

; GENERAL INFORMATION:

; APPLICANT: Matteucci, Mark D.

; APPLICANT: Krawczyk, Steven

; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED

; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF

; TITLE OF INVENTION: DUPLEX DNA

; NUMBER OF SEQUENCES: 158

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison & Foerster

; STREET: 545 Middlefield Road, Suite 200

; CITY: Menlo Park

; STATE: California

; COUNTRY: USA

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/03680

; FILING DATE: 19910524

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Murashige, Kate H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 4610-0011.40

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-327-7250

; TELEFAX: 415-327-2951

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

```
;
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US91-03680-19

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY. 864 AAGAGGAAGAGGAGG 878
Db 1 AAGAGGAGGAGGAGG 15

RESULT 535
PCT-US95-06379-19
; Sequence 19, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06379
; FILING DATE: May 13, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-PCT
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-19

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAAGAGGAGG 878
Db 1 AAGAGGAGGAGGAGG 15

RESULT 536
US-08-952-376-2/c
; Sequence 2, Application US/08952376
; Patent No. 6146855
; GENERAL INFORMATION:
; APPLICANT: Williams, Keith L
; APPLICANT: Vesey, Graham
; APPLICANT: Veal, Duncan
; APPLICANT: Ashbolt, Nicholas J
```

```
;
; APPLICANT: Dorsch, Matthias
; TITLE OF INVENTION: Method for the Detection of Viable
; TITLE OF INVENTION: Cryptosporidium parvum Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brinke, Hofer, Gilson & Lione
; STREET: 455 No. 6146855th Cityfront Plaza Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60611-5599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,376
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/AU96/00274
; FILING DATE: 06-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin, Alice
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-952-376-2

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAAATAAAA 1747
Db 15 TACTAAAAAATAAAA 1

RESULT 537
US-08-233-608-12/c
; Sequence 12, Application US/08233608
; Patent No. 5585238
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,608
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1739
```


TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Oligonucleotide primer JB446
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-233-608-12

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 612 CCCCACTCCAGCCTC 626
| | | | | | | | | | | | | | | | | |
Db 16 CACCACTCCAGCCTC 2

RESULT 538

US-08-531-747-4/c
Sequence 4, Application US/08531747
Patent No. 5631147
GENERAL INFORMATION:
APPLICANT: Lohman, Kenton L.
APPLICANT: Ostrerova, Natalie V.
APPLICANT: Van Cleve, Mark
APPLICANT: Reid, Robert A.
TITLE OF INVENTION: DETECTION OF NUCLEIC ACIDS IN CELLS BY
TITLE OF INVENTION: THERMOPHILIC STRAND DISPLACEMENT AMPLIFICATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,747
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3462
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-531-747-4

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 828 CAAAGAGGAGCTGC 842
| | | | | | | | | | | | | | | | | |
Db 15 CAATGAGGAGCTGC 1

RESULT 539
US-08-373-124A-194/c
Sequence 194, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-194

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAAGAGGAGG 878
| | | | | | | | | | | | | | | | | |
Db 17 AAGAGGAGGAGGAGG 3

RESULT 540
US-08-531-749-4/c
Sequence 4, Application US/08531749
Patent No. 5733752
GENERAL INFORMATION:
APPLICANT: Lohman, Kenton L.
APPLICANT: Ostrerova, Natalie V.

; APPLICANT: Van Cleve, Mark
; APPLICANT: Reid, Robert A.
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACIDS IN CELLS BY
; TITLE OF INVENTION: THERMOPHILIC STRAND DISPLACEMENT AMPLIFICATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/531,749
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3462
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-531-749-4

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 828 CAAAGAGGAAGCTGC 842
Db 15 CAATGAGGAAGCTGC 1

RESULT 541
US-08-178-476A-16/c
; Sequence 16, Application US/08178476A
; Patent No. 5756101
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: de Taisne, Charles
; APPLICANT: Chang, Sandra
; APPLICANT: Hui, George
; APPLICANT: Siddiqui, Wassim A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,476A
; FILING DATE: 07-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/724,109
; FILING DATE: 01-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2330
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-178-476A-16

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CAGCTTCGGGCCAG 1110
Db 17 CAGCTTCGAGGCCAG 3

RESULT 542
US-08-781-432-4/c
; Sequence 4, Application US/08781432
; Patent No. 5756702
; GENERAL INFORMATION:
; APPLICANT: Lohman, Kenton L.
; APPLICANT: Ostreerova, Natalie V.
; APPLICANT: Van Cleve, Mark
; APPLICANT: Reid, Robert A.
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACIDS IN CELLS BY
; TITLE OF INVENTION: THERMOPHILIC STRAND DISPLACEMENT AMPLIFICATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,432
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/531,747
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3462
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-781-432-4

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      828 CAAAGAGGAAGCTGC 842
Db      15 CAATGAGGAAGCTGC 1

RESULT 543
US-08-257-073-135/c
; Sequence 135, Application US/08257073
; Patent No. 5766597
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: de Taisne, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,073
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,305
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,183
; FILING DATE: 20-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2570
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066 CURTMS
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-257-073-135

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1096 CAGCTTCGCGCCAG 1110
Db      17 CAGCTTCGAGGCCAG 3

RESULT 544
US-08-887-480-12/c
; Sequence 12, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
```

```
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer JB446
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-887-480-12

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      612 CCCCACTCCAGCCTC 626
Db      16 CACCACTCCAGCCTC 2

RESULT 545
US-08-435-628-194/c
; Sequence 194, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-194

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAAGAGGAGG 878
| | | | | | | | | |
Db 17 AAGAGGAGGAGGAGG 3

RESULT 546
US-08-722-187-12/c
; Sequence 12, Application US/08722187
; Patent No. 5955274
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608

; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer JB446
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-722-187-12

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 612 CCCCACTCCAGCCTC 626
| | | | | | | | | |
Db 16 CACCACTCCAGCCTC 2

RESULT 547
US-08-964-020-2/c
; Sequence 2, Application US/08964020
; Patent No. 6077669
; GENERAL INFORMATION:
; APPLICANT: Vonk, Glenn P.
; APPLICANT: Little, Michael C.
; TITLE OF INVENTION: Kit and Method for Fluorescence Based
; TITLE OF INVENTION: Detection Assay
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick - Becton, Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: USA
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,020
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highet, David W.
; REGISTRATION NUMBER: 30,265
; REFERENCE/DOCKET NUMBER: p-4025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 847-5317
; TELEFAX: (201) 848-9228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-964-020-2

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;


```

;
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2777:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2777

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 AGGAAAAAAGC 47
Db 16 AGGAAAAAAGC 2

RESULT 551
US-08-584-040-2778/c
; Sequence 2778, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2778:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2778

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 AGGAAAAAAGC 47
Db 16 AGGAAAAAAGC 2

US-08-584-040-2779/c
; Sequence 2779, Application US/09370644B
; Patent No. 6433253
; GENERAL INFORMATION:
; APPLICANT: Kossmann et al.
; TITLE OF INVENTION: DEBRANCHING ENZYMES AND DNA SEQUENCES CODING THEM,
; TITLE OF INVENTION: SUITABLE FOR CHANGING THE DEGREE OF BRANCHING OF
; TITLE OF INVENTION: AMYLOPECTIN STARCH IN PLANTS
; FILE REFERENCE: 51413-3771
; CURRENT APPLICATION NUMBER: US/09/370,644B
; CURRENT FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 08/596,257
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 23
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Solanum tuberosum
US-09-370-644B-23

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1657 GACATCCACCTGTAT 1671
Db 15 GCCATCCACCTGTAT 1

RESULT 553
US-09-371-772B-1300/c
; Sequence 1300, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1300
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1300

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 AGGAAAAAAGC 47
Db 17 AGGAAAAAAGC 3
```


RESULT 554

US-09-371-772B-1301/c
; Sequence 1301, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1301
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1301

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 33 AGGAAAAAAGC 47
|||
Db 16 AGGAAAAAAGC 2

RESULT 555

US-09-371-772B-1302/c
; Sequence 1302, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1302
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1302

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 33 AGGAAAAAAGC 47
|||
Db 15 AGGAAAAAAGC 1

RESULT 556

US-09-371-772B-5090
; Sequence 5090, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5090
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5090

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 4.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 530 AGCCCCGCCACCTC 544
|
Db 3 AACCCCCGCCACCUC 17

RESULT 557

US-09-866-108A-6390
; Sequence 6390, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6390
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6390

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1177 GCCACGTGCTCCAG 1191
||| |||||
Db 3 GCCCGGTGCTCCAG 17

RESULT 558
US-09-866-108A-6391
; Sequence 6391, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6391
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6391

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1177 GCCACGTGCTCCAG 1191
||| |||||
Db 2 GCCCGGTGCTCCAG 16

RESULT 559

US-09-866-108A-6392
; Sequence 6392, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6392
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6392

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1177 GCCACGTGCTCCAG 1191
||| |||||
Db 1 GCCCGGTGCTCCAG 15

RESULT 560
US-09-866-108A-7876
; Sequence 7876, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6

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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7876
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7876

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      834 GGAAGCTGCTGGGGT 848
Db      3 GGGAGCTGCTGGGGT 17

RESULT 561
US-09-866-108A-7880
; Sequence 7880, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7880
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7880

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      837 AGCTGCTGGGGTCTC 851
Db      2 AGCTGCTGGGGTCAC 16

RESULT 562
US-09-866-108A-7881
; Sequence 7881, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7881
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7881

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      837 AGCTGCTGGGGTCTC 851
Db      1 AGCTGCTGGGGTCAC 15
```

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RESULT 563
US-09-866-108A-10020
; Sequence 10020, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10020
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10020

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      132 CGCTGTCTGGAGTCC 146
      ||| ||||| ||||| |||
Db      3 CGGTGTCTGGAGTCC 17

RESULT 564
US-09-866-108A-10021
; Sequence 10021, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10021
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10021

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      132 CGCTGTCTGGAGTCC 146
      ||| ||||| ||||| |||
Db      2 CGGTGTCTGGAGTCC 16

RESULT 565
US-09-866-108A-10281/c
; Sequence 10281, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10020
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10020
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10281
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10281

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1288 TTCACAGTGGATGCT 1302
Db 17 TTCAAAGTGGATGCT 3

RESULT 566
US-09-866-108A-10282/c
; Sequence 10282, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10282
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10282

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1288 TTCACAGTGGATGCT 1302
Db 16 TTCAAAGTGGATGCT 2

RESULT 567
US-09-866-108A-10283/c
; Sequence 10283, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10283
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10283

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1288 TTCACAGTGGATGCT 1302
Db 15 TTCAAAGTGGATGCT 1

RESULT 568
US-09-866-108A-10500
; Sequence 10500, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456

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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10500
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10500

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Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred.No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 805 CAGAGAGAGCCAGG 819
D_b 3 CGGAGAGAGCCAGG 17

RESULT 569
US-09-866-108A-10501
; Sequence 10501, Application US/09866108A
; Patent No. 686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006659
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006658
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663

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; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent NO. 6686188
; SEQ ID NO 10501
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10501

```

Query Match	0.8%	Score 13.4;	DB 1;	Length 17;
Best Local Similarity	93.3%	Pred. No. 4.6e+02;		
Matches 14; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 805 CAGAGAGAGCCAGGG 819
| | | | | | | | | |
Db 2 CGGAGAGAGCCAGGG 16

RESULT 570
US-09-866-108A-10503
; Sequence 10503, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: A6OMICA-7

Query Match	0.8%;	Score 13.4;	DB 1;	Length 17;
Best Local Similarity	93.3%;	Pred. NO. 4.6e+02;		
Matches 14; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 807 GAGAGAGCCAGGGCC 821
Db 2 GAGAGAGCCAGGGAC 16

RESULT 571
PCT-US91-03680-7/c
; Sequence 7, Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; APPLICANT: Krawczyk, Steven
; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
; TITLE OF INVENTION: DUPLEX DNA
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03680
; FILING DATE: 19910524
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4610-0011.40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 8
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N4,N4-ethanocytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 14
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 17
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "1,3-propanediol"
PCT-US91-03680-7
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAA 1751
Db 16 AAGAAAAAANAANA 1
RESULT 572
PCT-US95-04712-12/c
; Sequence 12, Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M

; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer JB446
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04712-12
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 612 CCCCACTCCAGCCTC 626
Db 16 CACCACTCCAGCCTC 2
RESULT 573
US-09-300-958A-65/c
; Sequence 65, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65

; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-65

Query Match 0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 3.9e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1748
:|||||
Db 14 BAAAAA1

RESULT 574
US-08-745-269-3/c
; Sequence 3, Application US/08745269
; Patent No. 5763183
; GENERAL INFORMATION:
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Koulou, Markku
; APPLICANT: Linnoila, Markku
; APPLICANT: Goldman, David
; APPLICANT: Virkkunen, Matti
; TITLE OF INVENTION: ALLELIC VARIATION
; TITLE OF INVENTION: OF THE 5HT7 SEROTONIN RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,269
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,394
; FILING DATE: 09-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH126.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-745-269-3

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA1748
:|||||
Db 13 AAAAAA1

RESULT 575
US-08-745-269-4/c
; Sequence 4, Application US/08745269
; Patent No. 5763183
; GENERAL INFORMATION:
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Koulou, Markku
; APPLICANT: Linnoila, Markku
; APPLICANT: Goldman, David
; APPLICANT: Virkkunen, Matti
; TITLE OF INVENTION: ALLELIC VARIATION
; TITLE OF INVENTION: OF THE 5HT7 SEROTONIN RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,269
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,394
; FILING DATE: 09-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael L
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH126.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-745-269-4

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA1748
:|||||
Db 13 AAAAAA1

RESULT 576
US-09-305-223-1
; Sequence 1, Application US/09305223
; Patent No. 6211354
; GENERAL INFORMATION:
; APPLICANT: HORIE, Ryuichi
; APPLICANT: ISHIGURO, Takahiko
; TITLE OF INVENTION: OPTICALLY ACTIVE DNA PROBE HAVING PHOSPHONIC DIESTER
; TITLE OF INVENTION: LINKAGE
; FILE REFERENCE: Q54283
; CURRENT APPLICATION NUMBER: US/09/305,223
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: JP 10-123298
; PRIOR FILING DATE: 1998-05-06

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; PRIOR APPLICATION NUMBER: JP 10-212569
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(6)
; OTHER INFORMATION: Between positions 5 and 6, a phosphonic diester
; OTHER INFORMATION: linkage is indicated (see page 21, line 12-13 and
; OTHER INFORMATION: lines 21-22 of the specification)
US-09-305-223-1

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 577
US-09-068-860-15
; Sequence 15, Application US/09068860
; Patent No. 6261770
; GENERAL INFORMATION:
; APPLICANT: WARTHOE, Peter R.
; TITLE OF INVENTION: METHOD TO CLONE MRNAS
; FILE REFERENCE: 674513-2001.1
; CURRENT APPLICATION NUMBER: US/09/068,860
; CURRENT FILING DATE: 1998-05-17
; EARLIER APPLICATION NUMBER: PCT/DK98/00186
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 0547/97
; EARLIER FILING DATE: 1997-05-13
; EARLIER APPLICATION NUMBER: 0432/98
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Thermophilic eubacteria
US-09-068-860-15

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 578
US-09-352-540A-6/c
; Sequence 6, Application US/09352540A
; Patent No. 6326175
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl
; APPLICANT: Tan, Ruoying
; APPLICANT: Rose, Michael J.
; TITLE OF INVENTION: Methods and Compositions for Producing
; TITLE OF INVENTION: Full Length cDNA Libraries
; FILE REFERENCE: 06514-087US1
; CURRENT APPLICATION NUMBER: US/09/352,540A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized Primer
US-09-352-540A-6

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 579
US-09-799-645-6/c
; Sequence 6, Application US/09799645
; Patent No. 6369199
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl
; APPLICANT: Tan, Ruoying
; APPLICANT: Rose, Michael J.
; TITLE OF INVENTION: Methods and Compositions for Producing
; TITLE OF INVENTION: Full Length cDNA Libraries
; FILE REFERENCE: 06514-087CON
; CURRENT APPLICATION NUMBER: US/09/799,645
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/352,540
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized Primer
US-09-799-645-6

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 580
US-09-619-103-19
; Sequence 19, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
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US-09-619-103-19

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 581

US-10-002-528-6/c
; Sequence 6, Application US/10002528
; Patent No. 6436676
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl
; APPLICANT: Tan, Ruoying
; APPLICANT: Rose, Michael J.
; TITLE OF INVENTION: Methods and Compositions for Producing
; TITLE OF INVENTION: Full Length cDNA Libraries
; FILE REFERENCE: 06514-087CON
; CURRENT APPLICATION NUMBER: US/10/002,528
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/799,645
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/352,540
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized Primer
US-10-002-528-6

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 582

US-09-475-947A-29
; Sequence 29, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 13
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-29

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
|||||

Db 1 CAAAAAAAAAAAAA 13

RESULT 583

US-08-455-627-8
; Sequence 8, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-627-8

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
|||||
Db 1 CAAAAAAAAAAAAA 13

RESULT 584

US-08-486-955A-2/c
; Sequence 2, Application US/08486955A
; Patent No. 5747299
; GENERAL INFORMATION:
; APPLICANT: FATHMAN, Garrison
; APPLICANT: BLOOM, Debra
; TITLE OF INVENTION: Anergy Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,955A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A59741-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-486-955A-2

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1747
Db 13 CAAAAA1

RESULT 585
US-08-294-424-33
; Sequence 33, Application US/08294424
; Patent No. 5800984
; GENERAL INFORMATION:
; APPLICANT: Vary, Calvin
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE DETECTION BY
; TITLE OF INVENTION: TRIPLE HELIX FORMATION
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,424
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/000,922
; FILING DATE: 16 JAN 1993
; APPLICATION NUMBER: US/07/629,601B
; FILING DATE: 17-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00088-037001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 33 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
US-08-294-424-33

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 861 AGGAGAGGAAGA 873
Db 2 AGGAGAGGAAGA 14

RESULT 586
US-08-689-856-8
; Sequence 8, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-689-856-8

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1747
Db 1 CAAAAA13

RESULT 587
US-08-371-377-8/c
; Sequence 8, Application US/08371377
; Patent No. 5851764
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Shen, Ruogian
; TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND
```

;; TITLE OF INVENTION: IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EXPRESSED
;; TITLE OF INVENTION: MOLECULES AND TRANSFORMATION-ASSOCIATED GENES
;; NUMBER OF SEQUENCES: 22
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10036
;; COMPUTER READABLE-FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/371,377
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 0575/37590-B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 278-0400
;; TELEFAX: (212) 391-0525
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "Synthetic DNA"
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-371-377-8

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
|||
Db 13 CAAAAAAAAAAAAA 1

RESULT 588
US-08-832-021-13/c
; Sequence 13, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-13

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAA 1747
|||
Db 13 CAAAAAAAAAAAAA 1

RESULT 589
US-08-832-021-14/c
; Sequence 14, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-14

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
|||
Db 13 CAAAAAAAAAAAAA 1

RESULT 590
US-08-832-021-15/c
; Sequence 15, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-15

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
|||
Db 13 CAAAAAAAAAAAAA 1

RESULT 591
 US-08-724-466B-12/c
 ; Sequence 12, Application US/08724466B
 ; Patent No. 6063606
 ; GENERAL INFORMATION:
 ; APPLICANT: Petkovich, P. Martin, White, Jay A.,
 ; APPLICANT: Beckett, Barbara R., Jones, Glenville
 ; TITLE OF INVENTION: Retinoid Metabolizing Protein
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; ZIP: M5L 1A9
 ; COUNTRY: Canada
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,466B
 ; FILING DATE: October 1, 1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/667,546
 ; FILING DATE: June 21, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 50767/00004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-724-466B-12

Query Match 0.7%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA1747
 Db 13 CAAAAA1

RESULT 592
 US-08-724-466B-13/c
 ; Sequence 13, Application US/08724466B
 ; Patent No. 6063606
 ; GENERAL INFORMATION:
 ; APPLICANT: Petkovich, P. Martin, White, Jay A.,
 ; APPLICANT: Beckett, Barbara R., Jones, Glenville
 ; TITLE OF INVENTION: Retinoid Metabolizing Protein
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; ZIP: M5L 1A9
 ; COUNTRY: Canada
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,466B
 ; FILING DATE: October 1, 1996

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/667,546
 ; FILING DATE: June 21, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 50767/00004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-724-466B-13

Query Match 0.7%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA1747
 Db 13 CAAAAA1

RESULT 593
 US-08-724-466B-15/c
 ; Sequence 15, Application US/08724466B
 ; Patent No. 6063606
 ; GENERAL INFORMATION:
 ; APPLICANT: Petkovich, P. Martin, White, Jay A.,
 ; APPLICANT: Beckett, Barbara R., Jones, Glenville
 ; TITLE OF INVENTION: Retinoid Metabolizing Protein
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; ZIP: M5L 1A9
 ; COUNTRY: Canada
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,466B
 ; FILING DATE: October 1, 1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/667,546
 ; FILING DATE: June 21, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 50767/00004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-724-466B-15

Query Match 0.7%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA1747
 Db 13 CAAAAA1

RESULT 594
 US-08-724-466B-16/c
 ; Sequence 16, Application US/08724466B
 ; Patent No. 6063606
 ; GENERAL INFORMATION:
 ; APPLICANT: Petkovich, P. Martin, White, Jay A.,
 ; APPLICANT: Beckett, Barbara R., Jones, Glenville
 ; TITLE OF INVENTION: Retinoid Metabolizing Protein
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Blake, Cassels & Graydon
 ; STREET: Box 25, Commerce Court West
 ; CITY: Toronto
 ; ZIP: M5L 1A9
 ; COUNTRY: Canada
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 ; COMPUTER: COMPAQ, IBM PC compatible
 ; OPERATING SYSTEM: MS-DOS 5.1
 ; SOFTWARE: WORD PERFECT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,466B
 ; FILING DATE: October 1, 1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/667,546
 ; FILING DATE: June 21, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunt, John C.
 ; REGISTRATION NUMBER: 36,424
 ; REFERENCE/DOCKET NUMBER: 50767/00004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 863-4344
 ; TELEFAX: (416) 863-2653
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-724-466B-16

Query Match 0.7%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA1747

Db |||||
 13 CAAAAAAAAAAAAA 1

RESULT 594
US-08-787-321-8
; Sequence 8, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-787-321-8

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
 |||||
Db 1 CAAAAAAAAAAAAA 13

RESULT 595
US-08-822-164D-12/c
; Sequence 12, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-12

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
 |||||
Db 13 CAAAAAAAAAAAAA 1

RESULT 596
US-08-882-164D-13/c
; Sequence 13, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-13

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
 |||||
Db 13 CAAAAAAAAAAAAA 1

RESULT 597
US-08-882-164D-15/c
; Sequence 15, Application US/08882164D
; Patent No. 6306624

GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-15

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA 1747
| | | | | | | | | | | | | | | | | |
Db 13 CAAAAA 1

RESULT 598
US-09-475-947A-94/c
; Sequence 94, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 14
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-94

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAA 1748
| | | | | | | | | | | | | | | | | |
Db 13 AAAAAA 1
RESULT 599
US-09-151-771B-18/c
; Sequence 18, Application US/09151771B
; Patent No. 6586204
; GENERAL INFORMATION:
; APPLICANT: Lehar, et al., Sophie M.
; TITLE OF INVENTION: APOPTOSIS GENE EI24, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 104322.170DIV
; CURRENT APPLICATION NUMBER: US/09/151,771B
; CURRENT FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer sequence
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: any nucleotide can be used
US-09-151-771B-18

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA 1748
| | | | | | | | | | | | | | | | | |
Db 14 CAAAAA 1

RESULT 600
US-09-151-771B-20/c
; Sequence 20, Application US/09151771B
; Patent No. 6586204
; GENERAL INFORMATION:
; APPLICANT: Lehar, et al., Sophie M.
; TITLE OF INVENTION: APOPTOSIS GENE EI24, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 104322.170DIV
; CURRENT APPLICATION NUMBER: US/09/151,771B
; CURRENT FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer sequence
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: any nucleotide can be used
US-09-151-771B-20

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAAA 1747
| | | | | | | | | | | | | | | | | |
Db 14 AAAAAA 1

RESULT 601
US-08-292-620A-359/c
; Sequence 359, Application US/08292620A
; Patent No. 5837542

GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-359

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 15 AAAAAAAAAAAAAA 3

RESULT 602
US-08-292-620A-364/c
Sequence 364, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF

two

TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 364:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-364

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 603
US-08-832-021-26/c
Sequence 26, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
APPLICANT: Combates, N.
APPLICANT: Pardinias, J.
APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 15

two

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-26

Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1

RESULT 604
US-08-832-021-27/c
; Sequence 27, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-27

Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1

RESULT 605
US-08-832-021-28/c
; Sequence 28, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-28

Query Match
0.7%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1

RESULT 606
US-08-832-021-36/c
; Sequence 36, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-36

Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 AGGAAAAAAAAAAAA 45
Db 15 AGGAAAAAAAAAAAA 3

RESULT 607
US-08-832-021-38/c
; Sequence 38, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-38

Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1

```
RESULT 608
US-08-832-021-39/c
; Sequence 39, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-39
```

```
Query Match      0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1735 CAAAAA1747
Db      13 CAAAAA1
```

```
RESULT 609
US-08-832-021-40/c
; Sequence 40, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-40
```

```
Query Match      0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1735 CAAAAA1747
Db      13 CAAAAA1
```

```
RESULT 610
US-08-832-021-50/c
; Sequence 50, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
```

```
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-50
```

```
Query Match      0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1735 CAAAAA1747
Db      13 CAAAAA1
```

```
RESULT 611
US-08-832-021-51/c
; Sequence 51, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-51
```

```
Query Match      0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1735 CAAAAA1747
Db      13 CAAAAA1
```

```
RESULT 612
US-09-071-845-359/c
; Sequence 359, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
```


;
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-359

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1748
Db 15 AAAAAAAAAAAAA 3

RESULT 613
US-09-071-845-364/c
; Sequence 364, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700

;
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 364:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-364

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAA 1

RESULT 614
US-09-081-646-842
; Sequence 842, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; TITLE OF INVENTION: Cancer Cells
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 842
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-081-646-842

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 ATGGGGCTGGGT 1037
|||||
Db 2 ATGGGGCTGGGT 14

RESULT 615

US-09-531-000-54/c
; Sequence 54, Application US/09531000
; Patent No. 6461810
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Marion D.
; APPLICANT: FRESCO, Jacques R.
; TITLE OF INVENTION: TRIPLEX IN-SITU HYBRIDIZATION
; FILE REFERENCE: 2448-103
; CURRENT APPLICATION NUMBER: US/09/531,000
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/23765
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/064,997
; PRIOR FILING DATE: 1997-11-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target
; OTHER INFORMATION: sequences
US-09-531-000-54

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AGAGGAAAAAAA 43
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Db 13 AGAGGAAAAAAA 1

RESULT 616

US-08-284-484A-4
; Sequence 4, Application US/08284484A
; Patent No. 5639873
; GENERAL INFORMATION:
; APPLICANT: Barascut, et al.
; TITLE OF INVENTION: Oligothionucleotides
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5639873ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,484A
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: MSA-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-284-484A-4

Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA 1747
|||||
Db 2 CAAAAA 14

RESULT 617

US-08-465-590-119
; Sequence 119, Application US/08465590
; Patent No. 5824770
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,590
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,438
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MPG-006C2DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-465-590-119

Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 865 AGAGGAAGAGGAG 877
|||||
Db 3 AGAGGAAGAGGAG 15

RESULT 618
US-08-711-417C-119
; Sequence 119, Application US/08711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-Sep-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 119:
US-08-711-417C-119
Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 865 AGAGGAAGAGGAG 877
| | | | | | | | | |
Db 3 AGAGGAAGAGGAG 15
RESULT 619
US-08-275-951-42/c
; Sequence 42, Application US/08275951
; Patent No. 6451968
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Kiely, John
; APPLICANT: Griffin, Michael
; APPLICANT: Coull, James M.
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS1577
; CURRENT APPLICATION NUMBER: US/08/275,951

; CURRENT FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 08/088,658
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/088,661
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-22
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1991-04-15
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 42
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence
; NAME/KEY: misc_feature
; LOCATION: (3)
; OTHER INFORMATION: N is Pseudoisocytosine
; NAME/KEY: misc_feature
; LOCATION: (5)..(6)
; OTHER INFORMATION: N is Pseudoisocytosine
; NAME/KEY: misc_feature
; LOCATION: (8)..(9)
; OTHER INFORMATION: Ethylene Glycol, Ethylene Glycol, Ethylene Glycol
; OTHER INFORMATION: Linkage
US-08-275-951-42
Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 30 AAGAGGAAAAA 45
| | | | | | | | | |
Db 16 AAGAGGAAANNANNA 1
RESULT 620
US-09-723-909-119
; Sequence 119, Application US/09723909
; Patent No. 6630141
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/723,909
; FILING DATE: 28-No. 6630141-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417
; FILING DATE: 05-Sep-1996
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438

```

; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 119:
US-09-723-909-119
Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 865 AGAGGAAGAGGAG 877
Db 3 AGAGGAAGAGGAG 15

RESULT 621
PCT-US93-08743-119
; Sequence 119, Application PC/TUS9308743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08743
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 946,233
; FILING DATE: 14-SEP-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US93-08743-119
Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 865 AGAGGAAGAGGAG 877
Db 3 AGAGGAAGAGGAG 15

RESULT 622
US-08-292-620A-1639/c
; Sequence 1639, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
```

```

; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1639:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-1639
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 623
US-08-292-620A-1790/c
; Sequence 1790, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
```

;
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1790:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-1790

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 624
US-08-292-620A-1801/c
; Sequence 1801, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

two

;
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1801:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-1801

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 625
US-08-292-620A-1823/c
; Sequence 1823, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

two

;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/292,620A
;; FILING DATE: August 17, 1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below:
;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 208/149
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1823:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-292-620A-1823

two

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 626
US-08-292-620A-1868/c
; Sequence 1868, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below:
;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 208/149
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1868:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-292-620A-1868

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 627
US-09-071-845-1639/c
; Sequence 1639, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/292,620
; APPLICATION NUMBER: August 17, 1994
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1639:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-1639

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 628
US-09-071-845-1790/c
; Sequence 1790, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1790:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-1790
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5
RESULT 629
US-09-071-845-1801/c
; Sequence 1801, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1801:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
US-09-071-845-1801

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 630
US-09-071-845-1823/c
; Sequence 1823, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1823:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-1823

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 631
US-09-071-845-1868/c
; Sequence 1868, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1868:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-1868

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 632
US-09-434-131A-12

; Sequence 12, Application US/09434131A
; Patent No. 6344345
; GENERAL INFORMATION:
; APPLICANT: HAYASHIZAKI, Yoshihide
; TITLE OF INVENTION: METHOD FOR PRODUCING DOUBLE-STRANDED DNA WHOSE TERMINAL
; PART IS ELIMINATED AND METHOD FOR
; DETERMINING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 024705-093
; CURRENT APPLICATION NUMBER: US/09/434,131A
; CURRENT FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: JP 316102/1998
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:hemimethylated
; OTHER INFORMATION: CDNA
; NAME/KEY: misc_feature
; LOCATION: (2)..(4)
; OTHER INFORMATION: Nucleotides 2-4 are n wherein n = any nucleotide.
US-09-434-131A-12

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1735 CAAAAA1750
Db 1 CNNNA16

RESULT 633

US-08-584-040-2547/c
; Sequence 2547, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES OR
; CONDITIONS RELATED TO LEVELS
; OF VASCULAR ENDOTHELIAL
; GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2547:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2547

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA1748
Db 17 AAAAAAAAAA5

RESULT 634

US-09-371-772B-1071/c
; Sequence 1071, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; ated to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1071
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1071

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA1748
Db 17 AAAAAAAAAA5

RESULT 635

US-09-371-772B-5091
; Sequence 5091, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; ated to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B

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; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5091
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5091
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Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 5.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 532 CCCCGGCCACCTC 544
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Db 2 CCCCGGCCACCUC 14
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RESULT 636

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US-09-371-772B-5092
; Sequence 5092, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5092
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5092
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Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 5.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 532 CCCCGGCCACCTC 544
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Db 1 CCCCGGCCACCUC 13
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RESULT 637

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US-09-866-108A-1381/c
; Sequence 1381, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
```

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; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1381
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1381
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Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1244 GCTTCACCTGCGT 1256
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Db 17 GCTTCACCTGCGT 5
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RESULT 638

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US-09-866-108A-1382/c
; Sequence 1382, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1382
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1382

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1244 GCTTCACCTGCGT 1256
Db 16 GCTTCACCTGCGT 4

RESULT 639
US-09-866-108A-1383/c
; Sequence 1383, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1383
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1383

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1244 GCTTCACCTGCGT 1256

Db 15 GCTTCACCTGCGT 3

RESULT 640
US-09-866-108A-1384/c
; Sequence 1384, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1384
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1384

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1244 GCTTCACCTGCGT 1256
Db 14 GCTTCACCTGCGT 2

RESULT 641
US-09-866-108A-1385/c
; Sequence 1385, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 15755
 ; SOFTWARE: Aeomica Sequence Listing Engine
 ; Patent No. 6686188
 ; SEQ ID NO 1385
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-866-108A-1385

Query Match 0.7%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1244 GCTTCACCTGCGT 1256
 Db 13 GCTTCACCTGCGT 1

RESULT 642
 US-08-126-564A-46
 ; Sequence 46, Application US/08126564A
 ; Patent No. 5436150
 ; GENERAL INFORMATION:
 ; APPLICANT: Chandrasegaran, Srinivasan
 ; TITLE OF INVENTION: Functional Domains in FokI
 ; TITLE OF INVENTION: Restriction Endonuclease
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cushman, Darby & Cushman
 ; STREET: 1100 New York Ave., N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0,
 ; SOFTWARE: Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/126,564A
 ; FILING DATE: 27-SEPTEMBER-93
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kokulis, Paul N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: PNK/4130/82506/CLB
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3503

; TELEFAX: 202-822-0944
 ; TELEX: 6714627 CUSH
 ; INFORMATION FOR SEQ ID NO: 46:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-126-564A-46

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 5.1e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 AATTAGGGGGAAGAG 34
 Db 1 ATTAAGGGGGAAGAG 16

RESULT 643
 US-08-031-147A-56
 ; Sequence 56, Application US/08031147A
 ; Patent No. 5514577
 ; GENERAL INFORMATION:
 ; APPLICANT: Draper et al.
 ; TITLE OF INVENTION: Oligonucleotide Therapies for
 ; TITLE OF INVENTION: Modulating the Effects of Herpesviruses
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz
 ; ADDRESSEE: Mackiewicz & No. 5514577ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/031,147A
 ; FILING DATE: March 12, 1993
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 485,297
 ; FILING DATE: February 26, 1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 852,132
 ; FILING DATE: April 28, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 954,185
 ; FILING DATE: September 29, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane Massey Licata
 ; REGISTRATION NUMBER: 32,257
 ; REFERENCE/DOCKET NUMBER: ISIS-0469
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; ANTI-SENSE: yes
 US-08-031-147A-56

Query Match 0.7%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 5.1e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGG 1030
| | | | | | | | | |
Db 1 GGGTTGGGTTGGG 16

RESULT 644
US-08-455-627-16/c
; Sequence 16, Application US/08455627
; Patent No. 571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-627-16

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 23 AGGGGGAGAGGAAA 38
| | | | | | | | | |
Db 16 AGGGGGAGAGGAAA 1

RESULT 645
US-08-748-591-18
; Sequence 18, Application US/08748591
; Patent No. 5759811
; GENERAL INFORMATION:
; APPLICANT: Epstein, Ervin
; APPLICANT: Hu, Zhilan
; APPLICANT: Bonifas, Jeanette
; TITLE OF INVENTION: Mutant Human Hedgehog Gene
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish and Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA

ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,591
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06510/067001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-748-591-18

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 GGGCCCTCCCGGCC 751
| | | | | | | | | |
Db 1 GGGCCCTCCCGGCC 16

RESULT 646
US-08-748-591-20
; Sequence 20, Application US/08748591
; Patent No. 5759811
; GENERAL INFORMATION:
; APPLICANT: Epstein, Ervin
; APPLICANT: Hu, Zhilan
; APPLICANT: Bonifas, Jeanette
; TITLE OF INVENTION: Mutant Human Hedgehog Gene
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish and Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,591
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06510/067001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single


```
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-748-591-20

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 736 GGGCCCCCTCCCGGCC 751
Db 1 GGGCCCCCTCCCGGCC 16

RESULT 647
US-08-689-856-16/c
; Sequence 16, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-689-856-16

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 23 AGGGGGGAAGAGGAAA 38
Db 16 AGGGGGGAAGAGAAA 1

RESULT 648
US-08-412-376-5/c
; Sequence 5, Application US/08412376
; Patent No. 5849900
; GENERAL INFORMATION:
; APPLICANT: Moelling, Karin
; TITLE OF INVENTION: Inhibition Of Viruses By Antisense
```

```
; TITLE OF INVENTION: Oligomers Capable Of Binding To Polypurine-Rich Tract Of Single
; MOLECULE TYPE: Stranded RNA Or RNA-DNA Hybrids
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5849900ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,376
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,184
; FILING DATE: 29-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yanko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: APOL-0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-412-376-5

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 23 AGGGGGGAAGAGGAAA 38
Db 16 AGGGGGGAAGAGAAA 1

RESULT 649
US-08-403-888A-39
; Sequence 39, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,888A
; FILING DATE: 12-JUN-1995
; CLASSIFICATION: 435
```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/954,185
;; FILING DATE: 29-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Paul K. Legaard
;; REGISTRATION NUMBER: 38,534
;; REFERENCE/DOCKET NUMBER: ISIS-1229
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 39:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-403-888A-39

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGG 1030
| | | | | | | | | | | | | | | |
Db 1 GGGGTTGGGTTGGG 16

RESULT 650
US-08-403-888A-55
; Sequence 55, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,888A
;; FILING DATE: 12-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/954,185
;; FILING DATE: 29-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Paul K. Legaard

;; REGISTRATION NUMBER: 38,534
;; REFERENCE/DOCKET NUMBER: ISIS-1229
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 55:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-403-888A-55

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGG 1030
| | | | | | | | | | | | | | | |
Db 1 GGGGTTGGGTTGGG 16

RESULT 651
US-08-403-888A-112
; Sequence 112, Application US/08403888A
; Patent No. 5952490
; GENERAL INFORMATION:
; APPLICANT: Hanecak et al.
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core
; TITLE OF INVENTION: Sequence
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,888A
;; FILING DATE: 12-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/954,185
;; FILING DATE: 29-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Paul K. Legaard

;; REGISTRATION NUMBER: 38,534
;; REFERENCE/DOCKET NUMBER: ISIS-1229
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 112:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

US-08-403-888A-112
Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGG 1030
| | | | | | | | | | | | | | | |
Db 1 GGGGTTGGGTTGGG 16

RESULT 652
US-08-739-069-1/c
; Sequence 1, Application US/08739069
; Patent No. 5962225
; GENERAL INFORMATION:
; APPLICANT: Ramberg, Elliot R.
; TITLE OF INVENTION: Methods and Compositions for Detection
; TITLE OF INVENTION: of Specific Nucleotide Sequences
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.

ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,069
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,938
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Merchant, Mary Anthony
REGISTRATION NUMBER: 39,771
REFERENCE/DOCKET NUMBER: 03038-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
US-08-739-069-1

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No: 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 23 AGGGGGGAAGAGGAAA 38
|||||
Db 16 AGGGGGGAAGAGAAA 1

RESULT 653
US-08-656-906-2
Sequence 2, Application US/08656906
Patent No. 5972901
GENERAL INFORMATION:
APPLICANT: Ferkol Jr., Thomas W.
APPLICANT: Davis, Pamela B.
APPLICANT: Ziady, Assem-Galal
TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
TITLE OF INVENTION: Mediated Gene Transfer
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,906
FILING DATE: 03-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 03-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/25809
FILING DATE: 23-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/216,534
FILING DATE: 23-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CASE-02280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-656-906-2

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No: 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 30 AAGAGGAAAAAAAAA 45
|||||
Db 1 AAGAGGAGAGAAAAA 16

RESULT 654
US-08-757-024-858/c
Sequence 858, Application US/08757024
Patent No. 6025339
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
NUMBER OF SEQUENCES: 952
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6025339th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 858:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-024-858

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No: 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 190 CAGCCGGAGCCCGCCA 205
Db 16 CAGCCTGTGCCCGCCA 1

RESULT 655
US-07-808-452-11
; Sequence 11, Application US/07808452
; Patent No. 6063612
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Antiviral Reagents Based on
; TITLE OF INVENTION: RNA-Binding Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/808,452
; FILING DATE: 19911213
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8255-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE, 12/A1
US-07-808-452-11

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 23 AGGGGGGAGAGGAAA 38
Db 1 AGGGGGGAGAGGAAA 16

RESULT 656
US-07-808-452-12/c
; Sequence 12, Application US/07808452
; Patent No. 6063612
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Antiviral Reagents Based on
; TITLE OF INVENTION: RNA-Binding Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/808,452
FILING DATE: 19911213
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8255-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE, 12/A-2
INDIVIDUAL ISOLATE: 12/A-2
US-07-808-452-12

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 23 AGGGGGGAGAGGAAA 38
Db 16 AGGGGGGAGAGGAAA 1

RESULT 657
US-09-313-121-1/c
; Sequence 1, Application US/09313121
; Patent No. 6100040
; GENERAL INFORMATION:
; APPLICANT: Ramberg, Elliot R.
; TITLE OF INVENTION: Methods and Compositions for Detection
; TITLE OF INVENTION: of Specific Nucleotide Sequences
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.A.
; ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/313,121
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/739,069
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 60/005,938
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Merchant, Mary Anthony

```
;
; REGISTRATION NUMBER: 39,771
; REFERENCE/DOCKET NUMBER: 03038-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 818-3700
; TELEFAX: (404) 818-3799
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
;
US-09-313-121-1

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      23 AGGGGGGAAGAGGAAA 38
      ||||| ||||| |||||
Db      16 AGGGGGGAAGAGGAAA 1

RESULT 658
US-09-217-847-2
; Sequence 2, Application US/09217847
; Patent No. 6200801
; GENERAL INFORMATION:
; APPLICANT: Ferkol Jr., Thomas W.
; APPLICANT: Davis, Pamela B.
; APPLICANT: Ziady, Assem-Galal
; TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
; TITLE OF INVENTION: Mediated Gene Transfer
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,847
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/656,906
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/25809
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/216,534
; FILING DATE: 23-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: CASE-02280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-09-217-847-2

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      30 AAGAGGAAAAAAAAA 45
      ||||| ||||| |||||
Db      1 AAGAGGAAAAAAAAA 16

RESULT 659
US-08-750-088A-38/c
; Sequence 38, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
;
US-08-750-088A-38

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      242 CGGGGGCCACCACCGGC 257
      ||||| ||||| |||||
Db      16 CGGGGGCCACCACCGGC 1

RESULT 660
US-09-633-848-1/c
; Sequence 1, Application US/09633848
; Patent No. 6458540
; GENERAL INFORMATION:
; APPLICANT: Ramberg, Elliot
```

```
; TITLE OF INVENTION: Methods and Compositions for Detection of Specific Nucleotide Seq
; FILE REFERENCE: 03038-0112 42892-215809
; CURRENT APPLICATION NUMBER: US/09/633,848
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/005,938
; PRIOR FILING DATE: 1995-10-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 Triplex Forming Oligonucleotide
US-09-633-848-1

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      23 AGGGGGGAAGAGGAAA 38
Db      16 AGGGGGGAAAGAAAA 1

RESULT 661
US-08-754-477A-37
; Sequence 37, Application US/08754477A
; Patent No. 6518411
; GENERAL INFORMATION:
; APPLICANT: Murray, Jeffrey
; APPLICANT: Semina, Elena
; TITLE OF INVENTION: RIEG COMPOSITIONS AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/754,477A
; FILING DATE: 22-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-022.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-754-477A-37

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1533 GGCCTGCAGCGCTGG 1548
Db      1 GGCCTCCAGCTCCTGG 16
```

```
RESULT 662
US-09-474-432B-1
; Sequence 1, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleoti
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-474-432B-1

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      605 ATGGGGGCCCACTCC 620
Db      1 AUGGGGCGACACUCC 16

RESULT 663
US-09-474-432B-21
; Sequence 21, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleoti
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 16
```

```

; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-474-432B-21

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      606 TGGGGGGCCCCCACTCCA 621
Db      1 UGGGGGCGACACUCCA 16

RESULT 664
US-09-829-855-40/c
; Sequence 40, Application US/09829855
; Patent No. 6613520
; GENERAL INFORMATION:
; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
; FILE REFERENCE: ASHBY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 16
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: unidentified soil organism
US-09-829-855-40

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      81 AGGTGCGGCGACGGAAG 96
Db      16 AGGTGCGGCGACGGAAG 1

RESULT 665
US-09-829-855-115/c
; Sequence 115, Application US/09829855
; Patent No. 6613520
; GENERAL INFORMATION:
; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
; FILE REFERENCE: ASHBY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTH: 16
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: unidentified soil organism
US-09-829-855-115

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      81 AGGTGCGGCGACGGAAG 96
Db      16 AGGTGCGGCGACGGAAG 1

RESULT 666
US-09-476-387-1
; Sequence 1, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hepatitis C Virus
US-09-476-387-1

Query Match      0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      605 ATGGGGGCCCCCACTCC 620
Db      1 AUGGGGGCGACACUCC 16

RESULT 667
US-09-476-387-21
; Sequence 21, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04

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; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hepatitis C Virus
US-09-476-387-21

Query Match          0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      606 TGGGGGCCCCACTCCA 621
Db      1 UGGGGGCGACACUCCA 16

RESULT 668
US-09-722-319-38/c
; Sequence 38, Application US/09722319
; Patent No. 6632607
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRANCOISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacterium
; TITLE OF INVENTION: Antibiotic Resistance
; FILE REFERENCE: 1657.0010001
; CURRENT APPLICATION NUMBER: US/09/722,319
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/750,088
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: PCT/EP95/02230
; PRIOR FILING DATE: 1995-06-09
; PRIOR APPLICATION NUMBER: EP 94870093.5
; PRIOR FILING DATE: 1994-06-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-722-319-38

Query Match          0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      242 CGGGGCCACCGCGC 257
Db      16 CGCGGCCACGACCGGC 1

RESULT 669
PCT-US92-10770-11
; Sequence 11, Application PC/TUS9210770
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Antiviral Reagents Based on
; TITLE OF INVENTION: RNA-Binding Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: SRI International
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10770
; FILING DATE: 19921211
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,452
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: P-2962
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-4550
; TELEFAX: (415) 859-3880
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE, 12/A1
PCT-US92-10770-11

Query Match          0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      23 AGGGGGGAAGAGGAAA 38
Db      1 AGGGGGGAAGAGGAAA 16

RESULT 670
PCT-US92-10770-12/c
; Sequence 12, Application PC/TUS9210770
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Antiviral Reagents Based on
; TITLE OF INVENTION: RNA-Binding Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI International
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10770
; FILING DATE: 19921211
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,452
```

```
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: P-2962
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-4550
; TELEFAX: (415) 859-3880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE,
; INDIVIDUAL ISOLATE: 12/A-2
PCT-US92-10770-12

Query Match          0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      23 AGGGGGGAAGAGGAAA 38
Db      16 AGGGGGGAAGAGAAA 1

RESULT 671
PCT-US92-10792-9
; Sequence 9, Application PC/TUS9210792
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Triple Helix Formation at
; TITLE OF INVENTION: (PUNPYN)-(PUNPYN) Tracts
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI International
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10792
; FILING DATE: 19921211
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,934
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,452
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: P-3141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-4550
; TELEFAX: (415) 859-3880
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: FIGURE 10, A-1
PCT-US92-10792-9

Query Match          0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      23 AGGGGGGAAGAGGAAA 38
Db      1 AGGGGGGAAGAGAAA 16

RESULT 672
PCT-US92-10792-10/c
; Sequence 10, Application PC/TUS9210792
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Triple Helix Formation at
; TITLE OF INVENTION: (PUNPYN)-(PUNPYN) Tracts
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI International
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10792
; FILING DATE: 19921211
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,934
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,452
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: P-3141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-4550
; TELEFAX: (415) 859-3880
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: FIGURE 10, A-2
PCT-US92-10792-10

Query Match          0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      23 AGGGGGGAAGAGGAAA 38
Db      16 AGGGGGGAAGAGAAA 1
```

RESULT 673
PCT-US94-02471-56
; Sequence 56, Application PC/TUS9402471
; GENERAL INFORMATION:
; APPLICANT: Draper et al.
; TITLE OF INVENTION: Oligonucleotide Therapies for
; TITLE OF INVENTION: Modulating the Effects of Herpesviruses
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02471
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 485,297
; FILING DATE: February 26, 1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,132
; FILING DATE: April 28, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 954,185
; FILING DATE: September 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISIS-0469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
PCT-US94-02471-56

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGG 1030
| | | | | | | | | | | | | | | |
Db 1 GGGTTGGGGTGGG 16

RESULT 674
PCT-US94-09143-46
; Sequence 46, Application PC/TUS9409143
; GENERAL INFORMATION:
; APPLICANT: Chandrasegaran, Srinivasan
; TITLE OF INVENTION: Functional Domains in FokI
; TITLE OF INVENTION: Restriction Endonuclease
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1100 New York Ave., N.W.
; CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09143
FILING DATE: 23-AUG-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,564
FILING DATE: 27-SEPTEMBER-93
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/4130/82506/CLB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3503
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-09143-46

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 19 AATTAGGGGGGAAGAG 34
| | | | | | | | | | | | | | | |
Db 1 ATTAAGGGGGGAAGAG 16

RESULT 675
US-08-152-313-67/c
; Sequence 67, Application US/08152313
; Patent No. 5561041
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,313
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100

```

; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
US-08-152-313-67

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1023 GGATGGGGCTGGGGTT 1038
Db 16 GGATGGGGCTCCGGT 1

RESULT 676
US-08-373-124A-2149/c
; Sequence 2149, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-2149

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1733 TACAAAAAATAAAAAA 1748
Db 16 TATAAAAAATAAAAAA 1

RESULT 677
US-08-579-223-67/c
; Sequence 67, Application US/08579223
; Patent No. 5726019
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,223
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/152,313
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
US-08-579-223-67

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1023 GGATGGGGCTGGGGTT 1038
Db 16 GGATGGGGCTCCGGT 1

RESULT 678
US-08-309-512-16
; Sequence 16, Application US/08309512
; Patent No. 5759828
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Tal, Ronny
; APPLICANT: Benzinan, Moshe
; APPLICANT: Gelfand, David H.
; APPLICANT: Ben-Bassat, Arie
; APPLICANT: Calhoon, Roger D.
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC ENZYMES
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/309,512
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,218
; FILING DATE: 29-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bortner, Scott R.
; REGISTRATION NUMBER: 34,298
; REFERENCE/DOCKET NUMBER: 8145-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; US-08-309-512-16

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 5.5e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 119 GGGGCTTCAAGACCGC 134
|:|:|:|:|:|:|:|:|
Db 2 GKGGMTTYAAYACMGC 17

RESULT 679
US-08-758-306-83/c
; Sequence 83, Application US/08/58306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
```

```
;
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-83

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1442 GCTGTTACAAGTGCGA 1457
|:|:|:|:|:|:|:|:|
Db 17 GCTGTTCCAAGTGCAA 2

RESULT 680
US-08-758-306-1067/c
; Sequence 1067, Application US/08/58306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1067:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-1067

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1442 GCTGTTACAAGTGGCA 1457
      ||||| |||||
Db      17 GCTGTTCCAAGTGGCA 2

RESULT 681
US-08-435-628-2149/c
; Sequence 2149, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1067:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-1067

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1733 TACAAAAAATAAAAAA 1748
      || ||||| |||||
Db      16 TATAAAAAATAAAAAA 1

RESULT 682
US-08-292-620A-1770/c
; Sequence 1770, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1770:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
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two

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1770
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 862 GGAAGAGGAAGAGGAG 877
Db 17 GCAAGAGGAAGAGCAG 2

RESULT 683
US-08-292-620A-1894/c
; Sequence 1894, Application US/082922620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1894:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1894
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 862 GGAAGAGGAAGAGGAG 877
Db 16 GCAAGAGGAAGAGCAG 1

RESULT 684
US-08-292-620A-1984/c
; Sequence 1984, Application US/082922620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1984:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1984
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 862 GGAAGAGGAAGAGGAG 877
Db 16 GCAAGAGGAAGAGCAG 1
```

two

two


```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-857

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 190 CAGCCGGAGCCCGCCA 205
Db 16 CAGCCTGTGCCCGCCA 1

RESULT 688
US-08-665-259-42/c
; Sequence 42, Application US/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide primer"
US-08-665-259-42

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1241 GCTGCTTCACCTGCGT 1256
Db 17 GCTCCTTCACCGCGT 2

RESULT 689
US-08-665-259-55/c
; Sequence 55, Application US/08665259
```

```
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide primer"
US-08-665-259-55

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1241 GCTGCTTCACCTGCGT 1256
Db 17 GCTCCTTCACCGCGT 2

RESULT 690
US-08-762-500-42/c
; Sequence 42, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
```

```
;
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide primer"
;
US-08-762-500-42

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1241 GCTGCTTCACCTGCGT 1256
Db 17 GCTCCTTCACCAGCGT 2

RESULT 691
US-08-762-500-55/c
; Sequence 55, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

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;
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide primer"
;
US-08-762-500-55

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1241 GCTGCTTCACCTGCGT 1256
Db 17 GCTCCTTCACCAGCGT 2

RESULT 692
US-08-463-903-89
; Sequence 89, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/08/463,903
; CURRENT FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 07/935,695
; EARLIER FILING DATE: 1992-08-21
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 89
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Aint2 primer
; LOCATION: 1..17
;
US-08-463-903-89

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 510 ACCAGACCGACAGGCA 525
Db 2 ACCAGACCGACAGTCA 17

RESULT 693
US-08-998-099-91
; Sequence 91, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
```

APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-08-998-099-91

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 5.5e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 415 GGGGGCCTTCGCCCTG 430
Db 1 GGAGGCCUCCACCCUG 16

RESULT 694

US-09-071-845-1770/c
; Sequence 1770, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1770:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-1770

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 862 GGAAGAGGAAGAGGAG 877
Db 17 GCAAGAGGAAGAGCAG 2

RESULT 695

US-09-071-845-1894/c
; Sequence 1894, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1894:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-1894

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 862 GGAAGAGGAAGAGGAG 877
Db 16 GCAAGAGGAAGAGCAG 1

RESULT 696

US-09-071-845-1984/c
; Sequence 1984, Application US/09071845
; Patent No. 6132967

GENERAL INFORMATION:

; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/071,845
; FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1984:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-1984

Query Match 0.7%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 862 GGAAGAGGAAGAGGAG 877
Db 16 GCAAGAGGAAGAGCAG 1

RESULT 697

US-09-021-701-74/c
; Sequence 74, Application US/09021701
; Patent No. 6251588

GENERAL INFORMATION:

; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.
; APPLICANT: Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; TITLE OF INVENTION: probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,701
; FILING DATE: 10-FEB-1998

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-021-701-74

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 773 GAGGTGAAGTCTGGGG 788
Db 17 GAGGAGAAGTCTGCGG 2

RESULT 698

US-09-021-701-75/c
; Sequence 75, Application US/09021701
; Patent No. 6251588

GENERAL INFORMATION:

; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.

APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
TITLE OF INVENTION: probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-75

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 773 GAGGTGAAGTCTGGG 788
Db 16 GAGGAGAAGTCTGCGG 1

RESULT 699
US-08-957-351-28
Sequence 28, Application US/08957351
Patent No. 6306586
GENERAL INFORMATION:
APPLICANT: Semina, Elena
APPLICANT: Murray, Jeffrey C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CATARACTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,351
FILING DATE: 24-OCT-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-024.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "probe"
US-08-957-351-28

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1533 GGCCTGCAGCGCCTGG 1548
Db 1 GGCCTGCAGCGCCTGG 16

RESULT 700
US-07-935-695-89
Sequence 89, Application US/07935695
Patent No. 6329507
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Kotite, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 89
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Aint2 primer
LOCATION: 1..17
OTHER INFORMATION: :
US-07-935-695-89

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 510 ACCAGACCGACAGGCA 525
Db 2 ACCAGACCGACAGTCA 17

RESULT 701
US-08-584-040-2519/c
Sequence 2519, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR

;; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
;; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
;; TITLE OF INVENTION: GROWTH FACTOR
;; NUMBER OF SEQUENCES: 8502
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 2519:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-584-040-2519

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 GAAGAGGAAAAAAA 44
|||
Db 16 GAAGAGGAACACAA 1

RESULT 702

US-08-584-040-2556/c
; Sequence 2556, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 2556:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-584-040-2556

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAAAA 1746
|||
Db 16 TTGGAAAAAAA 1

RESULT 703

US-08-584-040-2740/c
; Sequence 2740, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974


```
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2740:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2740

Query Match          0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1704 CCAATCAAGAAATAAT 1719
Db 17 CCAATTAGAAATATT 2
||||| |||||||

RESULT 704
US-08-584-040-7822/c
; Sequence 7822, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7822:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7822
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7822

Query Match          0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1749
Db 16 ACAAAACAAACAAACAA 1
||||| |||||||

RESULT 705
US-08-584-040-7824/c
; Sequence 7824, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7824:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7824

Query Match          0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1749
Db 16 ACAAAACAAACAAACAA 1
||||| |||||||
```

RESULT 706

US-08-679-645-880/c
; Sequence 880, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 880:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-679-645-880

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1749

|||||

Db 17 ACAAAATAAAACAA 2

RESULT 707

US-08-679-645-882/c
; Sequence 882, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:

; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 882:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-679-645-882

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1733 TACAAAAAAAAAAAAA 1748

|||||

Db 16 TACAAATAAAACAA 1

RESULT 708

US-09-593-012-23/c
; Sequence 23, Application US/09593012
; Patent No. 6387652
; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990

; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/081,773
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Aspergillus niger/foetidis/phoenicus
US-09-593-012-23

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 840 TGCTGGGGTCTCTGGC 855
||| ||||| |||
Db 16 TGTGGGGTCTCCGC 1

RESULT 709
US-09-474-432B-526
; Sequence 526, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 526
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-526

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1398 GGAGACTGTGAGAATT 1413
||||| :||| :|||
Db 2 GGAGAAUGUGAAAAUU 17

RESULT 710
US-09-474-432B-558/c
; Sequence 558, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka

; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleoti
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 558
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-558

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1751
||| ||| |||||
Db 17 AAACAAACACAAAAAA 2

RESULT 711
US-09-474-432B-559/c
; Sequence 559, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleoti
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 559
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-559

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1751
||||| |||||
Db 16 AAAAAACACAAAAAA 1

RESULT 712
US-09-474-432B-568
; Sequence 568, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 568
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-568

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 228 CCCCGCGGCACCCCG 243
Db 1 CCCUCGCGACACCCCG 16

RESULT 713
US-09-474-432B-825/c
; Sequence 825, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 825
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-474-432B-825
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 170 CCACCTGGCTGCCCCC 185
Db 17 CCCCTGGCTGCCCCC 2

RESULT 714
US-08-415-658-6/c
; Sequence 6, Application US/08415658
; Patent No. 6566105
; GENERAL INFORMATION:
; APPLICANT: GRIFANTINI, RENATA
; APPLICANT: FRASCOTTI, GIANNI
; APPLICANT: GALLI, GIULIANO
; APPLICANT: GRANDI, GUIDO
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF
; TITLE OF INVENTION: D-ALPHA-AMINO ACIDS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,658
; FILING DATE: 03-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT MI94 A 000726
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2264-085-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-415-658-6

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1506 CCCGCTGGATCGGCAC 1521
Db 16 CCCGCTGGATCGGCAC 1

RESULT 715
US-09-371-772B-1043/c
; Sequence 1043, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1043
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1043

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 29 GAAGAGGAAAAA 44
Db 16 GAAGAGGAAACA 1

RESULT 716

US-09-371-772B-1080/c
; Sequence 1080, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1080
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1080

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTACAAAAA 1746
Db 16 TTGGAAAAA 1

RESULT 717

US-09-371-772B-1264/c
; Sequence 1264, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1264
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1264

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1704 CCAATCAAGAAATAT 1719
Db 17 CCAATTAAGAAATATT 2

RESULT 718

US-09-371-772B-3606/c
; Sequence 3606, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3606
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3606

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 ACAAAAAA 1749
Db 16 ACAAAACA 1

RESULT 719

US-09-371-772B-3608/c
; Sequence 3608, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3608
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3608

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1749
||||| ||||| |||||
Db 16 ACAACAACAACAAAAA 1

RESULT 720
US-09-371-772B-5343/c
; Sequence 5343, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5343
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5343

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 721 GCCTCTCAGGCTTCTG 736
||||| ||||| |||||
Db 17 GCCTCTCCAGCTTCTG 2

RESULT 721
US-09-371-772B-5476/c
; Sequence 5476, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5476
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5476

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1631 CCATCCTTTGATTGAT 1646
||||| ||||| |||||
Db 17 CCATTCCTTGACTGAT 2

RESULT 722
US-09-371-772B-5562/c
; Sequence 5562, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5562
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5562

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1704 CCAATCAAGAAATAAT 1719
||||| ||||| |||||
Db 16 CCAATTAAGAAATATT 1

RESULT 723
US-09-371-772B-6785
; Sequence 6785, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan

```
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6785
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6785

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1188 CCAGCCCATCCTGGAC 1203
Db      2 CCAGACCAUGCUGGAC 17
      ||||| |||: |:||||
      ||||| |||: |:||||

RESULT 724
US-09-371-772B-6956/c
; Sequence 6956, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6956
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6956

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      398 GGCTCCCTGCAGACAG 413
Db      16 GGCTCCCTGCAGTCCG 1
      ||||| ||||| |||
      ||||| ||||| |||

RESULT 725
US-09-476-387-525
; Sequence 525, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
```

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; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-525

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1398 GGAGACTGTGAGAATT 1413
Db      2 GGAGAAUGUGAAAAAU 17
      ||||| |:|:| ||::
      ||||| |:|:| ||::

RESULT 726
US-09-476-387-557/c
; Sequence 557, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 557
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-557

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAA 1751
      ||| |||| | |||||
```


Db 17 AAACAAACAAACAAAAA 2

RESULT 727

US-09-476-387-558/c

; Sequence 558, Application US/09476387

; Patent No. 6617438

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Beigelman, Leo

; APPLICANT: Beaudry, Amber

; APPLICANT: Karpeisky, Alex

; APPLICANT: Adamic, Jasenka Matulic

; APPLICANT: Sweedler, Dave

; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot

; FILE REFERENCE: MBHB00-831-C (249/073)

; CURRENT APPLICATION NUMBER: US/09/476,387

; CURRENT FILING DATE: 2001-04-04

; PRIOR APPLICATION NUMBER: 09/474,432

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: 09/301,511

; PRIOR FILING DATE: 1999-04-28

; PRIOR APPLICATION NUMBER: 09/186,675

; PRIOR FILING DATE: 1998-11-04

; PRIOR APPLICATION NUMBER: 60/083,727

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/064,866

; PRIOR FILING DATE: 1997-11-05

; NUMBER OF SEQ ID NOS: 1524

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 558

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-09-476-387-558

Query Match 0.7%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 5.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751

Db 16 AAAAAAAAAACAAACAAA 1

RESULT 728

US-09-476-387-567

; Sequence 567, Application US/09476387

; Patent No. 6617438

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Beigelman, Leo

; APPLICANT: Beaudry, Amber

; APPLICANT: Karpeisky, Alex

; APPLICANT: Adamic, Jasenka Matulic

; APPLICANT: Sweedler, Dave

; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot

; FILE REFERENCE: MBHB00-831-C (249/073)

; CURRENT APPLICATION NUMBER: US/09/476,387

; CURRENT FILING DATE: 2001-04-04

; PRIOR APPLICATION NUMBER: 09/474,432

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: 09/301,511

; PRIOR FILING DATE: 1999-04-28

; PRIOR APPLICATION NUMBER: 09/186,675

; PRIOR FILING DATE: 1998-11-04

; PRIOR APPLICATION NUMBER: 60/083,727

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/064,866

; PRIOR FILING DATE: 1997-11-05

; NUMBER OF SEQ ID NOS: 1524

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 567

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-09-476-387-567

Query Match 0.7%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 5.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 228 CCCCCGCGCACCCCCG 243

Db 1 CCCUCGCAGCACCCCCG 16

RESULT 729

US-09-476-387-824/c

; Sequence 824, Application US/09476387

; Patent No. 6617438

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Beigelman, Leo

; APPLICANT: Beaudry, Amber

; APPLICANT: Karpeisky, Alex

; APPLICANT: Adamic, Jasenka Matulic

; APPLICANT: Sweedler, Dave

; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti

; FILE REFERENCE: MBHB00-831-C (249/073)

; CURRENT APPLICATION NUMBER: US/09/476,387

; CURRENT FILING DATE: 2001-04-04

; PRIOR APPLICATION NUMBER: 09/474,432

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: 09/301,511

; PRIOR FILING DATE: 1999-04-28

; PRIOR APPLICATION NUMBER: 09/186,675

; PRIOR FILING DATE: 1998-11-04

; PRIOR APPLICATION NUMBER: 60/083,727

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/064,866

; PRIOR FILING DATE: 1997-11-05

; NUMBER OF SEQ ID NOS: 1524

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 824

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo sapiens

US-09-476-387-824

Query Match 0.7%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 5.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 170 CCACCTGGCTGCCCCC 185

Db 17 CCCCTTGGCTGCCCCC 2

RESULT 730

US-09-827-998-376

; Sequence 376, Application US/09827998

; Patent No. 6656700

; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong

; APPLICANT: Shannon, Mark

; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

; FILE REFERENCE: MDHMORF-8

; CURRENT APPLICATION NUMBER: US/09/827,998

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/236,359

```
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 376
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-376

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1454 GCGAGGAGTGTGGCT 1469
Db      2 GCGAGGAGTGTGTGTT 17

RESULT 731
US-09-827-998-377
; Sequence 377, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 377
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-377

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1454 GCGAGGAGTGTGGCT 1469
Db      1 GCGAGGAGTGTGTGTT 16

RESULT 732
US-09-827-998-483
; Sequence 483, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 483
; LENGTH: 17
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-827-998-483

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      37 AAAAAAAAAAGCCAGAA 52
Db      2 AAAAAAAAAAGAAAGAA 17

RESULT 733
US-09-827-998-485
; Sequence 485, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 485
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-485

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      38 AAAAAAAAAAGCCAGAA 53
Db      1 AAAAAAAAAAGAAAGAA 16

RESULT 734
US-09-866-108A-645/C
; Sequence 645, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 645
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-645

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1089 CCGGGCCCCAGCTTCGC 1104
Db 17 CCGGGTCCAGCTTGGC 2

RESULT 735
US-09-866-108A-646/c
; Sequence 646, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 646
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-646

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1089 CCGGGCCCCAGCTTCGC 1104
Db 17 CCGGGTCCAGCTTGGC 2

RESULT 735
US-09-866-108A-646/c
; Sequence 646, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 646
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-646
```

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Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1089 CCGGGCCCCAGCTTCGC 1104
Db 16 CCGGGTCCAGCTTGGC 1

RESULT 736
US-09-866-108A-895
; Sequence 895, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 895
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-895

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1020 TCGGGATGGGCTGGG 1035
Db 2 TGGGAAGGGGCTTGG 17

RESULT 737
US-09-866-108A-897
; Sequence 897, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
```

```
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 897
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-897

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1021 GGGGATGGGCTGGG 1036
Db      1 GGGGAAGGGCTGGG 16

RESULT 738
US-09-866-108A-1424
; Sequence 1424, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1424
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1424

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      70 AGTCCCAACGAGGTG 85
Db      2 AGCCCCAAGGAGGTG 17

RESULT 739
US-09-866-108A-1425
; Sequence 1425, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1425
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1425
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Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 70 AGTCCCAACGAGGTG 85
||| ||||| |||||
Db 1 AGCCCAAGAGGTG 16

RESULT 740
US-09-866-108A-1530
; Sequence 1530, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1530
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1530

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1021 GGGGATGGGCTGGG 1036
||| ||||| |||||
Db 2 GGTGATGGGCTGGT 17

RESULT 741
US-09-866-108A-1531
; Sequence 1531, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1530
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1530

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1021 GGGGATGGGCTGGG 1036
||| ||||| |||||
Db 2 GGTGATGGGCTGGT 17

RESULT 742
US-09-866-108A-1638
; Sequence 1638, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1530
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1531

; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1531
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1531

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1021 GGGGATGGGCTGGG 1036
||| ||||| |||||
Db 1 GGTGATGGGCTGGT 16

RESULT 742
US-09-866-108A-1638
; Sequence 1638, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1531
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1531

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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1638
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1639

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      854 GCCCTGCAGGAAGG 869
      ||||| ||||| |||||
Db      2 GCCCCGCGAGGAGG 17

RESULT 743
US-09-866-108A-1639
; Sequence 1639, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1639
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
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```
US-09-866-108A-1639

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      854 GCCCTGCAGGAAGG 869
      ||||| ||||| |||||
Db      1 GCCCCGCGAGGAGG 16

RESULT 744
US-09-866-108A-2252/c
; Sequence 2252, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2252
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2252

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      672 AGTGAAGGTGGCACAG 687
      ||||| ||||| |||||
Db      17 AGTGAAGGTGGCTCGG 2

RESULT 745
US-09-866-108A-2253/c
; Sequence 2253, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
```



```
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2253
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2253

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      672 AGTGAAGGTGGCACAG 687
Db      16 AGTGAAGGTGGCTCGG 1

RESULT 746
US-09-866-108A-6140/c
; Sequence 6140, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2253
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2253
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```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6140
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6140

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      550 TACCGCACGGGCTCCC 565
Db      17 TACCGCACAGGGTCCC 2

RESULT 747
US-09-866-108A-6141/c
; Sequence 6141, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6141
; LENGTH: 17
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-866-108A-6141

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 550 TACCGCACGGGCTCCC 565
|||||
Db 16 TACCGCACAGGCTCCC 1

RESULT 748

US-09-866-108A-7436/c
; Sequence 7436, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 7436

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-7436

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 306 TCCATCTGACGAGTGT 321
|||||
Db 17 TCCATCTGACGACAGT 2

RESULT 749

US-09-866-108A-7437/c
; Sequence 7437, Application US/09866108A
; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 7436

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-7436

; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 7437

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-7437

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 306 TCCATCTGACGAGTGT 321
|||||
Db 16 TCCATCTGACGACAGT 1

RESULT 750

US-09-866-108A-10023

; Sequence 10023, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 7436

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-7437

```

; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10023
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-10023

```

```

Query Match      .      0.7%;      Score 12.8;      DB 1;      Length 17;
Best Local Similarity 87.5%;      Pred. NO. 5.5e+02;
Matches 14;      Conservative 0;      Mismatches 2;      Indels 0;      Gaps 0;

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Qy 133 GCTGCTGGAGTCCC 148
Db 1 GGTGCTGGAGTCCTC 16

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RESULT 751
US-09-866-108A-10228
; Sequence 10228, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeo mica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10228
; LENGTH: 17

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10228

```

Query Match	0.7%;	Score 12.8;	DB 1;	Length 17;
Best Local Similarity	87.5%;	Pred. No. 5.5e+02;		
Matches 14;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

Qy 1229 CCTACCACCTGGCTG 1244
 |||||
Db 2 CCTACCTCCTGGCTG 17

RESULT 752
US-09-866-108A-10229
; Sequence 10229, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10229
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10229

Query Match	0.7%;	Score 12.8;	DB 1;	Length 17;
Best Local Similarity	87.5%;	Pred. No. 5.5e+02;		
Matches 14;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;

Qy 1229 CCTACCACCTGGCTG 1244
Db 1 CCTACCTCCTGGCTG 16

RESULT 753
US-09-866-108A-10507
; Sequence 10507, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:

```
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10507
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10507

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      810 AGAGCCAGGCGCCAGG 825
      ||||| ||||| |||||
Db      1 AGAGCCAGGCGACGGG 16

RESULT 754
US-09-866-108A-10742/c
; Sequence 10742, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10507
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10507
```

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10742
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10742

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1226 AGGCCTACCACCTGG 1241
      ||||| ||||| |||||
Db      17 AGGCCAACCACTGG 2

RESULT 755
US-09-866-108A-10743/c
; Sequence 10743, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10743
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; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10743

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1226 AGGCTACCACCTGG 1241
Db 16 AGGCCAACCACTGG 1

RESULT 756
PCT-US94-12947A-67/c
; Sequence 67, Application PC/TUS9412947A
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12947A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: FD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
PCT-US94-12947A-67

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1023 GGATGGGGCTGGGTT 1038
Db 16 GGATGGGGCTCCGTT 1

RESULT 757
US-08-332-838-3/c
; Sequence 3, Application US/08332838
; Patent No. 5529916
; GENERAL INFORMATION:
; APPLICANT: Cormack, Brendan P.
; ATTORNEY/AGENT INFORMATION:
```

```
; TITLE OF INVENTION: Leukotriene A4 Hydrolase From Candida
; TITLE OF INVENTION: Albicans
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert,
; ADDRESSEE: Attn: R.M. Silva
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,838
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-60324/RFT/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-332-838-3

Query Match      0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1748
Db 14 CTAAAAAATAAAAAA 1

RESULT 758
US-08-435-684A-9
; Sequence 9, Application US/08435684A
; Patent No. 5707802
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Gurpreet S.
; APPLICANT: Kline, Bruce C.
; TITLE OF INVENTION: Nucleic Acid Probes for the Detection
; TITLE OF INVENTION: and Identification of Fungi
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba Corning Diagnostics Corp.
; STREET: 63 No. 5707802th Street
; CITY: Medfield
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02052
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS 6.2
; SOFTWARE: Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,684A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
```

; NAME: Morgenstern, Arthur S.
; REGISTRATION NUMBER: 28,244
; REFERENCE/DOCKET NUMBER: CCD-180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508 359-3836
; TELEFAX: 508 359-3885
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Nucleic acid probe for Histoplasma capsulatum
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-435-684A-9

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 224 CGATCCCGCGGC 237
Db 1 CAATCCCGCGGC 14

RESULT 759

US-08-373-127B-9
; Sequence 9, Application US/08373127B
; Patent No. 5763169

; GENERAL INFORMATION:
; APPLICANT: Sandhu, Gurpreet S.
; APPLICANT: Kline, Bruce C.
; TITLE OF INVENTION: Nucleic Acid Probes for the Detection
; TITLE OF INVENTION: and Identification of Fungi
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ciba Corning Diagnostics Corp.
; STREET: 63 No. 5763169th Street
; CITY: Medfield
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02052

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS 6.2
; SOFTWARE: Word 6.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,127B
; FILING DATE: January 13, 1995
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Morgenstern, Arthur S.
; REGISTRATION NUMBER: 28,244
; REFERENCE/DOCKET NUMBER: CCD-180
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 508 359-3836
; TELEFAX: 508 359-3885
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Nucleic acid probe for Histoplasma capsulatum
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-373-127B-9

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 224 CGATCCCGCGGC 237
Db 1 CAATCCCGCGGC 14

RESULT 760

US-08-494-577-10/c
; Sequence 10, Application US/08494577
; Patent No. 5786171

; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Hsieh, Chung-Ming
; TITLE OF INVENTION: AORTIC PREFERENTIALLY EXPRESSED GENE AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,577
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 436

; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/012001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

US-08-494-577-10

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA 1748
Db 14 CAAAAA 1

RESULT 761

US-08-795-868-10/c
; Sequence 10, Application US/08795868
; Patent No. 5846773

; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Hsieh, Chung-Ming
; TITLE OF INVENTION: A SINGLE GENE ENCODING AORTIC-SPECIFIC
; TITLE OF INVENTION: AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA

```
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,868
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/494,577
; FILING DATE: 22-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/032001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-795-868-10

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1748
Db 14 CBAATAAAAAAATA 1

RESULT 762
US-08-934-877A-9
; Sequence 9, Application US/08934877A
; Patent No. 5958693
; GENERAL INFORMATION:
; APPLICANT: SANDHU, Gurpreet S.
; APPLICANT: KLINE, Bruce C.
; TITLE OF INVENTION: DNA ISOLATION METHOD
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,877A
; FILING DATE: 22-SEP-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,684
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bern D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 080394/0108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399

; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,868
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/494,577
; FILING DATE: 22-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/032001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-795-868-10

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1748
Db 14 CBAATAAAAAAATA 1

RESULT 763
US-08-832-021-5/c
; Sequence 5, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-5

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAATAAAAA 1745
Db 14 TTAATAAAAAAATAAAAA 1

RESULT 764
US-08-832-021-7/c
; Sequence 7, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-7

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA1748
Db 14 CTA1

RESULT 765

US-08-832-021-8/c
; Sequence 8, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-8

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAA1747
Db 14 ATA1

RESULT 766

US-08-832-021-11/c
; Sequence 11, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-11

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA1748
Db 14 CGA1

RESULT 767

US-08-832-021-12/c
; Sequence 12, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-12

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAA1747
Db 14 AGA1

RESULT 768

US-08-724-466B-16/c
; Sequence 16, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 16:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-724-466B-16

Query Match          0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1748
Db 14 CTAATAAAAAATAAAA 1

RESULT 769
US-08-724-466B-17/c
; Sequence 17, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-724-466B-17

Query Match          0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAATAAAAAA 1745
Db 14 TTAATAAAAAATAAAA 1

RESULT 770
US-08-724-466B-18/c
; Sequence 18, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
```

```
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-724-466B-18

Query Match          0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAATAAAAA 1747
Db 14 ATAAAAATAAAAAA 1

RESULT 771
US-08-724-466B-20/c
; Sequence 20, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-724-466B-17

Query Match          0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAATAAAAAA 1745
Db 14 TTAATAAAAAATAAAA 1

RESULT 770
US-08-724-466B-18/c
; Sequence 18, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-724-466B-20

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAA 1748
Db 14 CGAAAA AAAAAA 1

RESULT 772

US-08-724-466B-22/c
Sequence 22, Application US/08724466B
Patent No. 6063606

GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-724-466B-22

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAA AAAAAA 1747
Db 14 AGAAAA AAAAAA 1

RESULT 773

US-08-871-678C-9
Sequence 9, Application US/08871678C

Patent No. 6180339
GENERAL INFORMATION:
APPLICANT: Sandhu, Gurpreet S, Kline, Bruce C
TITLE OF INVENTION: Nucleic Acid Probes for the Detection and
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Diagnostics Corporation
STREET: 63 No. 6180339th Street
CITY: Medfield
STATE: Massachusetts
COUNTRY: USA
ZIP: 02052

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS 6.2
SOFTWARE: Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,678C
FILING DATE: 06-JUNE-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,127
FILING DATE: 13-JANUARY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/435,684
FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Morgenstern, Arthur S.
REGISTRATION NUMBER: 28,244
REFERENCE/DOCKET NUMBER: CCD-180CIP11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508 359-3836
TELEFAX: 508 359-3885

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Nucleic acid probe for Histoplasma capsulatum
HYPOTHETICAL: No
ANTI-SENSE: No
US-08-871-678C-9

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 224 CGATCCCCCGCGC 237
Db 1 CAATCCCCCGCGC 14

RESULT 774

US-08-991-789A-130/c
Sequence 130, Application US/08991789A
Patent No. 6225054

GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 292
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,789A
; FILING DATE: 11-Dec-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-08-991-789A-130

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA1748
|
Db 14 CTAAAAA1

RESULT 775

US-08-882-164D-16/c
; Sequence 16, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653

; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-16

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA1748
|
Db 14 CTAAAAA1

RESULT 776

US-08-882-164D-17/c
; Sequence 17, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-17

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAA1745
|
Db 14 TTAAAAA1

RESULT 777

US-08-882-164D-18/c
; Sequence 18, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville

;/ TITLE OF INVENTION: Retinoid Metabolizing Protein
;/ NUMBER OF SEQUENCES: 43
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Blake, Cassels & Graydon
;/ STREET: Box 25, Commerce Court West
;/ CITY: Toronto
;/ STATE: Ontario
;/ COUNTRY: Canada
;/ ZIP: M5L 1A9
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
;/ COMPUTER: COMPAQ, IBM PC compatible
;/ OPERATING SYSTEM: MS-DOS 5.1
;/ SOFTWARE: WORD PERFECT
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/882,164D
;/ FILING DATE: June 25, 1997
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/667,546
;/ FILING DATE: June 21, 1996
;/ APPLICATION NUMBER: 08/724,466
;/ FILING DATE: October 1, 1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Hunt, John C.
;/ REGISTRATION NUMBER: 36,424
;/ REFERENCE/DOCKET NUMBER: 50767/00010
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (416) 863-4344
;/ TELEFAX: (416) 863-2653
;/ INFORMATION FOR SEQ ID NO: 18:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 14 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-882-164D-18

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAA 1747
| | | | | | | | | |
Db 14 ATAAAAAAAAAA 1

RESULT 778
US-08-882-164D-20/c
;/ Sequence 20, Application US/08882164D
;/ Patent No. 6306624
;/ GENERAL INFORMATION:
;/ APPLICANT: Petkovich, P. Martin, White, Jay A.,
;/ APPLICANT: Beckett, Barbara R., Jones, Glenville
;/ TITLE OF INVENTION: Retinoid Metabolizing Protein
;/ NUMBER OF SEQUENCES: 43
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Blake, Cassels & Graydon
;/ STREET: Box 25, Commerce Court West
;/ CITY: Toronto
;/ STATE: Ontario
;/ COUNTRY: Canada
;/ ZIP: M5L 1A9
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
;/ COMPUTER: COMPAQ, IBM PC compatible
;/ OPERATING SYSTEM: MS-DOS 5.1
;/ SOFTWARE: WORD PERFECT
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/882,164D
;/ FILING DATE: June 25, 1997
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/667,546
;/ FILING DATE: June 21, 1996

;/ APPLICATION NUMBER: 08/724,466
;/ FILING DATE: October 1, 1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Hunt, John C.
;/ REGISTRATION NUMBER: 36,424
;/ REFERENCE/DOCKET NUMBER: 50767/00010
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (416) 863-4344
;/ TELEFAX: (416) 863-2653
;/ INFORMATION FOR SEQ ID NO: 20:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 14 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-882-164D-20

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAA 1748
| | | | | | | | | |
Db 14 CGAAAAAAAAAA 1

RESULT 779
US-08-882-164D-22/c
;/ Sequence 22, Application US/08882164D
;/ Patent No. 6306624
;/ GENERAL INFORMATION:
;/ APPLICANT: Petkovich, P. Martin, White, Jay A.,
;/ APPLICANT: Beckett, Barbara R., Jones, Glenville
;/ TITLE OF INVENTION: Retinoid Metabolizing Protein
;/ NUMBER OF SEQUENCES: 43
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Blake, Cassels & Graydon
;/ STREET: Box 25, Commerce Court West
;/ CITY: Toronto
;/ STATE: Ontario
;/ COUNTRY: Canada
;/ ZIP: M5L 1A9
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
;/ COMPUTER: COMPAQ, IBM PC compatible
;/ OPERATING SYSTEM: MS-DOS 5.1
;/ SOFTWARE: WORD PERFECT
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/882,164D
;/ FILING DATE: June 25, 1997
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/667,546
;/ FILING DATE: June 21, 1996
;/ APPLICATION NUMBER: 08/724,466
;/ FILING DATE: October 1, 1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Hunt, John C.
;/ REGISTRATION NUMBER: 36,424
;/ REFERENCE/DOCKET NUMBER: 50767/00010
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (416) 863-4344
;/ TELEFAX: (416) 863-2653
;/ INFORMATION FOR SEQ ID NO: 22:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 14 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-882-164D-22

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      1734 ACAAAAAAAAAAAAAA 1747
      | | | | | | | | | |
Db      14 AGAAAAAAAAAAAAAA 1
      | | | | | | | | | |

RESULT 780
US-09-062-451-130/c
; Sequence 130, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062.451
; FILING DATE: 04-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.419C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-062-451-130

Query Match      0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAA 1748
      | | | | | | | | | |
Db      14 CTAAAAAAAAAAAAAA 1
      | | | | | | | | | |

RESULT 781
US-09-303-069-10/c
; Sequence 10, Application US/09303069A
; Patent No. 6350592
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Hsieh, Chung-Ming
; TITLE OF INVENTION: SINGLE GENE ENCODING AORTIC-SPECIFIC AND STRIATED-SPECIFIC
; TITLE OF INVENTION: MUSCLE CELL ISOFORMS AND USES THEREOF
; FILE REFERENCE: 05433/039001
; CURRENT APPLICATION NUMBER: US/09/303,069A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: US 09/134,250
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
```

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; SEQ ID NO 10
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic poly T anchoring primer
US-09-303-069-10

Query Match      0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAA 1748
      | | | | | | | | | |
Db      14 CBAAAAAAAAAAAAAA 1
      | | | | | | | | | |

RESULT 782
US-09-134-250-10/c
; Sequence 10, Application US/09134250B
; Patent No. 6399753
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Hsieh, Chung-Ming
; TITLE OF INVENTION: SINGLE GENE ENCODING AORTIC-SPECIFIC AND STRIATED-SPECIFIC
; TITLE OF INVENTION: MUSCLE CELL ISOFORMS AND USES THEREOF
; FILE REFERENCE: 05433/038001
; CURRENT APPLICATION NUMBER: US/09/134,250B
; CURRENT FILING DATE: 1998-08-14
; EARLIER APPLICATION NUMBER: US 08/795,868
; EARLIER FILING DATE: 1997-02-06
; EARLIER APPLICATION NUMBER: US 08/494,577
; EARLIER FILING DATE: 1995-06-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic poly T anchoring primer
US-09-134-250-10

Query Match      0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAA 1748
      | | | | | | | | | |
Db      14 CBAAAAAAAAAAAAAA 1
      | | | | | | | | | |

RESULT 783
US-09-598-326-130/c
; Sequence 130, Application US/09598326
; Patent No. 6423496
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 247
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,326
FILING DATE: 20-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-09-598-326-130

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1748
| |||||
Db 14 CTAATAAAAAAATAA 1

RESULT 784

US-09-370-838-47/c
Sequence 47, Application US/09370838
Patent No. 644425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 47
LENGTH: 14
TYPE: DNA
ORGANISM: Homo sapien
US-09-370-838-47

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1748
| |||||
Db 14 CTAATAAAAAAATAA 1

RESULT 785

US-09-475-947A-310
Sequence 310, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes

FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 310
LENGTH: 14
TYPE: DNA
ORGANISM: human
US-09-475-947A-310

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAATAAAAAA 1749
| |||||
Db 1 AAAAAAATAAAAAA 14

RESULT 786

US-09-289-198-130/c
Sequence 130, Application US/09289198
Patent No. 6586570
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289,198
CURRENT FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 09/062,451
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838,762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 130
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-289-198-130

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1748
| |||||
Db 14 CTAATAAAAAAATAA 1

RESULT 787

US-09-429-755-130/c
Sequence 130, Application US/09429755A
Patent No. 6656480
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.

;; APPLICANT: Misher, Lynda
;; APPLICANT: Retter, Marc W.
;; APPLICANT: Dillon, Davin C.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
;; FILE REFERENCE: 210121.419C6
;; CURRENT APPLICATION NUMBER: US/09/429,755A
;; CURRENT FILING DATE: 1999-10-28
;; NUMBER OF SEQ ID NOS: 315
;; SOFTWARE: FastSEQ for Windows Version 3.0
;; SEQ ID NO 130
;; LENGTH: 14
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Primer
US-09-429-755-130

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
| | | | | | | | | |
Db 14 CTAATAAAAAAAAAA 1

RESULT 788
US-08-041-599-2/c
; Sequence 2, Application US/08041599
; Patent No. 5393877
; GENERAL INFORMATION:
; APPLICANT: McLEAN, MICHAEL J.
; APPLICANT: HOLLAND, DAVID
; APPLICANT: GARMAN, ANDREW J.
; APPLICANT: SHEPPARD, ROBERT C.
; TITLE OF INVENTION: SYNTHESIS OF OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/041,599
; FILING DATE: 19930405
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 202706/SBI36848/US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-041-599-2

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
| | | | | | | | | |
Db 14 CGAAAAAAAAAAAAA 1

RESULT 789
US-08-337-025-2/c
; Sequence 2, Application US/08337025
; Patent No. 5552535
; GENERAL INFORMATION:
; APPLICANT: McLEAN, MICHAEL J.
; APPLICANT: HOLLAND, DAVID
; APPLICANT: GARMAN, ANDREW J.
; APPLICANT: SHEPPARD, ROBERT C.
; TITLE OF INVENTION: SYNTHESIS OF OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,025
; FILING DATE: 07-NOV-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,599
; FILING DATE: 05-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BIRD, DONALD J.
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 202706/SBI36848/US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-337-025-2

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
| | | | | | | | | |
Db 14 CGAAAAAAAAAAAAA 1

RESULT 790
US-08-363-240A-141
; Sequence 141, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION

;/ TITLE OF INVENTION: OF VASCULAR DISEASES
;/ NUMBER OF SEQUENCES: 1243
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Lyon & Lyon
;/ STREET: 633 West Fifth Street
;/ CITY: Suite 4700
;/ STATE: Los Angeles
;/ COUNTRY: California
;/ ZIP: 90071
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;/ MEDIUM TYPE: storage
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: IBM P.C. DOS 5.0
;/ SOFTWARE: Word Perfect 5.1
;/
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/363,240A
;/ FILING DATE: December 23, 1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER:
;/ FILING DATE:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Warburg, Richard
;/ REGISTRATION NUMBER: 32,327
;/ REFERENCE/DOCKET NUMBER: 210/096
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (213) 489-1600
;/ TELEFAX: (213) 955-0440
;/ TELEX: 67-3510
;/ INFORMATION FOR SEQ ID NO: 141:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 15 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-363-240A-141
;/
;/ Query Match 0.7%; Score 12.4; DB 1; Length 15;
;/ Best Local Similarity 78.6%; Pred. No. 5.3e+02;
;/ Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
;/
;/ QY 119 GGGGCTTCAAGACC 132
;/ |||||:|||||
;/ Db 2 GGGGCUUACACACC 15
;/
;/ RESULT 791
;/ US-08-363-240A-142
;/ Sequence 142, Application US/08363240A
;/ Patent No. 5705388
;/ GENERAL INFORMATION:
;/ APPLICANT: Couture, Larry
;/ APPLICANT: McSwiggen, James
;/ APPLICANT: Bisgaier, Charles
;/ APPLICANT: Pape, Michael
;/ TITLE OF INVENTION: METHOD AND REAGENT FOR
;/ TITLE OF INVENTION: PREVENTION, INHIBITION OF
;/ TITLE OF INVENTION: PROGRESSION AND REGRESSION
;/ TITLE OF INVENTION: OF VASCULAR DISEASES
;/ NUMBER OF SEQUENCES: 1243
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Lyon & Lyon
;/ STREET: 633 West Fifth Street
;/ CITY: Suite 4700
;/ STATE: Los Angeles
;/ COUNTRY: California
;/ ZIP: 90071
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;/ MEDIUM TYPE: storage
;/ COMPUTER: IBM Compatible

;/ OPERATING SYSTEM: IBM P.C. DOS 5.0
;/ SOFTWARE: Word Perfect 5.1
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/363,240A
;/ FILING DATE: December 23, 1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER:
;/ FILING DATE:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Warburg, Richard
;/ REGISTRATION NUMBER: 32,327
;/ REFERENCE/DOCKET NUMBER: 210/096
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (213) 489-1600
;/ TELEFAX: (213) 955-0440
;/ TELEX: 67-3510
;/ INFORMATION FOR SEQ ID NO: 142:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 15 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-363-240A-142
;/
;/ Query Match 0.7%; Score 12.4; DB 1; Length 15;
;/ Best Local Similarity 78.6%; Pred. No. 5.3e+02;
;/ Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
;/
;/ QY 119 GGGGCTTCAAGACC 132
;/ |||||:|||||
;/ Db 1 GGGGCUUACACACC 14
;/
;/ RESULT 792
;/ US-08-363-240A-757/c
;/ Sequence 757, Application US/08363240A
;/ Patent No. 5705388
;/ GENERAL INFORMATION:
;/ APPLICANT: Couture, Larry
;/ APPLICANT: McSwiggen, James
;/ APPLICANT: Bisgaier, Charles
;/ APPLICANT: Pape, Michael
;/ TITLE OF INVENTION: METHOD AND REAGENT FOR
;/ TITLE OF INVENTION: PREVENTION, INHIBITION OF
;/ TITLE OF INVENTION: PROGRESSION AND REGRESSION
;/ TITLE OF INVENTION: OF VASCULAR DISEASES
;/ NUMBER OF SEQUENCES: 1243
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Lyon & Lyon
;/ STREET: 633 West Fifth Street
;/ CITY: Suite 4700
;/ STATE: Los Angeles
;/ COUNTRY: U.S.A.
;/ ZIP: 90071
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;/ MEDIUM TYPE: storage
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: IBM P.C. DOS 5.0
;/ SOFTWARE: Word Perfect 5.1
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/363,240A
;/ FILING DATE: December 23, 1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER:
;/ FILING DATE:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Warburg, Richard
;/ REGISTRATION NUMBER: 32,327
;/ REFERENCE/DOCKET NUMBER: 210/096
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (213) 489-1600

```

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 757:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-757

Query Match      0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1651 CTCCTGACATCCA 1664
Db 14 CTCCTGACCTCCA 1

RESULT 793
US-08-585-684B-159/c
; Sequence 159, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-159

Query Match      0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 910 CTCCTGACGATGA 923
Db 14 CTCCTGACCTCCA 1

RESULT 794
US-08-819-867-68
; Sequence 68, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. Mceachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,867
; FILING DATE: March 14, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989ember 12, 1993
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-819-867-68

Query Match      0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1026 TGGGGCTGGGGTTG 1039
Db 2 TGGGGTTGGGGTTG 15

RESULT 795
US-08-832-021-18/c
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; Sequence 18, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-18

Query Match

Best Local Similarity 0.7%; Score 12.4; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1745

Db 14 TTA 1

RESULT 796

US-08-832-021-19/c

; Sequence 19, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-19

Query Match

Best Local Similarity 0.7%; Score 12.4; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1745

Db 14 TTA 1

RESULT 797

US-08-832-021-20/c

; Sequence 20, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-20

Query Match

Best Local Similarity 0.7%; Score 12.4; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1745

Db 14 TTA 1

RESULT 798

US-08-832-021-41/c

; Sequence 41, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 41

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-41

Query Match

Best Local Similarity 0.7%; Score 12.4; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA 1748

Db 14 CTA 1

RESULT 799

US-08-832-021-42/c

; Sequence 42, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 42
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-42

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
Db 14 CTAATAAAAAAAAAA 1

RESULT 800
US-08-832-021-43/c
; Sequence 43, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-43

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
Db 14 CTAATAAAAAAAAAA 1

RESULT 801
US-08-832-021-45/c
; Sequence 45, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-45
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Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
Db 14 CGAAAAAAAAAAAAA 1

RESULT 802
US-08-832-021-46/c
; Sequence 46, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-46
```

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Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
Db 14 CGAAAAAAAAAAAAA 1

RESULT 803
US-08-832-021-47/c
; Sequence 47, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-47
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Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
Db 14 CGAAAAAAAAAAAAA 1

RESULT 804
US-08-832-021-48/c
; Sequence 48, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-48
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Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
Db 14 CGAAAAAAAAAAAAA 1

RESULT 805
US-08-832-021-49/c
; Sequence 49, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-49
```

Db 14 CGAAAAAAAAAAAA 1

RESULT 804

US-08-832-021-54/c

; Sequence 54, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 54

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-54

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 5.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAA 1747

Db 14 ATAAAAAAAAAAAAA 1

RESULT 805

US-08-832-021-58/c

; Sequence 58, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 58

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-58

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 5.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 32 GAGGAAAAAAAAAA 45

Db 15 GAGAAAAAAAAAAAA 2

RESULT 806

US-09-038-073-159/c

; Sequence 159, Application US/09038073

; Patent No. 6194150

; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Daniel T.

; APPLICANT: Jarvis, Thale

; APPLICANT: McSwiggen, James

; TITLE OF INVENTION: METHOD AND REAGENT FOR THE

; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

; NUMBER OF SEQUENCES: 2751

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/038,073

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/585,684

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 218/078

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 159:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-038-073-159

Query Match 0.7%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 5.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 910 CCTCCAGAGGATGA 923

Db 14 CCTCCAGAGGTTGA 1

RESULT 807

US-09-446-765-4/c

; Sequence 4, Application US/09446765

; Patent No. 6313090

; GENERAL INFORMATION:

; APPLICANT: United States of America, as represented by the

; Secretary, Department of Health and Human Services,

; National Institutes of Health, Office of Technology

; Transfer, 6011 Executive Blvd., Suite 325, Rockville,

; Maryland 20852

; TITLE OF INVENTION: METHODS FOR TREATING PARASITIC INFECTIONS

; USING THIOPEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NEEDLE & ROSENBERG, P.C.

; STREET: Suite 1200, 127 Peachtree Street, NE

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30303

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/446,765
FILING DATE: 20-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Mary L
REGISTRATION NUMBER: 39,303
REFERENCE/DOCKET NUMBER: 14014.0233/P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-446-765-4

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CACCAAAATGCTGTC 1693
Db 15 CACCAAAATGCTCTC 2

RESULT 808
US-09-344-667-37
Sequence 37, Application US/09344667A
Patent No. 6361944
GENERAL INFORMATION:
APPLICANT: Mirkin, Chad A.
APPLICANT: Letsinger, Robert L.
APPLICANT: Mucic, Robert C.
APPLICANT: Storchhoff, James J.
APPLICANT: Elghanian, Robert
TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 4149-1-1-1
CURRENT APPLICATION NUMBER: US/09/344,667A
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: PCT/US97/12783
PRIOR FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/031,809
PRIOR FILING DATE: 1996-07-29
PRIOR APPLICATION NUMBER: 09/240,755
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: random
OTHER INFORMATION: synthetic sequence
US-09-344-667-37

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1714 AATAATAATCCCTC 1727
Db 2 AACATAATCCCTC 15
RESULT 809
US-08-464-011B-58
Sequence 58, Application US/08464011B
Patent No. 6368789
GENERAL INFORMATION:
APPLICANT: Michael D. West
Jerry W. Shay
Woodring E. Wright
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
RELATED TO TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,011B
FILING DATE: 05-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-08-464-011B-58

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1026 TGGGGCTGGGGTTG 1039
Db 2 TGGGGTTGGGGTTG 15

RESULT 810
US-09-693-352-37
Sequence 37, Application US/09693352
Patent No. 6417340

```
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 4149-1-1-1
; CURRENT APPLICATION NUMBER: US/09/693,352
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-693-352-37

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1714 AATAATAATCCCTC 1727
Db      2 AACATAATCCCTC 15

RESULT 811
US-09-693-005A-37
; Sequence 37, Application US/09693005A
; Patent No. 6495324
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-L
; CURRENT APPLICATION NUMBER: US/09/693,005A
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-693-005A-37

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1714 AATAATAATCCCTC 1727
Db      2 AACATAATCCCTC 15

RESULT 811
US-09-693-005A-37
; Sequence 37, Application US/09693005A
; Patent No. 6495324
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-L
; CURRENT APPLICATION NUMBER: US/09/693,005A
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-693-005A-37

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1714 AATAATAATCCCTC 1727
Db      2 AACATAATCCCTC 15

RESULT 812
US-09-603-830-37
; Sequence 37, Application US/09603830
; Patent No. 6506564
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 4149-1-1-1-1
; CURRENT APPLICATION NUMBER: US/09/603,830
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-603-830-37

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1714 AATAATAATCCCTC 1727
Db      2 AACATAATCCCTC 15

RESULT 813
US-09-976-978A-37
; Sequence 37, Application US/09976978A
; Patent No. 6532097
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-117
; CURRENT APPLICATION NUMBER: US/09/976,978A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
```


;; PRIOR APPLICATION NUMBER: 09/240,755
;; PRIOR FILING DATE: 1999-01-29
;; PRIOR APPLICATION NUMBER: PCT/US97/12783
;; PRIOR FILING DATE: 1997-07-21
;; PRIOR APPLICATION NUMBER: 60/031,809
;; PRIOR FILING DATE: 1996-07-29
;; PRIOR APPLICATION NUMBER: 60/200,161
;; PRIOR FILING DATE: 2000-04-26
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: Microsoft Word 2000
;; SEQ ID NO 37
;; LENGTH: 15
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: random
;; OTHER INFORMATION: synthetic sequence
US-09-976-978A-37

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1714 AATAATAATCCCTC 1727
Db 2 AACATAATCCCTC 15

RESULT 814
US-09-378-535-68
; Sequence 68, Application US/09378535
; Patent No. 6551774
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Calvin B. Harley
; Scott L. Weinrich
; Catherine M. Strahl
; Michael J. Mceachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO
; TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,535
; FILING DATE: 20-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/819,867
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 68:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-378-535-68

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1026 TGGGGCTGGGGTTG 1039
Db 2 TGGGGTTGGGGTTG 15

RESULT 815
US-09-961-949A-37
; Sequence 37, Application US/09961949A
; Patent No. 6582921
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-11
; CURRENT APPLICATION NUMBER: US/09/961,949A
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-09-961-949A-37

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1714 AATAATAATCCCTC 1727
Db 2 AACATAATCCCTC 15

RESULT 816
US-09-402-048-3/c
; Sequence 3, Application US/09402048

; Patent No. 6600028
; GENERAL INFORMATION:
; APPLICANT: BROWN ET AL
; TITLE OF INVENTION: TRICYCLIC BASE ANALOGS
; FILE REFERENCE: 28911/35902
; CURRENT APPLICATION NUMBER: US/09/402,048
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: PCT/GB98/00978
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: EP 97302265.0
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-402-048-3

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 382 CTCGAGCAGCAGCA 395
||| ||||| |||
Db 14 CTCGAGCAGCAGCA 1

RESULT 817
US-09-402-048-6/c
; Sequence 6, Application US/09402048
; Patent No. 6600028
; GENERAL INFORMATION:
; APPLICANT: BROWN ET AL
; TITLE OF INVENTION: TRICYCLIC BASE ANALOGS
; FILE REFERENCE: 28911/35902
; CURRENT APPLICATION NUMBER: US/09/402,048
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: PCT/GB98/00978
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: EP 97302265.0
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-402-048-6

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 382 CTCGAGCAGCAGCA 395
||| ||||| |||
Db 14 CTCGAGCAGCAGCA 1

RESULT 818
US-09-966-491A-37
; Sequence 37, Application US/09966491A
; Patent No. 6610491
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert

; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i4
; CURRENT APPLICATION NUMBER: US/09/966,491A
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-09-966-491A-37

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1714 AATAATAATCCCTC 1727
||| ||||| |||||
Db 2 AACATAATCCCTC 15

RESULT 819
US-09-957-313A-37
; Sequence 37, Application US/09957313A
; Patent No. 6645721
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i3
; CURRENT APPLICATION NUMBER: US/09/957,313A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-957-313A-37

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1714 AATAATAATCCCTC 1727
Db 2 AACATAATCCCTC 15

RESULT 820
US-09-898-210-1/c
; Sequence 1, Application US/09898210
; Patent No. 6664058
; GENERAL INFORMATION:
; APPLICANT: Kumar, Shiv
; APPLICANT: Nampalli, Satyam
; APPLICANT: Neagu, Constantin
; APPLICANT: McDougall, Mark
; APPLICANT: Loakes, David
; APPLICANT: Brown, Dan
; TITLE OF INVENTION: Base Analogues
; FILE REFERENCE: PA0036
; CURRENT APPLICATION NUMBER: US/09/898,210
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: GB0016258.6
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-09-898-210-1

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 382 CTCGAGCACACGCA 395
Db 14 CTCGAGCACATGCA 1

RESULT 821
US-09-966-312-37
; Sequence 37, Application US/09966312
; Patent No. 6673548
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-15
; CURRENT APPLICATION NUMBER: US/09/966,312
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783

; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-975-062A-37

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1714 AATAATAATCCCTC 1727
Db 2 AACATAATCCCTC 15

RESULT 822
US-09-975-062A-37
; Sequence 37, Application US/09975062A
; Patent No. 6677122
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-111
; CURRENT APPLICATION NUMBER: US/09/975,062A
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-975-062A-37

Query Match          0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1714 AATAATAATCCCTC 1727
Db 2 AACATAATCCCTC 15
```

RESULT 823
US-09-976-971A-37
; Sequence 37, Application US/09976971A
; Patent No. 6682895
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i18
; CURRENT APPLICATION NUMBER: US/09/976,971A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 37
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-09-976-971A-37

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1714 AATAATAATCCCTC 1727
||| ||||| |||||
Db 2 AACATAATCCCTC 15

RESULT 824
US-08-152-313-15
; Sequence 15, Application US/08152313
; Patent No. 5561041
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,313
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/152,313
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..16

; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..16
US-08-152-313-15

Query Match 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1188 CCAGCCCATCCTGG 1201
||||| |||||
Db 3 CCAGCCCATCCTGG 16

RESULT 825
US-08-579-223-15
; Sequence 15, Application US/08579223
; Patent No. 5726019
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,223
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/152,313
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..16

US-08-579-223-15

Query Match. 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1188 CCAGCCCATCCTGG 1201

Db 3 CCAGCCCTCCTGG 16

RESULT 826

US-08-282-197C-20
; Sequence 20, Application US/08282197C
; Patent No. 5871730
; GENERAL INFORMATION:
; APPLICANT: Brzezinski, Ryszard
; APPLICANT: Dery, Claude V
; APPLICANT: Beaulieu, Carole
; TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,197C
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Cimbala, Michele A

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 1050.0410000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

US-08-282-197C-20

Query Match 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 78.6%; Pred. No. 5.7e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 917 AGGATGAGCTGGAT 930

Db 2 AGGAGGAGCUGGAU 15

RESULT 827

US-07-792-600-27
; Sequence 27, Application US/07792600
; Patent No. 6008045
; GENERAL INFORMATION:
; APPLICANT: COPELAND, WILLIAM C.
; APPLICANT: WANG, TERESA S.-F.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: TEMPLATE-DEPENDENT ENZYMATIC SYNTHESIS OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Peter G. Carroll
; STREET: 220 Montgomery Street, Suite 710
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/792,600
; FILING DATE: 19911115
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: STDU-00097
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-792-600-27

Query Match 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 968 CGCCCAGCGGGGAG 981

Db 1 CGCCCAGCGGGGAG 14

RESULT 828

US-09-157-021-27
; Sequence 27, Application US/09157021A
; Patent No. 6100023

GENERAL INFORMATION:

APPLICANT: Copeland, William C.

APPLICANT: Wang, Teresa S. F.

TITLE OF INVENTION: Drug Design Assay

FILE REFERENCE: STDU-03484

CURRENT APPLICATION NUMBER: US/09/157,021A

CURRENT FILING DATE: 1998-09-18

EARLIER APPLICATION NUMBER: 07/792,600

EARLIER FILING DATE: 1991-11-15

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 27

LENGTH: 16

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-157-021-27

Query Match 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 968 CGCCCAGCGGGGAG 981

Db 1 CGCCCAGCGGGGAG 14

RESULT 829

US-09-156-842-27

; Sequence 27, Application US/09156842A

; Patent No. 6103473

; GENERAL INFORMATION:

; APPLICANT: Copeland, William C.

; APPLICANT: Wang, Teresa S. F.

; TITLE OF INVENTION: Drug Screening

; FILE REFERENCE: STDU-03485

; CURRENT APPLICATION NUMBER: US/09/156,842A

; CURRENT FILING DATE: 1998-09-18

; EARLIER APPLICATION NUMBER: 07/792,600

; EARLIER FILING DATE: 1991-11-15

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 16

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-156-842-27

Query Match 0.7%; Score 12.4; DB 1; Length 16;

Best Local Similarity 92.9%; Pred. No. 5.7e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 968 CGCCAGCGGGGAG 981

Db 1 CGCCAGCGGGCAG 14

RESULT 830

US-09-102-528-15/c

; Sequence 15, Application US/09102528

; Patent No. 6207883

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: DNA Sequences

; NUMBER OF SEQUENCES: 32

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/102,528

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB96/03191

; FILING DATE:

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-102-528-15

Query Match

Best Local Similarity 0.7%; Score 12.4; DB 1; Length 16;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 382 CTCCAGCACAGCA 395

Db 14 CTCCAGCACAGCA 1

RESULT 831

US-08-626-285-19/c

; Sequence 19, Application US/08626285

; Patent No. 6458530

; GENERAL INFORMATION:

; APPLICANT: Morris, Macdonald S.

; APPLICANT: Shoemaker, Daniel D.

; APPLICANT: Davis, Ronald W.

; APPLICANT: Mittmann, Michael P.

; TITLE OF INVENTION: Methods and Compositions for Selecting

; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/626,285

; FILING DATE: 04-APR-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Garrett-Wackowski, Eugenia

; REGISTRATION NUMBER: 37,330

; REFERENCE/DOCKET NUMBER: 16528X-017300US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-626-285-19

Query Match

Best Local Similarity 0.7%; Score 12.4; DB 1; Length 16;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1403 CTGTGAGAAATTGTT 1416

Db 15 CTGTGAGAAATTGTT 2

RESULT 832

US-09-300-958A-58/c

; Sequence 58, Application US/09300958A

; Patent No. 6495319

; GENERAL INFORMATION:

; APPLICANT: McClelland, Michael

; APPLICANT: Welsh, John

; APPLICANT: Trenkle, Thomas

; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of

; TITLE OF INVENTION: Using Same

; FILE REFERENCE: P-PH 3457

; CURRENT APPLICATION NUMBER: US/09/300,958A

; CURRENT FILING DATE: 1999-04-27

; PRIOR APPLICATION NUMBER: 60/083,331

; PRIOR FILING DATE: 1998-04-27

; PRIOR APPLICATION NUMBER: 60/098,070

; PRIOR FILING DATE: 1998-08-27

; PRIOR APPLICATION NUMBER: 60/118,624

; PRIOR FILING DATE: 1999-02-04

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 58

; LENGTH: 16

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-58

Query Match 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 GGAAAAAAAAGC 47
| | | | | | | | | |
Db 16 GAAAAAAAAGC 3

RESULT 833

US-09-300-958A-84/c
Sequence 84, Application US/09300958A
Patent No. 6495319

GENERAL INFORMATION:

APPLICANT: McClelland, Michael
APPLICANT: Welsh, John
APPLICANT: Trenkle, Thomas
TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
FILE OF INVENTION: Using Same
FILE REFERENCE: P-PH 3457
CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/098,070
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/118,624
PRIOR FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 84
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-84

Query Match 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 GGAAAAAAAAGC 47
| | | | | | | | | |
Db 16 GAAAAAAAAGC 3

RESULT 834

US-09-527-972-17/c
Sequence 17, Application US/09527972
Patent No. 6642438

GENERAL INFORMATION:

APPLICANT: Clendennen, Stephanie K.
APPLICANT: Kellogg, Jill A.
APPLICANT: Phan, Chau B.
APPLICANT: Mathews, Helena V.
APPLICANT: Webb, Nancy M.
TITLE OF INVENTION: Banana and Melon Promoters for
FILE REFERENCE: 4257-0019.30
CURRENT APPLICATION NUMBER: US/09/527,972
CURRENT FILING DATE: 2000-03-17
EARLIER APPLICATION NUMBER: US 60/125,310
EARLIER FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-09-527-972-17

Query Match 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 GGAAAAAAAAGC 47
| | | | | | | | | |
Db 16 GAAAAAAAAGC 3

RESULT 835

US-09-591-514-27
Sequence 27, Application US/09591514
Patent No. 6670161

GENERAL INFORMATION:

APPLICANT: Copeland, William C.
APPLICANT: Wang, Teresa S. F.
TITLE OF INVENTION: Drug Design Assay
FILE REFERENCE: STDU-03484
CURRENT APPLICATION NUMBER: US/09/591,514
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US/09/157,021
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 07/792,600
PRIOR FILING DATE: 1991-11-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-591-514-27

Query Match 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 968 CGCCGAGCGGGAG 981
| | | | | | | | | |
Db 1 CGCCGAGCGGGAG 14

RESULT 836

PCT-US94-12947A-15

Sequence 15, Application PC/TUS9412947A

GENERAL INFORMATION:

APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
TITLE OF INVENTION: ANALYSIS OF SPUTUM
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12947A
FILING DATE: 10-NOV-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.


```
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: FD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..16
; PCT-US94-12947A-15

Query Match 0.7%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1188 CCAGCCCATCCTGG 1201
Db 3 CCAGCCCATCCTGG 16

RESULT 837
US-08-351-748-2/c
; Sequence 2, Application US/08351748
; Patent No. 5599672
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; APPLICANT: Pardee, Arthur B.
; APPLICANT: Bianchi, Cesario F.
; TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
; TITLE OF INVENTION: MESSENGER RNAs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,748
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/033,084
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan Esq., Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: 181411-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248-4000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-351-748-2
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Query Match 0.7%; Score 12.2; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.8e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1747
Db 13 BAAAAA1

RESULT 838
US-08-430-536A-2/c
; Sequence 2, Application US/08430536A
; Patent No. 5665547
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; APPLICANT: Pardee, Arthur B.
; TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
; TITLE OF INVENTION: MESSENGER RNAs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,536A
; FILING DATE: 25-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Herschbach Ph.D., Brenda M.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 181411-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248-4000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-430-536A-2

Query Match 0.7%; Score 12.2; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.8e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1747
Db 13 BAAAAA1

RESULT 839
US-08-684-547-2/c
; Sequence 2, Application US/08684547
; Patent No. 5965409
; GENERAL INFORMATION:
; APPLICANT: Pardee Ph.D., Arthur B.
; APPLICANT: Liang Ph.D., Peng
; TITLE OF INVENTION: SYSTEM FOR COMPARING LEVELS OR AMOUNTS
; TITLE OF INVENTION: OF mRNAs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
```

STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,547
FILING DATE: 19-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jarrell Ph.D., Brenda H.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 0181411-0013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248-4000
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-684-547-2

Query Match 0.7%; Score 12.2; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.8e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
:|||||
Db 13 BAAAAAAAAAAAAA 1

RESULT 840

PCT-US93-02246-2/c
Sequence 2, Application PC/TUS9302246
GENERAL INFORMATION:
APPLICANT: Liang, Peng
APPLICANT: Pardee, Arthur B.
TITLE OF INVENTION: Identifying, Isolating and Cloning
TITLE OF INVENTION: Messenger RNAs
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate, Hall & Stewart
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02190
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC, compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02246
FILING DATE: 19930311
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/850,343
FILING DATE: 11-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pasternack, Sam
REGISTRATION NUMBER: 29,576
REFERENCE/DOCKET NUMBER: DFCI234CIP
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617 227-5020
TELEFAX: 617 227-7566
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-02246-2

Query Match 0.7%; Score 12.2; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.8e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
:|||||
Db 13 BAAAAAAAAAAAAA 1

RESULT 841

US-09-042-225-4/c
Sequence 4, Application US/09042225A
Patent No. 6207812
GENERAL INFORMATION:
APPLICANT: Terek, Richard M.
TITLE OF INVENTION: CHONDROSARCOMA ASSOCIATED GENES
FILE REFERENCE: 04930/021001
CURRENT APPLICATION NUMBER: US/09/042,225A
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(14)
OTHER INFORMATION: n = A,T,C or G
US-09-042-225-4

Query Match 0.7%; Score 12.2; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 5.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
:|||||
Db 13 BAAAAAAAAAAAAA 1

RESULT 842

US-09-390-324B-1/c
Sequence 1, Application US/09390324B
Patent No. 6342376
GENERAL INFORMATION:
APPLICANT: Kozian, Detlef
APPLICANT: Reuner, Birgit
TITLE OF INVENTION: Two-color differential display as a method for
detecting regulated genes
FILE REFERENCE: 2481-1635
CURRENT APPLICATION NUMBER: US/09/390,324B
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence

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; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(14)
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: "V=A,C,G; N=A,C,G,T"
US-09-390-324B-1
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Query Match 0.7%; Score 12.2; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 5.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1735 CAAAAAAAAAAAA 1747
:|||||
Db 13 BAAAAAAAAAAAA 1
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RESULT 843
US-10-015-593-1/c
; Sequence 1, Application US/10015593
; Patent No. 6645741
; GENERAL INFORMATION:
; APPLICANT: Kozian, Detlef
; APPLICANT: Reuner, Birgit
; TITLE OF INVENTION: Two-color differential display as a method for
; TITLE OF INVENTION: detecting regulated genes
; FILE REFERENCE: 2481-1635
; CURRENT APPLICATION NUMBER: US/10/015,593
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/390,324
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(14)
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: "V=A,C,G; N=A,C,G,T"
US-10-015-593-1
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Query Match 0.7%; Score 12.2; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 5.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1735 CAAAAAAAAAAAA 1747
:|||||
Db 13 BAAAAAAAAAAAA 1
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Search completed: August 16, 2004, 15:26:41
Job time : 18 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 16:46:04 ; Search time 18 Seconds
(without alignments)
3.751 Million cell updates/sec

Title: us-10-008-789-3
Perfect score: 1755
Sequence: 1 cgccgggcaggtcccaaaa.....aaaaaaaaaaaaaaaaaaaa 1755

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1017 seqs, 19236 residues

Total number of hits satisfying chosen parameters: 2034

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1028 summaries

Database : rstdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	2.8	50	1	AU102457
2	48.4	2.8	50	1	AU102453
3	48.4	2.8	50	1	AU102454
4	48.4	2.8	50	1	AU102455
C 5	33.4	1.9	43	1	AI954491
C 6	30	1.7	31	1	AI000255
7	24.8	1.4	33	1	AL048719
C 8	23.4	1.3	25	1	AA482614
C 9	23.4	1.3	26	1	R26779
C 10	23.4	1.3	29	1	CF299155
C 11	23.4	1.3	29	1	TA378G07P
C 12	22.8	1.3	26	1	CF299646
C 13	22.4	1.3	25	1	CF317007
C 14	22.4	1.3	25	1	N59260
C 15	22.4	1.3	27	1	N34515
16	22.4	1.3	28	1	CF337400
C 17	22.4	1.3	29	1	CF314795
C 18	22	1.3	23	1	BX559898
C 19	22	1.3	28	1	T52836
C 20	21.8	1.2	26	1	CF280688
C 21	21.8	1.2	26	1	AZ358846
C 22	21.8	1.2	27	1	CF333518
C 23	21.8	1.2	27	1	R59382
C 24	21.8	1.2	29	1	CF334023
C 25	21.4	1.2	23	1	CF329694
26	21.4	1.2	25	1	AZ330737
C 27	21.4	1.2	26	1	AW333508
C 28	21.4	1.2	27	1	N52529
C 29	21.4	1.2	27	1	N89936
C 30	21.4	1.2	28	1	AZ824574
C 31	21	1.2	21	1	CF311914
C 32	21	1.2	21	1	AZ792613
33	21	1.2	22	1	AZ304806

34	21	1.2	22	1	AZ505769
35	21	1.2	23	1	AZ315640
36	21	1.2	24	1	AL048765
37	21	1.2	24	1	CF326993
38	21	1.2	24	1	AZ404871
39	21	1.2	24	1	AZ786257
40	21	1.2	25	1	AL048782
C 41	21	1.2	25	1	N27663
C 42	21	1.2	25	1	CG726337
C 43	21	1.2	27	1	CF299084
44	21	1.2	27	1	CF310745
C 45	21	1.2	28	1	AL587582
C 46	21	1.2	28	1	AZ481286
C 47	21	1.2	28	1	AZ809971
C 48	20.8	1.2	27	1	N51845
C 49	20.6	1.2	27	1	N29432
C 50	20.4	1.2	22	1	AW332181
C 51	20.4	1.2	22	1	AW332399
C 52	20.4	1.2	22	1	CF299342
C 53	20.4	1.2	22	1	CF300133
C 54	20.4	1.2	22	1	CF310366
55	20.4	1.2	22	1	CF310486
C 56	20.4	1.2	22	1	CF311269
57	20.4	1.2	22	1	CF311713
58	20.4	1.2	22	1	CF312498
C 59	20.4	1.2	22	1	CF330679
C 60	20.4	1.2	22	1	CF333430
C 61	20.4	1.2	22	1	CF334781
C 62	20.4	1.2	22	1	CF336250
63	20.4	1.2	22	1	CF337580
C 64	20.4	1.2	22	1	CF338524
C 65	20.4	1.2	22	1	AZ310066
66	20.4	1.2	22	1	AZ351527
67	20.4	1.2	22	1	AZ357630
68	20.4	1.2	22	1	AZ388103
C 69	20.4	1.2	22	1	AZ401908
C 70	20.4	1.2	22	1	AZ424307
C 71	20.4	1.2	22	1	AZ428818
C 72	20.4	1.2	22	1	AZ459654
C 73	20.4	1.2	22	1	AZ463503
C 74	20.4	1.2	22	1	AZ463652
75	20.4	1.2	22	1	AZ582403
76	20.4	1.2	22	1	AZ607658
77	20.4	1.2	22	1	AZ654691
78	20.4	1.2	22	1	AZ760533
C 79	20.4	1.2	22	1	AZ779844
C 80	20.4	1.2	22	1	AZ785019
C 81	20.4	1.2	22	1	AZ787098
C 82	20.4	1.2	22	1	AZ787606
C 83	20.4	1.2	22	1	AZ792704
C 84	20.4	1.2	22	1	AZ810674
C 85	20.4	1.2	22	1	AZ820439
86	20.4	1.2	22	1	AZ841661
C 87	20.4	1.2	22	1	AZ843514
88	20.4	1.2	22	1	AZ946102
89	20.4	1.2	22	1	TA131B09P
90	20.4	1.2	22	1	TA329F10P
C 91	20.4	1.2	22	1	TA35C12Q
92	20.4	1.2	22	1	TA380A07P
C 93	20.4	1.2	23	1	CF279238
C 94	20.4	1.2	23	1	CF297943
C 95	20.4	1.2	23	1	CF310501
C 96	20.4	1.2	23	1	CF319212
97	20.4	1.2	23	1	CF322953
98	20.4	1.2	23	1	CF329042
C 99	20.4	1.2	23	1	CF332379
100	20.4	1.2	23	1	CF334657
C 101	20.4	1.2	23	1	AZ309219
102	20.4	1.2	23	1	AZ309851
C 103	20.4	1.2	23	1	AZ312314
C 104	20.4	1.2	23	1	AZ313922
105	20.4	1.2	23	1	AZ351354
106	20.4	1.2	23	1	AZ357645

C 107	20.4	1.2	23	1	AZ419236	ACCESSION:AZ419236	180	20.4	1.2	26	1	CF282426	ACCESSION:CF282426
C 108	20.4	1.2	23	1	AZ425710	ACCESSION:AZ425710	C 181	20.4	1.2	26	1	CF296851	ACCESSION:CF296851
C 109	20.4	1.2	23	1	AZ461220	ACCESSION:AZ461220	C 182	20.4	1.2	26	1	CF297087	ACCESSION:CF297087
C 110	20.4	1.2	23	1	AZ465327	ACCESSION:AZ465327	C 183	20.4	1.2	26	1	CF299701	ACCESSION:CF299701
C 111	20.4	1.2	23	1	AZ481702	ACCESSION:AZ481702	C 184	20.4	1.2	26	1	CF302874	ACCESSION:CF302874
C 112	20.4	1.2	23	1	AZ588254	ACCESSION:AZ588254	C 185	20.4	1.2	26	1	CF311369	ACCESSION:CF311369
C 113	20.4	1.2	23	1	AZ593540	ACCESSION:AZ593540	C 186	20.4	1.2	26	1	CF331439	ACCESSION:CF331439
C 114	20.4	1.2	23	1	AZ610785	ACCESSION:AZ610785	C 187	20.4	1.2	26	1	CF336199	ACCESSION:CF336199
C 115	20.4	1.2	23	1	AZ647637	ACCESSION:AZ647637	C 188	20.4	1.2	26	1	AZ359871	ACCESSION:AZ359871
C 116	20.4	1.2	23	1	AZ654903	ACCESSION:AZ654903	C 189	20.4	1.2	26	1	AZ376664	ACCESSION:AZ376664
C 117	20.4	1.2	23	1	AZ778751	ACCESSION:AZ778751	C 190	20.4	1.2	26	1	AZ389765	ACCESSION:AZ389765
C 118	20.4	1.2	23	1	AZ787184	ACCESSION:AZ787184	C 191	20.4	1.2	26	1	AZ414673	ACCESSION:AZ414673
C 119	20.4	1.2	23	1	AZ792751	ACCESSION:AZ792751	C 192	20.4	1.2	26	1	AZ593300	ACCESSION:AZ593300
C 120	20.4	1.2	23	1	AZ801003	ACCESSION:AZ801003	C 193	20.4	1.2	26	1	AZ612722	ACCESSION:AZ612722
C 121	20.4	1.2	23	1	AZ859570	ACCESSION:AZ859570	C 194	20.4	1.2	26	1	AZ624441	ACCESSION:AZ624441
C 122	20.4	1.2	23	1	AZ939608	ACCESSION:AZ939608	C 195	20.4	1.2	26	1	AZ627846	ACCESSION:AZ627846
C 123	20.4	1.2	23	1	BH000534	ACCESSION:BH000534	C 196	20.4	1.2	26	1	AZ652515	ACCESSION:AZ652515
C 124	20.4	1.2	23	1	TA151C02Q	ACCESSION:AL473028	C 197	20.4	1.2	26	1	AZ800453	ACCESSION:AZ800453
C 125	20.4	1.2	23	1	TA274B03P	ACCESSION:AL484584	C 198	20.4	1.2	26	1	AZ963974	ACCESSION:AZ963974
C 126	20.4	1.2	23	1	TA353A10P	ACCESSION:AL494456	C 199	20.4	1.2	26	1	TA324D07P	ACCESSION:AL493390
C 127	20.4	1.2	24	1	BG670391	ACCESSION:BG670391	C 200	20.4	1.2	27	1	AW327923	ACCESSION:AW327923
C 128	20.4	1.2	24	1	BX554611	ACCESSION:BX554611	C 201	20.4	1.2	27	1	CF291968	ACCESSION:CF291968
C 129	20.4	1.2	24	1	CA853764	ACCESSION:CA853764	C 202	20.4	1.2	27	1	CF310560	ACCESSION:CF310560
C 130	20.4	1.2	24	1	CF276855	ACCESSION:CF276855	C 203	20.4	1.2	27	1	CF329725	ACCESSION:CF329725
C 131	20.4	1.2	24	1	CF301561	ACCESSION:CF301561	C 204	20.4	1.2	27	1	CF330557	ACCESSION:CF330557
C 132	20.4	1.2	24	1	CF312319	ACCESSION:CF312319	C 205	20.4	1.2	27	1	CF335229	ACCESSION:CF335229
C 133	20.4	1.2	24	1	CF320862	ACCESSION:CF320862	C 206	20.4	1.2	27	1	N34459	ACCESSION:N34459
C 134	20.4	1.2	24	1	AZ328848	ACCESSION:AZ328848	C 207	20.4	1.2	27	1	R31539	ACCESSION:R31539
C 135	20.4	1.2	24	1	AZ363562	ACCESSION:AZ363562	C 208	20.4	1.2	27	1	AZ344642	ACCESSION:AZ344642
C 136	20.4	1.2	24	1	AZ386491	ACCESSION:AZ386491	C 209	20.4	1.2	27	1	AZ401672	ACCESSION:AZ401672
C 137	20.4	1.2	24	1	AZ390642	ACCESSION:AZ390642	C 210	20.4	1.2	27	1	AZ486791	ACCESSION:AZ486791
C 138	20.4	1.2	24	1	AZ438069	ACCESSION:AZ438069	C 211	20.4	1.2	27	1	AZ511894	ACCESSION:AZ511894
C 139	20.4	1.2	24	1	AZ459280	ACCESSION:AZ459280	C 212	20.4	1.2	27	1	AZ580921	ACCESSION:AZ580921
C 140	20.4	1.2	24	1	AZ644621	ACCESSION:AZ644621	C 213	20.4	1.2	27	1	AZ616094	ACCESSION:AZ616094
C 141	20.4	1.2	24	1	AZ812579	ACCESSION:AZ812579	C 214	20.4	1.2	27	1	AZ623186	ACCESSION:AZ623186
C 142	20.4	1.2	24	1	AZ834990	ACCESSION:AZ834990	C 215	20.4	1.2	27	1	AZ627847	ACCESSION:AZ627847
C 143	20.4	1.2	24	1	AZ970038	ACCESSION:AZ970038	C 216	20.4	1.2	27	1	AZ809295	ACCESSION:AZ809295
C 144	20.4	1.2	24	1	AZ984490	ACCESSION:AZ984490	C 217	20.4	1.2	27	1	AZ862643	ACCESSION:AZ862643
C 145	20.4	1.2	24	1	AZ993423	ACCESSION:AZ993423	C 218	20.4	1.2	27	1	AZ941721	ACCESSION:AZ941721
C 146	20.4	1.2	24	1	TA169D12P	ACCESSION:AL478922	C 219	20.4	1.2	27	1	AZ970621	ACCESSION:AZ970621
C 147	20.4	1.2	24	1	TA27B08Q	ACCESSION:AL453584	C 220	20.4	1.2	27	1	TA355B06P	ACCESSION:AL493923
C 148	20.4	1.2	24	1	TA354C06P	ACCESSION:AL494439	C 221	20.2	1.2	25	1	CF317378	ACCESSION:CF317378
C 149	20.4	1.2	24	1	TA371F11P	ACCESSION:AL495622	C 222	20.2	1.2	25	1	CC883604	ACCESSION:CC883604
C 150	20.4	1.2	24	1	TA95B08P	ACCESSION:AL459003	C 223	20	1.1	20	1	AW334823	ACCESSION:AW334823
C 151	20.4	1.2	25	1	AL587648	ACCESSION:AL587648	C 224	20	1.1	20	1	CF280913	ACCESSION:CF280913
C 152	20.4	1.2	25	1	CF291048	ACCESSION:CF291048	C 225	20	1.1	20	1	CF282035	ACCESSION:CF282035
C 153	20.4	1.2	25	1	CF291646	ACCESSION:CF291646	C 226	20	1.1	20	1	CF282414	ACCESSION:CF282414
C 154	20.4	1.2	25	1	CF299288	ACCESSION:CF299288	C 227	20	1.1	20	1	CF299822	ACCESSION:CF299822
C 155	20.4	1.2	25	1	CF300333	ACCESSION:CF300333	C 228	20	1.1	20	1	CF301720	ACCESSION:CF301720
C 156	20.4	1.2	25	1	CF301712	ACCESSION:CF301712	C 229	20	1.1	20	1	CF302027	ACCESSION:CF302027
C 157	20.4	1.2	25	1	CF316323	ACCESSION:CF316323	C 230	20	1.1	20	1	CF310604	ACCESSION:CF310604
C 158	20.4	1.2	25	1	CF317714	ACCESSION:CF317714	C 231	20	1.1	20	1	CF313067	ACCESSION:CF313067
C 159	20.4	1.2	25	1	CF319073	ACCESSION:CF319073	C 232	20	1.1	20	1	CF313569	ACCESSION:CF313569
C 160	20.4	1.2	25	1	CF330786	ACCESSION:CF330786	C 233	20	1.1	20	1	CF319133	ACCESSION:CF319133
C 161	20.4	1.2	25	1	CF638767	ACCESSION:CF638767	C 234	20	1.1	20	1	CF321721	ACCESSION:CF321721
C 162	20.4	1.2	25	1	N33150	ACCESSION:N33150	C 235	20	1.1	20	1	CF328565	ACCESSION:CF328565
C 163	20.4	1.2	25	1	AZ344725	ACCESSION:AZ344725	C 236	20	1.1	20	1	CF333173	ACCESSION:CF333173
C 164	20.4	1.2	25	1	AZ350777	ACCESSION:AZ350777	C 237	20	1.1	20	1	CF334170	ACCESSION:CF334170
C 165	20.4	1.2	25	1	AZ381039	ACCESSION:AZ381039	C 238	20	1.1	20	1	CF336525	ACCESSION:CF336525
C 166	20.4	1.2	25	1	AZ386891	ACCESSION:AZ386891	C 239	20	1.1	20	1	CF337494	ACCESSION:CF337494
C 167	20.4	1.2	25	1	AZ389458	ACCESSION:AZ389458	C 240	20	1.1	20	1	T50579	ACCESSION:T50579
C 168	20.4	1.2	25	1	AZ609234	ACCESSION:AZ609234	C 241	20	1.1	20	1	AZ307671	ACCESSION:AZ307671
C 169	20.4	1.2	25	1	AZ623157	ACCESSION:AZ623157	C 242	20	1.1	20	1	AZ333980	ACCESSION:AZ333980
C 170	20.4	1.2	25	1	AZ788646	ACCESSION:AZ788646	C 243	20	1.1	20	1	AZ341530	ACCESSION:AZ341530
C 171	20.4	1.2	25	1	AZ832800	ACCESSION:AZ832800	C 244	20	1.1	20	1	AZ343031	ACCESSION:AZ343031
C 172	20.4	1.2	25	1	AZ949287	ACCESSION:AZ949287	C 245	20	1.1	20	1	AZ351273	ACCESSION:AZ351273
C 173	20.4	1.2	25	1	AZ980407	ACCESSION:AZ980407	C 246	20	1.1	20	1	AZ357623	ACCESSION:AZ357623
C 174	20.4	1.2	25	1	TA154D03P	ACCESSION:AL472971	C 247	20	1.1	20	1	AZ369734	ACCESSION:AZ369734
C 175	20.4	1.2	25	1	TA324E10P	ACCESSION:AL493396	C 248	20	1.1	20	1	AZ386573	ACCESSION:AZ386573
C 176	20.4	1.2	26	1	AL587774	ACCESSION:AL587774	C 249	20	1.1	20	1	AZ396481	ACCESSION:AZ396481
C 177	20.4	1.2	26	1	AW327613	ACCESSION:AW327613	C 250	20	1.1	20	1	AZ442328	ACCESSION:AZ442328
C 178	20.4	1.2	26	1	BQ583199	ACCESSION:BQ583199	C 251	20	1.1	20	1	AZ463331	ACCESSION:AZ463331
C 179	20.4	1.2	26	1	CF278359	ACCESSION:CF278359	C 252	20	1.1	20	1	AZ477734	ACCESSION:AZ477734

399	19	1.1	19	1	AZ385952	ACCESSION:AZ385952	472	18.8	1.1	23	1	AZ330773	ACCESSION:AZ330773
400	19	1.1	19	1	AZ391509	ACCESSION:AZ391509	473	18.8	1.1	23	1	AZ382013	ACCESSION:AZ382013
401	19	1.1	19	1	AZ410050	ACCESSION:AZ410050	C 474	18.8	1.1	23	1	AZ486853	ACCESSION:AZ486853
402	19	1.1	19	1	AZ414413	ACCESSION:AZ414413	C 475	18.8	1.1	23	1	AZ627841	ACCESSION:AZ627841
403	19	1.1	19	1	AZ422604	ACCESSION:AZ422604	C 476	18.8	1.1	23	1	AZ645254	ACCESSION:AZ645254
C 404	19	1.1	19	1	AZ424716	ACCESSION:AZ424716	C 477	18.8	1.1	23	1	TA55C06P	ACCESSION:AL455778
C 405	19	1.1	19	1	AZ441329	ACCESSION:AZ441329	C 478	18.8	1.1	24	1	AW247159	ACCESSION:AW247159
C 406	19	1.1	19	1	AZ442365	ACCESSION:AZ442365	C 479	18.8	1.1	24	1	CF281313	ACCESSION:CF281313
C 407	19	1.1	19	1	AZ453930	ACCESSION:AZ453930	480	18.8	1.1	24	1	AZ448207	ACCESSION:AZ448207
C 408	19	1.1	19	1	AZ460906	ACCESSION:AZ460906	C 481	18.8	1.1	24	1	AZ458112	ACCESSION:AZ458112
C 409	19	1.1	19	1	AZ471494	ACCESSION:AZ471494	C 482	18.8	1.1	24	1	AZ621257	ACCESSION:AZ621257
C 410	19	1.1	19	1	AZ476576	ACCESSION:AZ476576	C 483	18.8	1.1	25	1	AU265663	ACCESSION:AU265663
C 411	19	1.1	19	1	AZ486786	ACCESSION:AZ486786	484	18.8	1.1	25	1	AZ329925	ACCESSION:AZ329925
C 412	19	1.1	19	1	AZ490652	ACCESSION:AZ490652	485	18.8	1.1	25	1	AZ404078	ACCESSION:AZ404078
C 413	19	1.1	19	1	AZ508040	ACCESSION:AZ508040	486	18.8	1.1	25	1	AZ515233	ACCESSION:AZ515233
414	19	1.1	19	1	AZ579119	ACCESSION:AZ579119	487	18.8	1.1	25	1	TA12F02Q	ACCESSION:AL451366
415	19	1.1	19	1	AZ583970	ACCESSION:AZ583970	C 488	18.4	1.0	20	1	CF308984	ACCESSION:CF308984
416	19	1.1	19	1	AZ585865	ACCESSION:AZ585865	489	18.4	1.0	20	1	AZ375620	ACCESSION:AZ375620
417	19	1.1	19	1	AZ593210	ACCESSION:AZ593210	C 490	18.4	1.0	20	1	AZ486787	ACCESSION:AZ486787
C 418	19	1.1	19	1	AZ616154	ACCESSION:AZ616154	491	18.4	1.0	20	1	AZ579122	ACCESSION:AZ579122
C 419	19	1.1	19	1	AZ627844	ACCESSION:AZ627844	C 492	18.4	1.0	20	1	AZ645312	ACCESSION:AZ645312
420	19	1.1	19	1	AZ631701	ACCESSION:AZ631701	493	18.4	1.0	20	1	AZ849506	ACCESSION:AZ849506
421	19	1.1	19	1	AZ633821	ACCESSION:AZ633821	494	18.4	1.0	20	1	AZ949997	ACCESSION:AZ949997
422	19	1.1	19	1	AZ643659	ACCESSION:AZ643659	C 495	18.4	1.0	21	1	BX548564	ACCESSION:BX548564
C 423	19	1.1	19	1	AZ644698	ACCESSION:AZ644698	C 496	18.4	1.0	21	1	BX564412	ACCESSION:BX564412
424	19	1.1	19	1	AZ648335	ACCESSION:AZ648335	C 497	18.4	1.0	21	1	CF296213	ACCESSION:CF296213
C 425	19	1.1	19	1	AZ649888	ACCESSION:AZ649888	C 498	18.4	1.0	21	1	CF333393	ACCESSION:CF333393
426	19	1.1	19	1	AZ764497	ACCESSION:AZ764497	C 499	18.4	1.0	21	1	AZ317208	ACCESSION:AZ317208
427	19	1.1	19	1	AZ764522	ACCESSION:AZ764522	C 500	18.4	1.0	21	1	AZ486776	ACCESSION:AZ486776
428	19	1.1	19	1	AZ764534	ACCESSION:AZ764534	C 501	18.4	1.0	21	1	AZ610868	ACCESSION:AZ610868
429	19	1.1	19	1	AZ770387	ACCESSION:AZ770387	502	18.4	1.0	21	1	AZ764492	ACCESSION:AZ764492
430	19	1.1	19	1	AZ778858	ACCESSION:AZ778858	503	18.4	1.0	21	1	AZ822825	ACCESSION:AZ822825
431	19	1.1	19	1	AZ779901	ACCESSION:AZ779901	504	18.4	1.0	21	1	AZ853429	ACCESSION:AZ853429
432	19	1.1	19	1	AZ781876	ACCESSION:AZ781876	C 505	18.4	1.0	23	1	CF291486	ACCESSION:CF291486
C 433	19	1.1	19	1	AZ787634	ACCESSION:AZ787634	C 506	18.4	1.0	23	1	CF311534	ACCESSION:CF311534
C 434	19	1.1	19	1	AZ788058	ACCESSION:AZ788058	C 507	18.4	1.0	24	1	CF337747	ACCESSION:CF337747
C 435	19	1.1	19	1	AZ789590	ACCESSION:AZ789590	C 508	18.4	1.0	24	1	AZ626101	ACCESSION:AZ626101
C 436	19	1.1	19	1	AZ792713	ACCESSION:AZ792713	509	18.2	1.0	23	1	AZ662734	ACCESSION:AZ662734
437	19	1.1	19	1	AZ795403	ACCESSION:AZ795403	C 510	18	1.0	18	1	BQ582676	ACCESSION:BQ582676
C 438 -	19	1.1	19	1	AZ801970	ACCESSION:AZ801970	C 511	18	1.0	18	1	BQ590027	ACCESSION:BQ590027
C 439	19	1.1	19	1	AZ822225	ACCESSION:AZ822225	C 512	18	1.0	18	1	CF277873	ACCESSION:CF277873
440	19	1.1	19	1	AZ841581	ACCESSION:AZ841581	C 513	18	1.0	18	1	CF297446	ACCESSION:CF297446
441	19	1.1	19	1	AZ841622	ACCESSION:AZ841622	C 514	18	1.0	18	1	CF299027	ACCESSION:CF299027
442	19	1.1	19	1	AZ861896	ACCESSION:AZ861896	C 515	18	1.0	18	1	CF299674	ACCESSION:CF299674
443	19	1.1	19	1	AZ936798	ACCESSION:AZ936798	C 516	18	1.0	18	1	CF301325	ACCESSION:CF301325
444	19	1.1	19	1	AZ985501	ACCESSION:AZ985501	C 517	18	1.0	18	1	CF301760	ACCESSION:CF301760
445	19	1.1	19	1	BH000498	ACCESSION:BH000498	C 518	18	1.0	19	1	CF291665	ACCESSION:CF291665
C 446	19	1.1	20	1	AL587572	ACCESSION:AL587572	C 519	18	1.0	19	1	CF293167	ACCESSION:CF293167
C 447	19	1.1	20	1	AL587727	ACCESSION:AL587727	C 520	18	1.0	19	1	CF309821	ACCESSION:CF309821
C 448	19	1.1	20	1	CF282002	ACCESSION:CF282002	C 521	18	1.0	19	1	CF311778	ACCESSION:CF311778
C 449	19	1.1	20	1	CF316662	ACCESSION:CF316662	C 522	18	1.0	19	1	CF331361	ACCESSION:CF331361
C 450	19	1.1	20	1	CF318278	ACCESSION:CF318278	C 523	18	1.0	19	1	CF335293	ACCESSION:CF335293
C 451	19	1.1	20	1	CF320843	ACCESSION:CF320843	C 524	18	1.0	20	1	AL587759	ACCESSION:AL587759
452	19	1.1	20	1	AZ341237	ACCESSION:AZ341237	C 525	18	1.0	20	1	CA853586	ACCESSION:CA853586
C 453	19	1.1	20	1	AZ486784	ACCESSION:AZ486784	C 526	18	1.0	20	1	AZ345856	ACCESSION:AZ345856
454	19	1.1	20	1	AZ638704	ACCESSION:AZ638704	C 527	18	1.0	20	1	AZ370699	ACCESSION:AZ370699
455	19	1.1	20	1	AZ821905	ACCESSION:AZ821905	528	18	1.0	22	1	AZ843648	ACCESSION:AZ843648
456	19	1.1	20	1	AZ858419	ACCESSION:AZ858419	C 529	18	1.0	22	1	TA211D06P	ACCESSION:AL478564
C 457	19	1.1	21	1	AL587702	ACCESSION:AL587702	530	18	1.0	22	1	TA231E08Q	ACCESSION:AL480935
C 458	19	1.1	21	1	CF302218	ACCESSION:CF302218	C 531	18	1.0	22	1	TA386H07Q	ACCESSION:AL498291
C 459	19	1.1	21	1	CF314260	ACCESSION:CF314260	C 532	18	1.0	23	1	AW334124	ACCESSION:AW334124
460	19	1.1	22	1	AL048750	ACCESSION:AL048750	533	18	1.0	23	1	CF293321	ACCESSION:CF293321
C 461	19	1.1	22	1	CF328832	ACCESSION:CF328832	534	18	1.0	24	1	AZ764519	ACCESSION:AZ764519
C 462	19	1.1	22	1	AZ309907	ACCESSION:AZ309907	535	17.8	1.0	21	1	AL048772	ACCESSION:AL048772
C 463	19	1.1	23	1	AL587621	ACCESSION:AL587621	536	17.8	1.0	23	1	AW335179	ACCESSION:AW335179
464	19	1.1	24	1	AZ764496	ACCESSION:AZ764496	C 537	17.4	1.0	19	1	AW248747	ACCESSION:AW248747
465	19	1.1	24	1	AZ764513	ACCESSION:AZ764513	C 538	17.4	1.0	19	1	CF291899	ACCESSION:CF291899
466	19	1.1	25	1	AZ774476	ACCESSION:AZ774476	C 539	17.4	1.0	19	1	CF292072	ACCESSION:CF292072
C 467	18.8	1.1	22	1	CF298427	ACCESSION:CF298427	C 540	17.4	1.0	19	1	CF292144	ACCESSION:CF292144
468	18.8	1.1	22	1	TA303G05P	ACCESSION:AL497383	541	17.4	1.0	19	1	CF310688	ACCESSION:CF310688
C 469	18.8	1.1	23	1	BX550903	ACCESSION:BX550903	C 542	17.4	1.0	19	1	CF319596	ACCESSION:CF319596
C 470	18.8	1.1	23	1	CF279593	ACCESSION:CF279593	C 543	17.4	1.0	19	1	CF329136	ACCESSION:CF329136
C 471	18.8	1.1	23	1	CF333801	ACCESSION:CF333801	544	17.4	1.0	19	1	AZ345795	ACCESSION:AZ345795

C 545	17.4	1.0	19	1	AZ363907	ACCESSION:AZ363907	C 618	16.	0.9	16	1	CF311057	ACCESSION:CF311057
C 546	17.4	1.0	19	1	AZ447251	ACCESSION:AZ447251	C 619	16	0.9	16	1	CF314377	ACCESSION:CF314377
C 547	17.4	1.0	19	1	AZ450180	ACCESSION:AZ450180	C 620	16	0.9	16	1	CF315789	ACCESSION:CF315789
C 548	17.4	1.0	19	1	AZ513919	ACCESSION:AZ513919	C 621	16	0.9	16	1	CF316056	ACCESSION:CF316056
C 549	17.4	1.0	19	1	AZ645841	ACCESSION:AZ645841	C 622	16	0.9	16	1	CF317718	ACCESSION:CF317718
C 550	17.4	1.0	19	1	AZ650252	ACCESSION:AZ650252	C 623	16	0.9	16	1	CF318894	ACCESSION:CF318894
C 551	17.4	1.0	19	1	AZ650575	ACCESSION:AZ650575	C 624	16	0.9	16	1	CF320356	ACCESSION:CF320356
C 552	17.4	1.0	19	1	AZ654747	ACCESSION:AZ654747	C 625	16	0.9	16	1	CF322722	ACCESSION:CF322722
C 553	17.4	1.0	20	1	CF282165	ACCESSION:CF282165	C 626	16	0.9	16	1	CF327923	ACCESSION:CF327923
C 554	17.4	1.0	20	1	CF330490	ACCESSION:CF330490	C 627	16	0.9	16	1	CF328223	ACCESSION:CF328223
C 555	17.4	1.0	20	1	CF333052	ACCESSION:CF333052	C 628	16	0.9	16	1	CF333386	ACCESSION:CF333386
C 556	17.4	1.0	21	1	CF319625	ACCESSION:CF319625	C 629	16	0.9	17	1	BQ590128	ACCESSION:BQ590128
C 557	17.4	1.0	21	1	CF330439	ACCESSION:CF330439	C 630	16	0.9	17	1	CF294668	ACCESSION:CF294668
C 558	17.4	1.0	21	1	AZ308846	ACCESSION:AZ308846	C 631	16	0.9	17	1	CF295988	ACCESSION:CF295988
C 559	17.4	1.0	21	1	AZ627840	ACCESSION:AZ627840	C 632	16	0.9	17	1	CF297251	ACCESSION:CF297251
C 560	17.4	1.0	22	1	CF302435	ACCESSION:CF302435	C 633	16	0.9	17	1	CF298341	ACCESSION:CF298341
C 561	17.4	1.0	23	1	AL048695	ACCESSION:AL048695	C 634	16	0.9	17	1	CF302447	ACCESSION:CF302447
C 562	17.4	1.0	23	1	BQ590647	ACCESSION:BQ590647	C 635	16	0.9	17	1	CF313013	ACCESSION:CF313013
C 563	17.4	1.0	23	1	BX560037	ACCESSION:BX560037	C 636	16	0.9	17	1	CF336950	ACCESSION:CF336950
C 564	17.2	1.0	22	1	BQ591193	ACCESSION:BQ591193	C 637	16	0.9	19	1	CF300236	ACCESSION:CF300236
C 565	17.2	1.0	22	1	CF297521	ACCESSION:CF297521	C 638	16	0.9	19	1	CF311668	ACCESSION:CF311668
C 566	17.2	1.0	22	1	AZ442146	ACCESSION:AZ442146	C 639	16	0.9	19	1	CF325356	ACCESSION:CF325356
C 567	17.2	1.0	22	1	TA110B07P	ACCESSION:TA110B07P	C 640	16	0.9	19	1	AZ764517	ACCESSION:AZ764517
C 568	17	1.0	17	1	BQ590687	ACCESSION:BQ590687	C 641	16	0.9	20	1	CF336815	ACCESSION:CF336815
C 569	17	1.0	17	1	BQ591177	ACCESSION:BQ591177	C 642	16	0.9	21	1	CF282313	ACCESSION:CF282313
C 570	17	1.0	17	1	CF290854	ACCESSION:CF290854	C 643	16	0.9	21	1	CF28316019	ACCESSION:CF28316019
C 571	17	1.0	17	1	CF295807	ACCESSION:CF295807	C 644	16	0.9	21	1	AZ963501	ACCESSION:AZ963501
C 572	17	1.0	17	1	CF298589	ACCESSION:CF298589	C 645	15.8	0.9	19	1	CF298134	ACCESSION:CF298134
C 573	17	1.0	17	1	CF299639	ACCESSION:CF299639	C 646	15.8	0.9	19	1	CF329137	ACCESSION:CF329137
C 574	17	1.0	17	1	CF310219	ACCESSION:CF310219	C 647	15.8	0.9	19	1	AZ345499	ACCESSION:AZ345499
C 575	17	1.0	17	1	CF334566	ACCESSION:CF334566	C 648	15.8	0.9	19	1	AZ509929	ACCESSION:AZ509929
C 576	17	1.0	18	1	AL048754	ACCESSION:AL048754	C 649	15.8	0.9	19	1	AZ611602	ACCESSION:AZ611602
C 577	17	1.0	18	1	CF301057	ACCESSION:CF301057	C 650	15.8	0.9	19	1	AZ775624	ACCESSION:AZ775624
C 578	17	1.0	18	1	CF301151	ACCESSION:CF301151	C 651	15.8	0.9	19	1	AZ786336	ACCESSION:AZ786336
C 579	17	1.0	18	1	CF320418	ACCESSION:CF320418	C 652	15.8	0.9	20	1	AW333777	ACCESSION:AW333777
C 580	17	1.0	19	1	CF327587	ACCESSION:CF327587	C 653	15.4	0.9	17	1	AW248574	ACCESSION:AW248574
C 581	17	1.0	19	1	AZ853220	ACCESSION:AZ853220	C 654	15.4	0.9	17	1	BQ591181	ACCESSION:BQ591181
C 582	17	1.0	20	1	CF298018	ACCESSION:CF298018	C 655	15.4	0.9	17	1	BQ591588	ACCESSION:BQ591588
C 583	17	1.0	20	1	CF298207	ACCESSION:CF298207	C 656	15.4	0.9	17	1	CF276637	ACCESSION:CF276637
C 584	17	1.0	20	1	CF319428	ACCESSION:CF319428	C 657	15.4	0.9	17	1	CF291802	ACCESSION:CF291802
C 585	17	1.0	20	1	AZ818055	ACCESSION:AZ818055	C 658	15.4	0.9	17	1	CF299997	ACCESSION:CF299997
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C 587	17	1.0	22	1	AZ310057	ACCESSION:AZ310057	C 660	15.4	0.9	19	1	AA953971	ACCESSION:AA953971
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C 589	16.8	1.0	20	1	CF300961	ACCESSION:CF300961	C 662	15.2	0.9	20	1	AZ316368	ACCESSION:AZ316368
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C 591	16.8	1.0	20	1	AZ343730	ACCESSION:AZ343730	C 664	15.2	0.9	20	1	AZ368518	ACCESSION:AZ368518
C 592	16.8	1.0	20	1	AZ633741	ACCESSION:AZ633741	C 665	15.2	0.9	20	1	AZ959504	ACCESSION:AZ959504
C 593	16.8	1.0	21	1	AW248782	ACCESSION:AW248782	C 666	15	0.9	15	1	BE230585	ACCESSION:BE230585
C 594	16.8	1.0	21	1	CF293087	ACCESSION:CF293087	C 667	15	0.9	15	1	BQ582543	ACCESSION:BQ582543
C 595	16.8	1.0	21	1	CF319122	ACCESSION:CF319122	C 668	15	0.9	15	1	BQ585820	ACCESSION:BQ585820
C 596	16.8	1.0	21	1	AZ597932	ACCESSION:AZ597932	C 669	15	0.9	15	1	BQ590410	ACCESSION:BQ590410
C 597	16.8	1.0	21	1	AZ647578	ACCESSION:AZ647578	C 670	15	0.9	15	1	BQ590656	ACCESSION:BQ590656
C 598	16.4	0.9	18	1	BM658677	ACCESSION:BM658677	C 671	15	0.9	15	1	BQ591170	ACCESSION:BQ591170
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C 604	16.4	0.9	19	1	CF278272	ACCESSION:CF278272	C 677	15	0.9	15	1	CF290920	ACCESSION:CF290920
C 605	16.4	0.9	19	1	CF298472	ACCESSION:CF298472	C 678	15	0.9	15	1	CF291029	ACCESSION:CF291029
C 606	16.4	0.9	19	1	CF309636	ACCESSION:CF309636	C 679	15	0.9	15	1	CF291103	ACCESSION:CF291103
C 607	16.4	0.9	19	1	CF326845	ACCESSION:CF326845	C 680	15	0.9	15	1	CF291717	ACCESSION:CF291717
C 608	16.4	0.9	19	1	CF334610	ACCESSION:CF334610	C 681	15	0.9	15	1	CF291798	ACCESSION:CF291798
C 609	16.4	0.9	19	1	AZ360314	ACCESSION:AZ360314	C 682	15	0.9	15	1	CF292458	ACCESSION:CF292458
C 610	16.4	0.9	21	1	CF309614	ACCESSION:CF309614	C 683	15	0.9	15	1	CF292461	ACCESSION:CF292461
C 611	16.2	0.9	21	1	AZ346714	ACCESSION:AZ346714	C 684	15	0.9	15	1	CF296652	ACCESSION:CF296652
C 612	16	0.9	16	1	BQ590166	ACCESSION:BQ590166	C 685	15	0.9	15	1	CF298148	ACCESSION:CF298148
C 613	16	0.9	16	1	BQ590207	ACCESSION:BQ590207	C 686	15	0.9	15	1	CF298630	ACCESSION:CF298630
C 614	16	0.9	16	1	BQ592600	ACCESSION:BQ592600	C 687	15	0.9	15	1	CF298733	ACCESSION:CF298733
C 615	16	0.9	16	1	BQ592965	ACCESSION:BQ592965	C 688	15	0.9	15	1	CF298805	ACCESSION:CF298805
C 616	16	0.9	16	1	BQ595717	ACCESSION:BQ595717	C 689	15	0.9	15	1	CF298889	ACCESSION:CF298889
C 617	16	0.9	16	1	CF279325	ACCESSION:CF279325	C 690	15	0.9	15	1	CF299602	ACCESSION:CF299602

C 837	13	0.7	13	1	CF291726	ACCESSION:CF291726	C 910	13	0.7	14	1	BQ591949	ACCESSION:BQ591949
C 838	13	0.7	13	1	CF291903	ACCESSION:CF291903	C 911	13	0.7	15	1	CF543203	ACCESSION:CF543203
C 839	13	0.7	13	1	CF298590	ACCESSION:CF298590	C 912	12.8	0.7	16	1	AA937877	ACCESSION:AA937877
C 840	13	0.7	13	1	CF298592	ACCESSION:CF298592	C 913	12.8	0.7	16	1	AW248540	ACCESSION:AW248540
C 841	13	0.7	13	1	CF298736	ACCESSION:CF298736	C 914	12.8	0.7	17	1	AW246528	ACCESSION:AW246528
C 842	13	0.7	13	1	CF298764	ACCESSION:CF298764	C 915	12.8	0.7	50	1	AU102457	ACCESSION:AU102457
C 843	13	0.7	13	1	CF298795	ACCESSION:CF298795	C 916	12.6	0.7	29	1	CF334023	ACCESSION:CF334023
C 844	13	0.7	13	1	CF298908	ACCESSION:CF298908	C 917	12.4	0.7	14	1	CF301021	ACCESSION:CF301021
C 845	13	0.7	13	1	CF299133	ACCESSION:CF299133	C 918	12.4	0.7	15	1	AW246551	ACCESSION:AW246551
C 846	13	0.7	13	1	CF299359	ACCESSION:CF299359	C 919	12.4	0.7	15	1	CF332179	ACCESSION:CF332179
C 847	13	0.7	13	1	CF299937	ACCESSION:CF299937	C 920	12.4	0.7	16	1	AW245338	ACCESSION:AW245338
C 848	13	0.7	13	1	CF300118	ACCESSION:CF300118	C 921	12.2	0.7	24	1	AZ764496	ACCESSION:AZ764496
C 849	13	0.7	13	1	CF300587	ACCESSION:CF300587	C 922	12.2	0.7	24	1	AZ764513	ACCESSION:AZ764513
C 850	13	0.7	13	1	CF300658	ACCESSION:CF300658	C 923	12.2	0.7	24	1	AZ764519	ACCESSION:AZ764519
C 851	13	0.7	13	1	CF300929	ACCESSION:CF300929	C 924	12.2	0.7	26	1	TA321GL1P	ACCESSION:AL492371
C 852	13	0.7	13	1	CF301247	ACCESSION:CF301247	C 925	12.2	0.7	50	1	AU102454	ACCESSION:AU102454
C 853	13	0.7	13	1	CF301286	ACCESSION:CF301286	C 926	12	0.7	12	1	BG668943	ACCESSION:BG668943
C 854	13	0.7	13	1	CF302158	ACCESSION:CF302158	C 927	12	0.7	12	1	BQ582536	ACCESSION:BQ582536
C 855	13	0.7	13	1	CF302830	ACCESSION:CF302830	C 928	12	0.7	12	1	BQ588719	ACCESSION:BQ588719
C 856	13	0.7	13	1	CF302898	ACCESSION:CF302898	C 929	12	0.7	12	1	BQ594698	ACCESSION:BQ594698
C 857	13	0.7	13	1	CF310516	ACCESSION:CF310516	C 930	12	0.7	12	1	CF279278	ACCESSION:CF279278
C 858	13	0.7	13	1	CF310517	ACCESSION:CF310517	C 931	12	0.7	12	1	CF291428	ACCESSION:CF291428
C 859	13	0.7	13	1	CF312721	ACCESSION:CF312721	C 932	12	0.7	12	1	CF291800	ACCESSION:CF291800
C 860	13	0.7	13	1	CF313171	ACCESSION:CF313171	C 933	12	0.7	12	1	CF291801	ACCESSION:CF291801
C 861	13	0.7	13	1	CF314239	ACCESSION:CF314239	C 934	12	0.7	12	1	CF291885	ACCESSION:CF291885
C 862	13	0.7	13	1	CF314874	ACCESSION:CF314874	C 935	12	0.7	12	1	CF291886	ACCESSION:CF291886
C 863	13	0.7	13	1	CF315395	ACCESSION:CF315395	C 936	12	0.7	12	1	CF292107	ACCESSION:CF292107
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C 865	13	0.7	13	1	CF316440	ACCESSION:CF316440	C 938	12	0.7	12	1	CF298686	ACCESSION:CF298686
C 866	13	0.7	13	1	CF316637	ACCESSION:CF316637	C 939	12	0.7	12	1	CF298872	ACCESSION:CF298872
C 867	13	0.7	13	1	CF3182								

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c 984	11.8	0.7	50	1	AU102455	ACCESSION:AU102455
985	11.4	0.6	13	1	CF291168	ACCESSION:CF291168
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c 989	11	0.6	11	1	BQ589109	ACCESSION:BQ589109
c 990	11	0.6	11	1	BQ590590	ACCESSION:BQ590590
c 991	11	0.6	11	1	BQ595827	ACCESSION:BQ595827
c 992	11	0.6	11	1	BQ595834	ACCESSION:BQ595834
c 993	11	0.6	11	1	CF281971	ACCESSION:CF281971
c 994	11	0.6	11	1	CF290941	ACCESSION:CF290941
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c 997	11	0.6	11	1	CF291454	ACCESSION:CF291454
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c1001	11	0.6	11	1	CF297318	ACCESSION:CF297318
c1002	11	0.6	11	1	CF297948	ACCESSION:CF297948
c1003	11	0.6	11	1	CF298806	ACCESSION:CF298806
c1004	11	0.6	11	1	CF299648	ACCESSION:CF299648
c1005	11	0.6	11	1	CF299849	ACCESSION:CF299849
c1006	11	0.6	11	1	CF300174	ACCESSION:CF300174
c1007	11	0.6	11	1	CF301288	ACCESSION:CF301288
1008	11	0.6	11	1	CF301713	ACCESSION:CF301713
c1009	11	0.6	11	1	CF301744	ACCESSION:CF301744
c1010	11	0.6	11	1	CF302896	ACCESSION:CF302896
c1011	11	0.6	11	1	CF307845	ACCESSION:CF307845
c1012	11	0.6	11	1	CF309987	ACCESSION:CF309987
c1013	11	0.6	11	1	CF311911	ACCESSION:CF311911
1014	11	0.6	11	1	CF311912	ACCESSION:CF311912
c1015	11	0.6	11	1	CF314533	ACCESSION:CF314533
c1016	11	0.6	11	1	CF318741	ACCESSION:CF318741
c1017	11	0.6	11	1	CF326997	ACCESSION:CF326997
1018	11	0.6	11	1	CF326998	ACCESSION:CF326998
1019	11	0.6	11	1	CF327885	ACCESSION:CF327885
c1020	11	0.6	11	1	CF328618	ACCESSION:CF328618
1021	11	0.6	11	1	CF328619	ACCESSION:CF328619
c1022	11	0.6	11	1	CF329242	ACCESSION:CF329242
c1023	11	0.6	11	1	CF329344	ACCESSION:CF329344
1024	11	0.6	11	1	CF329345	ACCESSION:CF329345
c1025	11	0.6	11	1	CF331049	ACCESSION:CF331049
c1026	11	0.6	11	1	CF331066	ACCESSION:CF331066
c1027	11	0.6	11	1	CF331814	ACCESSION:CF331814
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ALIGNMENTS

RESULT 1						
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LOCUS	AU102457	Sugano Homo sapiens	cdna library	Homo sapiens	cdna clone	
DEFINITION	REC01020, mRNA sequence.					
ACCESSION	AU102457					
VERSION	AU102457.1	GI:13551977				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
	1 (bases 1 to 50)					
	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,					
	Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,					
	Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.					
TITLE	Diverse transcriptional initiation revealed by fine, large-scale					
	mapping of mRNA start sites					
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)					
MEDLINE	21270072					
PUBMED	11375929					
COMMENT	Contact: Yutaka Suzuki					

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Institute of Medical Science, University of Tokyo						
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan						
Email: ysuzuki@ims.u-tokyo.ac.jp						
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and						
Sugano,S. Construction and characterization of a full						
length-enriched and a 5'-end-enriched cdna library. Gene 200 (1-2),						
149-156 (1997).						
FEATURES	Location/Qualifiers					
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Best Local Similarity	100.0%; Pred. No. 0.067;					
Matches	50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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Db	1 GTTTTCTTTCTGGAGTCCCAACGAGGTGCGGACGGAAGGGGGTGA 50					
RESULT 2						
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LOCUS	AU102453	50 bp	mRNA	linear	EST 30-AUG-2001	
DEFINITION	AU102453 Sugano Homo sapiens	cdna library	Homo sapiens	cdna clone		
	CAS11875, mRNA sequence.					
ACCESSION	AU102453					
VERSION	AU102453.1	GI:13551973				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 50)					
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,					
	Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,					
	Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.					
TITLE	Diverse transcriptional initiation revealed by fine, large-scale					
	mapping of mRNA start sites					
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)					
MEDLINE	21270072					
PUBMED	11375929					
COMMENT	Contact: Yutaka Suzuki					

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Institute of Medical Science, University of Tokyo						
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Email: ysuzuki@ims.u-tokyo.ac.jp						
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and						
Sugano,S. Construction and characterization of a full						
length-enriched and a 5'-end-enriched cdna library. Gene 200 (1-2),						
149-156 (1997).						
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Best Local Similarity	98.0%; Pred. No. 0.1;					
Matches	49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
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RESULT 3						

AU102454
LOCUS
DEFINITION AU102454 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC01208, mRNA sequence.
ACCESSION AU102454
VERSION AU102454.1 GI:13551974
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source Location/Qualifiers
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Qy 49 AGAAAGTCTTTCTTTCTGGAGTCCCAACGAGGTGCGGACGGAAG 98
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Db 1 AGAAATGTTTCTTTCTGGAGTCCCAACGAGGTGCGGACGGAAG 50
RESULT 4
AU102455
LOCUS
DEFINITION AU102455 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC10032, mRNA sequence.
ACCESSION AU102455
VERSION AU102455.1 GI:13551975
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source Location/Qualifiers
1..50
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Query Match 2.8%; Score 48.4; DB 1; Length 50;
Best Local Similarity 98.0%; Pred. No. 0.1;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 47 CCAGAAAAAGTTTCTTTCTGGAGTCCCAACGAGGTGCGGACGGAAG 96
| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 CAAGAAAAAGTTTCTTTCTGGAGTCCCAACGAGGTGCGGACGGAAG 50
RESULT 5
AI954491/c
LOCUS
DEFINITION AI954491 43 bp mRNA linear EST 09-MAR-2000
wx83d04.x1 NCI CGAP Ov38 Homo sapiens cDNA clone IMAGE:2550247 3'
similar to SW:TRIG_HUMAN Q15654 THYROID RECEPTOR INTERACTING
PROTEIN 6 ; mRNA sequence.
ACCESSION AI954491
VERSION AI954491.1 GI:5746801
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeff Struwing, M.D., Michael R. Emmert-Buck,
M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. CDNA
Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert length: 1014 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
source Location/Qualifiers
1..43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2550247"
/tissue_type="normal epithelium"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Ov38"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies."
Query Match 1.9%; Score 33.4; DB 1; Length 43;
Best Local Similarity 86.0%; Pred. No. 6.1;
Matches 37; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1348 CCAAGATGCTCAGTGTGGGTGGGCCATATATGCCTGAGCCAG 1390
|| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 43 CCTTGTGCTCGGTGCGGTGGGCCGTAGTGCCTGAGCCAG 1

RESULT 6
AI000255/c
LOCUS
DEFINITION
AI000255
ov10a02.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1636874 3'
similar to SW:TR16_HUMAN Q15654 THYROID RECEPTOR INTERACTING
PROTEIN 6 ; , mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 680 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source

1. .31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1636874"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid3"

/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. mRNA
source: 2 pooled kidneys. Library went through one round
of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo."

Query Match 1.7%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 TTGCCCCCAGATGCTCAGTGTGGGTGG 1371
|||||
DB 31 TTGCCCCCAGATGCTCAGTGTGGGTGG 2

RESULT 7
AL048719

LOCUS
DEFINITION
AL048719
DKFZp566G233.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566G233, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
1. .33
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566G233"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

FEATURES
source

Query Match 1.4%; Score 24.8; DB 1; Length 33;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1728 GAGTTTACAAAAA
DB 6 GGGTTACAAAAA

AA482614
LOCUS
DEFINITION
AA482614.1 GI:2210292
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1356 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 1.

RESULT 8
AA482614/c

LOCUS
DEFINITION
AA482614.1 GI:2210292
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1356 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source

1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5935790"
/db_xref="taxon:9606"
/clone="IMAGE:724270"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NBHOT"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a

QY 1728 GAGTTTACAAAAA
DB 6 GGGTTACAAAAA

AA482614
LOCUS
DEFINITION
AA482614.1 GI:2210292
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1356 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 1.

Query Match 1.7%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 TTGCCCCCAGATGCTCAGTGTGGGTGG 1371
|||||
DB 31 TTGCCCCCAGATGCTCAGTGTGGGTGG 2

RESULT 7
AL048719

LOCUS
DEFINITION
AL048719
DKFZp566G233.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566G233, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGCGCGGTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "

Query Match 1.3%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1246 TTCACCTGGTGGTGTGTACCGCG 1270
|||||
Db 25 TTCACGTGGTGGTGTGTACCGCG 1

RESULT 9
R26779/c
LOCUS
DEFINITION Yh44f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:132611 3' similar to gb:M85164 SERUM RESPONSE FACTOR
ACCESSORY PROTEIN 1A (HUMAN);, mRNA sequence.

ACCESSION R26779.1 GI:782914
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 26)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1384
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1384 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source
1. .26
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:538233"
/db_xref="taxon:9606"
/clone="IMAGE:132611"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Nb2HP"
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAAATTCGCGCGCGAGCAATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

Query Match 1.3%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 67;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1755
|||||
Db 25 TTTAAAAA 1

RESULT 10
CF299155/c
LOCUS
DEFINITION CF299155 29 bp mRNA linear EST 15-AUG-2003
7LEAF--03-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-B02, mRNA sequence.

ACCESSION CF299155
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .29
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-B02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 23.4; DB 1; Length 29;
Best Local Similarity 96.0%; Pred. No. 72;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1755
|||||
Db 26 TTTAAAAA 2

RESULT 11
TA378G07P/c
LOCUS
DEFINITION TA378G07P 29 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 378g07, forward sequence, genomic survey sequence.
ACCESSION AL497621
VERSION AL497621.1 GI:11873343
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE
AUTHORS 1 (bases 1 to 29)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source Location/Qualifiers
1. .29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="378g07"
Query Match 1.3%; Score 23.4; DB 1; Length 29;
Best Local Similarity 96.0%; Pred. No. 72;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1731 TTACAAAAA 1755
Db 25 TTTAAAAA 1
RESULT 12
CF299646/c 26 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-L24.bi Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-L24, mRNA sequence.
ACCESSION CF299646
VERSION CF299646.1 GI:33671407
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source Location/Qualifiers
1. .26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-L24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 1.3%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 79;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1730 GTTACAAAAA 1755
Db 26 GATTAAAAA 1
RESULT 13
CF317007/c 25 bp mRNA linear EST 15-AUG-2003
LOCUS HD--06-I14.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--06-I14, mRNA sequence.
ACCESSION CF317007
VERSION CF317007.1 GI:33688768
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source Location/Qualifiers
1. .25
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--06-I14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 1.3%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1732 TTACAAAAA 1755
Db 25 TTAAAAA 2
RESULT 14
N59260/c 25 bp mRNA linear EST 23-FEB-1996
LOCUS y282d11.s1 Soares multiple sclerosis 2NbhMSP Homo sapiens CDNA
DEFINITION clone IMAGE:289557 3, similar to gb:M77693 DIAMINE
ACETYLTRANSFERASE (HUMAN);, mRNA sequence.
ACCESSION N59260

VERSION N59260.1 GI:1203150
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1.
FEATURES
source
1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3905397"
/db_xref="taxon:9606"
/clone="IMAGE:289557"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares multiple sclerosis 2NbHMSp"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH). "
Query Match 1.3%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 86;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1731 TTTACAAAAA 1754
Db 24 TTTAAAAA 1
RESULT 15
N34515/c
LOCUS N34515 27 bp mRNA linear EST 16-JAN-1996
DEFINITION YY55b01.s1 Soares multiple sclerosis 2NbHMSp Homo sapiens cDNA
Clone IMAGE:277510 3' similar to gb:S78694 PROTEIN-LYSINE 6-OXIDASE
PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION N34515
VERSION N34515.1 GI:1155657
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 27)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1.
FEATURES
source
1. .27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3895793"
/db_xref="taxon:9606"
/clone="IMAGE:277510"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares multiple sclerosis 2NbHMSp"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH). "
Query Match 1.3%; Score 22.4; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 90;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1731 TTTACAAAAA 1755
Db 25 TTTCAAAAAA 1
RESULT 16
CF337400
LOCUS CF337400 28 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--07-N04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--07-N04, mRNA sequence.
ACCESSION CF337400
VERSION CF337400.1 GI:33823200
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 28)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..28

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="JMT--07-N04"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

CDNA library (JMT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match

Best Local Similarity 1.3%; Score 22.4; DB 1; Length 28;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1732 TTACAAAAA 1755

|||||

1 TTA 24

RESULT 17

CF314795/c

LOCUS

DEFINITION HD--03-H09.g1 OsHDAC1-overexpressing transgenic rice plasmid CDNA
library (HD) Oryza sativa CDNA clone HD--03-H09, mRNA sequence.

ACCESSION

CF314795

VERSION

CF314795.1 GI:33686556

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 29)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..29

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HD--03-H09"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid

CDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.3%; Score 22.4; DB 1; Length 29;

Best Local Similarity 95.8%; Pred. No. 95;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1731 TTTACAAAA 1754

|||||

25 TTTAAAA 2

RESULT 18

BX559898/c

LOCUS

DEFINITION

BX559898 Glossina morsitans morsitans adult infected gut Glossina

morsitans morsitans cDNA clone Tse46d05_plc, mRNA sequence.

ACCESSION

BX559898

VERSION

BX559898.1

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans

Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Hippoboscoidae; Glossinidae; Glossina.

1 (bases 1 to 23)

Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,

Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.

Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune

response genes

Genome Biol. 4 (10), R63 (2003)

22881942

PUBMED

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxtion, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'

end of the cDNA all plc reads are from

the 3' end.

FEATURES

source

1..23

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse46d05_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected

gut"

/note="country: Zimbabwe; EST from adult gut infected with

T.brucei"

Query Match

Best Local Similarity 100.0%; Pred. No. 91;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1734 ACAAAAA 1755

|||||

22 ACA 1

RESULT 19

T52836/c

LOCUS

T52836

28 bp

mRNA

linear

EST 06-FEB-1995

DEFINITION ya81b09.sl Stratagene ovary (#937217) Homo sapiens cDNA clone
IMAGE:68057 3' similar to similar to gb:X53463 GLUTATHIONE
PEROXIDASE-GASTROINTESTINAL (HUMAN), mRNA sequence.

ACCESSION T52836
VERSION T52836.1 GI:654696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,P., Thierry-Mieg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Marra,M.

TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 51
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 51 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 1.
Location/Qualifiers
1. .28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:504314"
/db_xref="taxon:9606"
/clone="IMAGE:68057"
/sex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5'
GAATTCGGCAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3,"

Query Match 1.3%; Score 22; DB 1; Length 28;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1755
|||||
Db 22 ACAAAAAAAAAAAAAAAAAA 1

RESULT 20
CF280688/c
LOCUS CF280688 26 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-H09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-H09, mRNA sequence.

ACCESSION CF280688
VERSION CF280688.1 GI:33658074
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--07-H09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred.No. 1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAAAAAAAAAAAAAA 1755
|||||
Db 26 TTTCACAAAAAAAAAAAAAAAAA 2

RESULT 21
AZ358846/c
LOCUS AZ358846 26 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0101M24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0101M24 F, genomic survey sequence.

ACCESSION AZ358846
VERSION AZ358846.1 GI:10472546
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0101 row: M column: 24
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.


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FEATURES
source
Location/Qualifiers
1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0101M24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWd42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1755
||| |||||
Db 25 TTTTAAAAA 1

RESULT 22
CF333518/c
LOCUS
DEFINITION
JMT--02-H05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--02-H05, mRNA sequence.
CF333518
ACCESSION
VERSION
CF333518.1 GI:33815326
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 27)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1. .27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-H05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
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```
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1755
||| |||||
Db 25 TTTTAAAAA 1

RESULT 23
R59382/c
LOCUS
DEFINITION
R59382
YH17e07.s1 Soares infant brain IN1B Homo sapiens cDNA clone
IMAGE:37726 3' similar to gb:M65131 METHYLMALONYL-COA MUTASE
PRECURSOR (HUMAN);, mRNA sequence.
R59382
ACCESSION
VERSION
R59382.1 GI:830077
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 27)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: polyt not found
Seq primer: SP6
High quality sequence stop: 1.

FEATURES
source
Location/Qualifiers
1. .27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:410267"
/db_xref="taxon:9606"
/clone="IMAGE:37726"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain IN1B"
/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
AACTGGAAGAATTCCGGCCGACGAAATTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lafmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
```

```
Query Match      1.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1755
Db 26 TTGAAAAA 2

RESULT 24
CF334023/c
LOCUS
DEFINITION JMT--03-C14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-C14, mRNA sequence.
ACCESSION CF334023
VERSION CF334023.1 GI:33816351
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..29
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-C14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      1.2%; Score 21.8; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1730 GTTACAAAAA 1754
Db 25 GTTACTGAAAAA 1

RESULT 25
CF329694/c
LOCUS
DEFINITION NACL--05-B19.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-B19, mRNA sequence.
ACCESSION CF329694
VERSION CF329694.1 GI:33807601
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
```

```
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-B19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1754
Db 23 TTAAAAA 1

RESULT 26
AZ330737
LOCUS
DEFINITION 1M0056F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0056F09 F, genomic survey sequence.
ACCESSION AZ330737
VERSION AZ330737.1 GI:10392737
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: F column: 09
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"

source
```


/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0056F09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1753
|||||
Db 3 TTTAAAAA 25

RESULT 27
AW333508/c
LOCUS AW333508 26 bp mRNA linear EST 31-JAN-2000
DEFINITION S22F8 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AW333508
VERSION AW333508.1 GI:6829865
KEYWORDS EST.
SOURCE Pneumocystis carinii
ORGANISM Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 26)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers

1. .26
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1753
|||||
Db 23 TTTATAAAAA 1

RESULT 28
N52529/c
LOCUS N52529 27 bp mRNA linear EST 15-FEB-1996
DEFINITION yv35a12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:244702 3' similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
HIN-1 (HUMAN);, mRNA sequence.
ACCESSION N52529
VERSION N52529.1 GI:1193695
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 27)
Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1.

FEATURES
source
1. .27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3793948"
/db_xref="taxon:9606"
/clone="IMAGE:244702"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAGAAATAATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 1.2%; Score 21.4; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1755
|||||
Db 27 TTCNAAAAA 4

RESULT 29

N89936/c
LOCUS
DEFINITION
N89936 27 bp mRNA linear EST 02-APR-1996
zb23e12.s1 Soares fetal lung NBHL19W Homo sapiens cDNA clone
IMAGE:302926 3' similar to gb:X59066 ATP SYNTHASE ALPHA CHAIN,
MITOCHONDRIAL PRECURSOR (HUMAN); mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 27)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE
JOURNAL
COMMENT
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ET primer
High quality sequence stop: 8.
FEATURES
source
1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1247858"
/db_xref="taxon:9606"
/clone="IMAGE:302926"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung_NBHL19W"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGGCCGAATTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."
Query Match 1.2%; Score 21.4; DB 1; Length 27;
Best Local Similarity 95.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1733 TACAAAAA 1755
Db 25 TGCAAAAA 3
RESULT 30
AZ824574/c
LOCUS
DEFINITION
AZ824574 28 bp DNA linear GSS 20-FEB-2001
2M0099D17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0099D17 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
TITLE
JOURNAL
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: D column: 17
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES
source
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0099D17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 1.2%; Score 21.4; DB 1; Length 28;
Best Local Similarity 95.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1733 TACAAAAA 1755
Db 23 TAAAAA 1
RESULT 31
CF311914/c
LOCUS
DEFINITION
CF311914 21 bp mRNA linear EST 15-AUG-2003
ABF--07-G07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-G07, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--07-G07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA... 1755
|||||...
Db 21 CAAAAA... 1

RESULT 32
AZ792613/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ792613 21 bp DNA linear GSS 16-FEB-2001
2M0045M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045M12 F, genomic survey sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ792613
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: M column: 12
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source

Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0045M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAA... 1754
|||||...
Db 21 ACAA... 1

RESULT 33
AZ304806
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ304806 22 bp DNA linear GSS 29-SEP-2000
1M005K17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M005K17 F, genomic survey sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ304806
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0005 row: K column: 17
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

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source      1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0005K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid.R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 1.2%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
 |||||||

Db 1 CAAAAAAAAAAAAAAAAAAAAA 21

RESULT 34

AZ505769

LOCUS 22 bp DNA linear GSS 05-OCT-2000

DEFINITION 1M0346A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0346A10 R, genomic survey sequence.

ACCESSION AZ505769

VERSION AZ505769.1 GI:10687085

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0346 row: A column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22

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source      1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0005K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid.R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 1.2%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
 |||||||

Db 1 CAAAAAAAAAAAAAAAAAAAAA 21

RESULT 35

AZ315640

LOCUS 23 bp DNA linear GSS 29-SEP-2000

DEFINITION 1M0033O04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0033O04 F, genomic survey sequence.

ACCESSION AZ315640

VERSION AZ315640.1 GI:10362861

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: O column: 04
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23

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source      1. .23
/organism="Mus musculus"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      1.2%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 3 CAAAAAAAAAAAAAAAAAAAAA 23

RESULT 36
AL048765
LOCUS
DEFINITION
AL048765 24 bp mRNA linear EST 04-SEP-2003
KFZP566M233.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
KFZP566M233, mRNA sequence.
ACCESSION
AL048765.1 GI:4727836
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Koehrer, K., Bever, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE
EST (Koehrer, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
Location/Qualifiers
1..24
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566M233"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      1.2%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 3 CAAAAAAAAAAAAAAAAAAAAA 23

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0033O04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      1.2%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 3 CAAAAAAAAAAAAAAAAAAAAA 23

RESULT 36
AL048765
LOCUS
DEFINITION
AL048765 24 bp mRNA linear EST 04-SEP-2003
KFZP566M233.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
KFZP566M233, mRNA sequence.
ACCESSION
AL048765.1 GI:4727836
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Koehrer, K., Bever, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE
EST (Koehrer, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
Location/Qualifiers
1..24
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566M233"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      1.2%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 3 CAAAAAAAAAAAAAAAAAAAAA 23

RESULT 37
CF326993
LOCUS
DEFINITION
CF326993 24 bp mRNA linear EST 18-AUG-2003
NACL--01-E17.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-E17, mRNA sequence.
ACCESSION
CF326993
VERSION
CF326993.1 GI:33802241
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 24)
REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--01-E17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      1.2%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 2 CAAAAAAAAAAAAAAAAAAAAA 22

RESULT 38
AZ404871
LOCUS
DEFINITION
AZ404871 24 bp DNA linear GSS 03-OCT-2000
1M0173J14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0173J14 R, genomic survey sequence.
ACCESSION
AZ404871
VERSION
AZ404871.1 GI:10528884
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss

```


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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0173 row: J column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
source

1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0173J14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

1.2%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA
Db 4 CAAAAA

RESULT 39
AZ786257
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

24 bp DNA linear GSS 16-FEB-2001
2M0031H1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0031H11 R, genomic survey sequence.

AZ786257
AZ786257.1 GI:12923835
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: H column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
source

1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0031H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

1.2%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA
Db 1 CAAAAA

RESULT 40
AL048782
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

25 bp mRNA linear EST 04-SEP-2003
DKFZp5660013_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp5660013, mRNA sequence.

AL048782
AL048782.1 GI:4727853
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehrer, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

1. .25
/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="DKFZp5660013"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      1.2%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1754
Db 5 ACACAAAAA 25

RESULT 41
N27663/c
LOCUS N27663
DEFINITION yw50906.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255706 3' similar to gb:J05032 ASPARTYL-TRNA SYNTHETASE (HUMAN);, mRNA sequence.
ACCESSION N27663
VERSION N27663.1 GI:1142144
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 25)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.
Location/Qualifiers
1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3866115"
/db_xref="taxon:9606"
/clone="IMAGE:255706"
/sex="Female"
/tissue_type="olfactory epithelium"
/dev_stage="35 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Weizmann Olfactory Epithelium"
/note="Organ: nose; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Olfactory epithelium, normal. Average insert size: 0.8 kb; Uni-ZAP XR Vector. Library constructed by N. Walker, D. Lancet, Weizmann Institute of Science. ~5' adaptor sequence: 5' GAATTCGGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match      1.2%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA 1755
Db 22 CAAAAA 2

RESULT 42
CG726337/c
LOCUS CG726337
DEFINITION 1119089E12.2EL_Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION CG726337
VERSION CG726337.1 GI:37764992
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 25)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119089 row: E column: 12
Class: transposon-tagged.
Location/Qualifiers
1. .25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match      1.2%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA 1755
Db 23 CAAAAA 3

RESULT 43
```



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CF299084/c
LOCUS       CF299084                27 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--02-P02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--02-P02, mRNA sequence.
ACCESSION    CF299084
VERSION      CF299084.1  GI:33670845
KEYWORDS     EST.
SOURCE       Oryza sativa
              ORGANISM
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 27)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..27
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-P02"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     Query Match      1.2%; Score 21; DB 1; Length 27;
     Best Local Similarity 100.0%; Pred. No. 1.3e+02;
     Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db      23 CAAAAAAAAAAAAAAAAAAAAA 3

RESULT 44
LOCUS      CF310745
DEFINITION ABF--05-J07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
              library (ABF) Oryza sativa cDNA clone ABF--05-J07, mRNA sequence.
ACCESSION   CF310745
VERSION     CF310745.1  GI:33682506
KEYWORDS    EST.
SOURCE      Oryza sativa
              ORGANISM
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 27)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..27
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-P02"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     Query Match      1.2%; Score 21; DB 1; Length 27;
     Best Local Similarity 100.0%; Pred. No. 1.3e+02;
     Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db      23 CAAAAAAAAAAAAAAAAAAAAA 3

RESULT 44
LOCUS      CF310745
DEFINITION ABF--05-J07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
              library (ABF) Oryza sativa cDNA clone ABF--05-J07, mRNA sequence.
ACCESSION   CF310745
VERSION     CF310745.1  GI:33682506
KEYWORDS    EST.
SOURCE      Oryza sativa
              ORGANISM
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 27)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..27
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-P02"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

     Query Match      1.2%; Score 21; DB 1; Length 27;
     Best Local Similarity 100.0%; Pred. No. 1.3e+02;
     Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db      5 CAAAAAAAAAAAAAAAAAAAAA 25

RESULT 45
LOCUS      AL587582/c
DEFINITION   AL587582 BP Chicken Brain Library Gallus gallus cDNA clone
              ROS059D03, mRNA sequence.
ACCESSION    AL587582
VERSION      AL587582.1  GI:13192616
KEYWORDS     EST.
SOURCE       Gallus gallus (chicken)
              ORGANISM
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                Phasianinae; Gallus.
REFERENCE    1 (bases 1 to 28)
AUTHORS      Murray,F.
TITLE        BP Chicken Brain Library
JOURNAL      Unpublished (2001)
COMMENT      Contact: Frazer Murray
              Dept. Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UK
              Tel: +44 (0)131 527 4200
              Fax: +44 (0)131 440 0434
              Email: frazer.murray@bbsrc.ac.uk
              GCGGCCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetechn
              (*6854-

     Seq primer: M13F.

FEATURES             Location/Qualifiers
     source           1..28
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS059D03"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
                     unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from
                     Clonetechn (*6854-1)"

     Query Match      1.2%; Score 21; DB 1; Length 28;
     Best Local Similarity 100.0%; Pred. No. 1.3e+02;
     Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1735	CAAAAAAAAAAAAAAAAAAAAAA	1755
Db	26	CAAAAAAAAAAAAAAAAAAAAAA	6
RESULT 46			
AZ481286/c			
LOCUS	AZ481286 28 bp DNA linear GSS 04-OCT-2000		
DEFINITION	1M0303L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0303L24 F, genomic survey sequence.		
ACCESSION	AZ481286		
VERSION	AZ481286.1 GI:10642351		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0303 row: L column: 24 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 28.		
FEATURES			
source			
1. .28			
/organism="Mus musculus"			
/mol_type="genomic DNA"			
/strain="C57BL/6J"			
/db_xref="taxon:10090"			
/clone="UUGC1M0303L24"			
/sex="Male"			
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"			
/clone_lib="Mouse 10kb plasmid UUGC1M library"			
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
Query Match 1.2%; Score 21; DB 1; Length 28;			
Best Local Similarity 100.0%; Pred. No. 1.3e+02;			
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1735	CAAAAAAAAAAAAAAAAAAAAAA	1755

QY	1735	CAAAAAAAAAAAAAAAAAAAAAA	1755
Db	28	CAAAAAAAAAAAAAAAAAAAAAA	8
RESULT 47			
AZ809971/c			
LOCUS	AZ809971 28 bp DNA linear GSS 20-FEB-2001		
DEFINITION	2M0074C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0074C14 F, genomic survey sequence.		
ACCESSION	AZ809971		
VERSION	AZ809971.1 GI:12976769		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0074 row: C column: 14 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 28.		
FEATURES			
source			
1. .28			
/organism="Mus musculus"			
/mol_type="genomic DNA"			
/strain="C57BL/6J"			
/db_xref="taxon:10090"			
/clone="UUGC2M0074C14"			
/sex="Male"			
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"			
/clone_lib="Mouse 10kb plasmid UUGC1M library"			
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
Query Match 1.2%; Score 21; DB 1; Length 28;			
Best Local Similarity 100.0%; Pred. No. 1.3e+02;			
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1735	CAAAAAAAAAAAAAAAAAAAAAA	1755

QY	1735	CAAAAAAAAAAAAAAAAAAAAAA	1755
Db	28	CAAAAAAAAAAAAAAAAAAAAAA	8
RESULT 47			
AZ809971/c			
LOCUS	AZ809971 28 bp DNA linear GSS 20-FEB-2001		
DEFINITION	2M0074C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0074C14 F, genomic survey sequence.		
ACCESSION	AZ809971		
VERSION	AZ809971.1 GI:12976769		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0074 row: C column: 14 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 28.		
FEATURES	Location/Qualifiers		
source	1. .28		
	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UUGC2M0074C14"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	1.2%; Score 21; DB 1; Length 28;		
Best Local Similarity	100.0%; Pred. No. 1.3e+02;		
Matches 21; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1735	CAAAAAAAAAAAAAAAAAAAAAA	1755

Db

|||||

28 CAAAAAAAAAAAAAAAAAAAAA

8

RESULT 48

N51845/c

LOCUS

DEFINITION

Y202d07.s1 Soares multiple sclerosis 2NBHSP Homo sapiens cDNA clone IMAGE:281869 3' similar to gb:M85164 SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (HUMAN);, mRNA sequence.

ACCESSION

N51845

VERSION

N51845.1

GI:1193011

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 27)

AUTHORS

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.

TITLE

Generation and analysis of 280,000 human expressed sequence tags

JOURNAL

Genome Res. 6 (9), 807-828 (1996)

MEDLINE

97044478

PUBMED

8889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 450 Std Error: 0.00
Seq primer: ml3 -40 forward
High quality sequence stop: 1.

FEATURES

source

1. .27

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3900397"

/db_xref="taxon:9606"

/clone="IMAGE:281869"

/sex="male"

/tissue_type="multiple sclerosis lesions"

/dev_stage="Age 46"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares multiple sclerosis 2NBHSP"

/note="Vector: pT7T3D (Pharmacia) with a modified polylinker V type: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCGATTTT TTT TTT TTT TTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Patima Bonaldo."

Query Match

Best Local Similarity

1.2%; Score 20.8; DB 1; Length 27;

Matches

22; Conservative

0; Mismatches

3; Indels

0; Gaps

0;

Qy

1729 AGTTTACAAAAAAAAAAAAAAAAAAAAA

1753

Db

|||||

25 ANTTTAAAAAAAAAAAAAAAAAAAAA

1

RESULT 50

AW332181/c

LOCUS

DEFINITION

AW332181 S5C7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

ACCESSION

AW332181

VERSION

AW332181.1

GI:6828538

FEATURES

source

1. .27

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3888877"

/db_xref="taxon:9606"

/clone="IMAGE:259171"

/dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares placenta 8to9weeks_2NBHP8to9W"

/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCGATTTT TTT TTT TTT TTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Patima Bonaldo."

Query Match

Best Local Similarity

1.2%; Score 20.6; DB 1; Length 27;

Matches

23; Conservative

0; Mismatches

4; Indels

0; Gaps

0;

Qy

1728 GAGTTTACAAAAAAAAAAAAAAAAAAAAA

1754

Db

|||||

27 GAGGAAAAAAAAAAAAAAAAAAAAA

1

RESULT 49

N29432/c

LOCUS

DEFINITION

N29432 YW86h10.s1 Soares placenta 8to9weeks 2NBHP8to9W Homo sapiens cDNA clone IMAGE:259171 3' similar to gb:X64559 TETRALECTIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION

N29432

VERSION

N29432.1

GI:1147952

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 27)

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1.

FEATURES

source

1. .27

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3888877"

/db_xref="taxon:9606"

/clone="IMAGE:259171"

/dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares placenta 8to9weeks_2NBHP8to9W"

/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCGATTTT TTT TTT TTT TTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Patima Bonaldo."

Query Match

Best Local Similarity

1.2%; Score 20.6; DB 1; Length 27;

Matches

23; Conservative

0; Mismatches

4; Indels

0; Gaps

0;

Qy

1728 GAGTTTACAAAAAAAAAAAAAAAAAAAAA

1754

Db

|||||

27 GAGGAAAAAAAAAAAAAAAAAAAAA

1

RESULT 50

AW332181/c

LOCUS

DEFINITION

AW332181 S5C7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

ACCESSION

AW332181

VERSION

AW332181.1

GI:6828538

```
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Pneumocystis carinii
Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 22)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES
source
1..22
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note=Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | |
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 52
CF299342/c
LOCUS
DEFINITION
CF299342
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone_lib="7LEAF--03-F06"
/tissue_type="Leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note=Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | |
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 53
CF300133/c
LOCUS
DEFINITION
CF300133
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="Leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note=Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | |
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 51
AW332399/c
LOCUS
DEFINITION
S8A2 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Pneumocystis carinii
Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 22)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES
source
1..22
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note=Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
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Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAA 1755
1 AAAAAAAAAAAAAAAAAA 22

Db

RESULT 59
CF330679/c
LOCUS
DEFINITION NACL--06-H22.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-H22, mRNA sequence.
ACCESSION CF330679
VERSION CF330679.1 GI:33809583
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-H22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAA 1755
1 AAAAAAAAAAAAAAAAAA 22

Db

RESULT 60
CF333430/c
LOCUS
DEFINITION JMT--02-F04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-F04, mRNA sequence.
ACCESSION CF333430
VERSION CF333430.1 GI:33815154
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-F04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAA 1755
1 AAAAAAAAAAAAAAAAAA 22

Db

RESULT 61
CF334781/c
LOCUS
DEFINITION JMT--04-D05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--04-D05, mRNA sequence.
ACCESSION CF334781
VERSION CF334781.1 GI:33817904
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--04-D05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."


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Query Match      1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. NO. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 77

AZ654691	AZ654691	22 bp	DNA	linear	GSS 14-DEC-2000
LOCUS	1M0529D05F Mouse	10kb	plasmid	UUGc1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0529D05 F,	genomic survey sequence.			

Query Match

1.28; Score 20.4; DB 1; Length 22;

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Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
    | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 78
AZ760533
LOCUS
DEFINITION 1M0554A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0554A24 F, genomic survey sequence.
                22 bp DNA linear GSS 16-FEB-2001

```

RESULT 78
AZ760533
LOCUS
DEFINITION
AZ760533
ACCESSION
VERSION
KEYWORDS

AZ760533
1M0554A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0554A24 F, genomic survey sequence.
22 bp DNA linear
GSS 16-FEB-2001
GI:12868477
GSS.

Query Match

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;

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FEATURES
source
high quality sequence stop: 22.
Location/Qualifiers
1. 22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554A24"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```


QY	1734	ACAAAAA	1755	
Db	22	AAAAAAAAAAAAAAAAAAAA	1	
RESULT 81				
AZ787098/c				
LOCUS	AZ787098	22 bp	DNA	linear
DEFINITION	2M0033A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0033A05 F, genomic survey sequence.			
ACCESSION	AZ787098			
VERSION	AZ787098.1	GI:12925520		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0033 row: A column: 05 Seq primer: CGTTGTAACGACGCCAGT Class: plasmid ends High quality sequence stop: 22.			
FEATURES	Location/Qualifiers			
source	1..22			
	/organism="Mus musculus"			
	/mol_type="genomic DNA"			
	/strain="C57BL/6J"			
	/db_xref="taxon:10090"			
	/clone="UUGC2M0033A05"			
	/sex="Male"			
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"			
	/clone_lib="Mouse 10kb plasmid UUGC1M library"			
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
Query Match	1.2%;	Score 20.4;	DB 1;	Length 22;
Best Local Similarity	95.5%;	Pred. No. 1.4e+02;		
Matches	21;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	1734	ACAAAAA	1755	

Db	22	AAAAAAAAAAAAAAAAAAAA	1	
RESULT 82				
AZ787606/c				
LOCUS	AZ787606	22 bp	DNA	linear
DEFINITION	2M0034G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0034G12 F, genomic survey sequence.			
ACCESSION	AZ787606			
VERSION	AZ787606.1	GI:12926565		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0034 row: G column: 12 Seq primer: CGTTGTAACGACGCCAGT Class: plasmid ends High quality sequence stop: 22.			
FEATURES	Location/Qualifiers			
source	1..22			
	/organism="Mus musculus"			
	/mol_type="genomic DNA"			
	/strain="C57BL/6J"			
	/db_xref="taxon:10090"			
	/clone="UUGC2M0034G12"			
	/sex="Male"			
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"			
	/clone_lib="Mouse 10kb plasmid UUGC1M library"			
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
Query Match	1.2%;	Score 20.4;	DB 1;	Length 22;
Best Local Similarity	95.5%;	Pred. No. 1.4e+02;		
Matches	21;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	1734	ACAAAAA	1755	

Db	22	AAAAAAAAAAAAAAAAAAAAA	1
RESULT 83	AZ792704	22 bp	DNA
LOCUS	2M0045A24F	Mouse 10kb plasmid	UUGC1M library
DEFINITION	clone UUGC2M0045A24 F, genomic survey sequence.		
ACCESSION	AZ792704		
VERSION	AZ792704.1	GI:12936911	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0045 row: A column: 24 Seq primer: CGTTGTAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 22.		
FEATURES	Location/Qualifiers		
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	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UUGC2M0045A24"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	1.2%;	Score 20.4;	DB 1; Length 22;
Best Local Similarity	95.5%;	Pred. No. 1.4e+02;	
Matches	21; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
Qy	1734	ACAAAAAAAAAAAAAAAAAAAAA	1755
Db	22	AAAAAAAAAAAAAAAAAAAAA	1

RESULT 84	AZ810674/c	22 bp	DNA
LOCUS	2M0076E19F	Mouse 10kb plasmid	UUGC1M library
DEFINITION	clone UUGC2M0076E19 F, genomic survey sequence.		
ACCESSION	AZ810674		
VERSION	AZ810674.1	GI:12978158	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0076 row: E column: 19 Seq primer: CGTTGTAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 22.		
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	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UUGC2M0076E19"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	1.2%;	Score 20.4;	DB 1; Length 22;
Best Local Similarity	95.5%;	Pred. No. 1.4e+02;	
Matches	21; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
Qy	1734	ACAAAAAAAAAAAAAAAAAAAAA	1755
Db	22	AAAAAAAAAAAAAAAAAAAAA	1

AZ843514/c	AZ843514	22 bp	DNA	linear	GSS 20-FEB-2001
LOCUS	2M0142124F	Mouse 10kb	plasmid	UUC1M	library Mus musculus genomic
DEFINITION	clone UUC2M0142124 F,	genomic survey	sequence.		
ACCESSION	AZ843514				
VERSION	AZ843514.1	GI:13013422			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 22)				
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
	University of Utah Genome Center				
	University of Utah				
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA				
	Tel: 801 585 5606				
	Fax: 801 585 7177				
	Email: ddunn@genetics.utah.edu				
	Insert Length: 10000	Std Error: 0.00			
	Plate: 0142	row: 1	column: 24		
	Seq primer: CGTTGTAAACGACGGCCAGT				
	Class: plasmid ends				
	High quality sequence stop: 22.				

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Query Match      1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734  ACACAAAAAAAAAAAAAAAAAAAA 1755
          | | | | | | | | | | | | | | | | | |
Db      22  AAAAAAAAAAAAAAAAAAAAAA 1
          | | | | | | | | | | | | | | | | | |

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RESULT 88
AZ946102

LOCUS	AZ946102	22 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	2M0207D13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0207D13 R, genomic survey sequence.				
ACCESSION	AZ946102				
VERSION	AZ946102.1 GI:13812911				
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 22) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0207 row: D column: 13 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 22. Location/Qualifiers				
FEATURES					

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Query Match      1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1734 ACACAAAAAAAAAAAAAAAAAAAAA 1755

DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 22

RESULT 89			
TA131B09P			
LOCTS	TA131B09P	22 bp	DNA linear
			GSS 13-DEC-2000

DEFINITION	T. brucei sheared genomic DNA clone 131b09, forward sequence, genomic survey sequence.
ACCESSION	AL464164
VERSION	AL464164.1 GI:11834427
KEYWORDS	GSS.
SOURCE	Trypanosoma brucei
ORGANISM	Trypanosoma brucei
	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE	1 (bases 1 to 22)
AUTHORS	Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ .

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FEATURES
  source
    Location/Qualifiers
      1..22
        /organism="Trypanosoma brucei"
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        /clone="131b09"

Query Match      1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

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FEATURES
  source
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      1. .22
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        /db_xref="taxon:5691"
        /clone="329f10"

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Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative -0; Mismatches 1; Indels 0; Gaps 0

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Query Match      1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0
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RESULT 92
TA380A07P
LOCUS
DEFINITION
    TA380A07P
    22 bp DNA linear GSS 13-DEC-2000
    T. brucei sheared genomic DNA clone 380a07, forward sequence,
    genomic survey sequence.
ACCESSION
AL497713
VERSION
AL497713.1 GI:11873435
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 22)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
    1..22
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    /db_xref="taxon:5691"
    /clone="380a07"
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Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
| | | | | | | | | | | | | | | | | | | | |
RESULT 93
CF279238/c
LOCUS
DEFINITION
    CF279238
    23 bp mRNA linear EST 14-AUG-2003
    14ETL--05-H12.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
    Oryza sativa cDNA clone 14ETL--05-H12, mRNA sequence.
ACCESSION
CF279238
VERSION
CF279238.1 GI:33656624
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
| | | | | | | | | | | | | | | | | | | | |
RESULT 92
TA380A07P
LOCUS
DEFINITION
    TA380A07P
    22 bp DNA linear GSS 13-DEC-2000
    T. brucei sheared genomic DNA clone 380a07, forward sequence,
    genomic survey sequence.
ACCESSION
AL497713
VERSION
AL497713.1 GI:11873435
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 22)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
    1..22
    /organism="Trypanosoma brucei"
    /mol_type="genomic DNA"
    /strain="TREU927"
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    /clone="380a07"
Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | |
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RESULT 93
CF279238/c
LOCUS
DEFINITION
    CF279238
    23 bp mRNA linear EST 14-AUG-2003
    14ETL--05-H12.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
    Oryza sativa cDNA clone 14ETL--05-H12, mRNA sequence.
ACCESSION
CF279238
VERSION
CF279238.1 GI:33656624
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
| | | | | | | | | | | | | | | | | | | | |
```

```
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 23 AAAAAAAAAAAAAAAAAAAAAA 2
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RESULT 94
CF297943/c
LOCUS
DEFINITION
    CF297943
    23 bp mRNA linear EST 15-AUG-2003
    7LEAF--01-B24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
    sativa cDNA clone 7LEAF--01-B24, mRNA sequence.
ACCESSION
CF297943
VERSION
CF297943.1 GI:33669704
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="7LEAF--01-B24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | |
Db 23 AAAAAAAAAAAAAAAAAAAAAA 2
| | | | | | | | | | | | | | | | | | | | |
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RESULT 94
CF297943/c
LOCUS
DEFINITION
    CF297943
    23 bp mRNA linear EST 15-AUG-2003
    7LEAF--01-B24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
    sativa cDNA clone 7LEAF--01-B24, mRNA sequence.
ACCESSION
CF297943
VERSION
CF297943.1 GI:33669704
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Location/Qualifiers
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | |
Db 23 AAAAAAAAAAAAAAAAAAAAAA 2
| | | | | | | | | | | | | | | | | | | | |
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Db      23 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 95
CF310501/c
LOCUS   23 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--05-C24.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--05-C24, mRNA sequence.
ACCESSION CF310501
VERSION   CF310501.1 GI:33682262
KEYWORDS  EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL  Unpublished (2003)
COMMENT  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/cultivar="Nackdong"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then hrsd. for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      23 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 96
CF319212/c
LOCUS   23 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION HD--09-K06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-K06, mRNA sequence.
ACCESSION CF319212
VERSION   CF319212.1 GI:33690973
KEYWORDS  EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL  Unpublished (2003)
COMMENT  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF--05-C24"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then hrsd. for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      23 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 97
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LOCUS   23 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION HDN--02-I09.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--02-I09, mRNA
sequence.
ACCESSION CF322953
VERSION   CF322953.1 GI:33794126
KEYWORDS  EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL  Unpublished (2003)
COMMENT  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--02-I09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      23 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 97
CF322953
LOCUS   23 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION HDN--02-I09.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--02-I09, mRNA
sequence.
ACCESSION CF322953
VERSION   CF322953.1 GI:33794126
KEYWORDS  EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL  Unpublished (2003)
COMMENT  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--02-I09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
```

```
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..23
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-K06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      23 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 97
CF322953
LOCUS   23 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION HDN--02-I09.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--02-I09, mRNA
sequence.
ACCESSION CF322953
VERSION   CF322953.1 GI:33794126
KEYWORDS  EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL  Unpublished (2003)
COMMENT  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--02-I09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
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Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1734 ACACAAAAAAAAAAAAAAAAAAAAA 1755

Db 23 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT	111
AZ481702/c	
LOCUS	
DEFINITION	AZ481702 23 bp DNA linear GSS 04-OCT-2000 IM0306E11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0306E11 F, genomic survey sequence.

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;

```

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1734 AAAAAAAAAAAAAAAAAAAAAA 1755
        .| ||||| ||||| |||||
Db       23 AAAAAAAAAAAAAAAAAAAAAA 2

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RESULT 112
 AZ588254/c
 LOCUS
 DEFINITION
 AZ588254 23 bp DNA linear GSS 13-DEC-2000
 IM0396024F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0396024 F, genomic survey sequence.

RESULT 112	AZ588254/c	LOCUS	AZ588254	23 bp	DNA	linear	GSS 13-DEC-2000
		DEFINITION	1M0396024F Mouse 10kb plasmid UUGClm library Mus musculus genomic clone UUGClm0396024 F, genomic survey sequence.				

SOURCE ORGANISM	
Mus musculus (house mouse)	
Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 23)	
REFERENCE AUTHORS	
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	

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Query Match      1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 23 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 113
AZ593540/c
LOCUS
DEFINITION
clone UUGC1M0405C07 F, genomic survey sequence.
ACCESSION
AZ593540
VERSION
AZ593540.1 GI:11715730
KEYWORDS
SOURCE
GSS.
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0405 row: C column: 07
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0405C07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 23 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 114
AZ610785
LOCUS
DEFINITION
AZ610785
VERSION
AZ610785.1 GI:11732975
KEYWORDS
SOURCE
GSS.
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0436 row: N column: 07
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0436N07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 ||||| 22

RESULT 115
AZ647637/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ647637 23 bp DNA linear GSS 14-DEC-2000
1M0514E09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0514E09 F, genomic survey sequence.

AZ647637
GSS.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0514 row: E column: 09
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
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/clone="UUGC1M0514E09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| |||||

Db 23 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 116
AZ654903
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ654903 23 bp DNA linear GSS 14-DEC-2000
1M0529D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529D03 R, genomic survey sequence.

AZ654903
GSS.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

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/organism="Mus musculus"
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/strain="C57BL/6J"
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| |||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22


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RESULT 117
AZ778751
LOCUS      23 bp DNA linear GSS 16-FEB-2001
DEFINITION Mus musculus UUC1M library genomic survey sequence.
ACCESSION  ZM0014O08F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUGC2M0014O08 F, genomic survey sequence.
VERSION    AZ778751
KEYWORDS   AZ778751.1 GI:12908711
SOURCE     GSS.
ORGANISM   Mus musculus (house mouse)
REFERENCE  Mus musculus
AUTHORS    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
           University of Utah Genome Center
           University of Utah
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0014 row: O column: 08
           Seq primer: CGTTGTAACGACGGCCAGT
           Class: plasmid ends
           High quality sequence stop: 23.
FEATURES   Location/Qualifiers
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               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC2M0014O08"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUC1M library"
               /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match      1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
1 AAAAAAAAAAAAAAAAAAAAAA 22

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RESULT 119
AZ792751/c
LOCUS
DEFINITION
2M0045K24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045K24 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: K column: 24
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0045K24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
|AAAAAAAAAAAAAAAAAAAAA|
Db 23 AAAAAAAAAAAAAAAAAAAAAA 2
AAAAAAAAAAAAAAAAAAAAA

RESULT 120

AZ801003
LOCUS
DEFINITION
2M0059J16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0059J16 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: J column: 16
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0059J16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
|AAAAAAAAAAAAAAAAAAAAA|
Db 1 ATAAAAAAAAAAAAAAAAAAAAA 22
AAAAAAAAAAAAAAAAAAAAA

RESULT 121
AZ859570


```

clone UUGC2M0288B03 R, genomic survey sequence.
ACCESSION BH000534
VERSION BH000534.1 GI:13871760
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: B column: 03
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
source
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288B03"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACACAGGAACACGCTATGACC 1755
| | | | | | | | | | | | | | | | | | | | |
Db 23 AAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 124
TA151C02Q 23 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 151c02, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION TA151C02Q
VERSION TA151C02Q.1 GI:11851281
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 23)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="151c02"
Query Match 1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACACAGGAACACGCTATGACC 1755
| | | | | | | | | | | | | | | | | | | | |
Db 23 AAAAAAAAAAAAAAAAAAAAAAAAAA 22
RESULT 125
TA274B03P/c 23 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 274b03, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION TA274B03P
VERSION TA274B03P.1 GI:11851281
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 23)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In

```


TITLE	Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes
JOURNAL	Genome Biol. 4 (10), R63 (2003)
MEDLINE	22881942
PUBMED	14519198
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

```

FEATURES
source
Location/Qualifiers
1. 24
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse16d06_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T. brucei;"

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```
Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1734 ACACAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | |
Db 24 AAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 129	CA853764	24 bp	mRNA	linear	EST 01-AUG-2003
CA853764/C	B12A03.seq	cdNA Peking library 12hr	SCN3	Glycine max	cdNA clone
LOCUS	B12A03 5',	mRNA sequence.			
DEFINITION					

CA853764
 CA853764.1
 GI:33390569
 EST.
 Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabaales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE	1 (bases 1 to 24)
AUTHORS	Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE	Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL	Unpublished (2002)
COMMENT	Contact: Alkharouf, N.W. Soybean Genomics and Improvement Laboratory (SGIL) US Department of Agriculture (USDA), ARS, PSI Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,

```

FEATURES
  source
    1. .24
      Location/Qualifiers
        Email: alkharon@ba.ars.usda.gov.
        Fax: 301 504 5728.
        Tel: 301 504 5750
        USA

```

```

/db_xref="taxon:3847"
/clone="B12A03"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."

```

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1734	ACAAAAAAAAAAAAAAAAAAAA	1755
Db	24	AAAAAAAAAAAAAAAAAAAAAA	3

RESULT 130					
CF276855					
LOCUS	CF276855	24 bp	mRNA	linear	EST 14-AUG-2003
DEFINITION	14ETL--02-C19.g1	Rice etiolated leaf	plasmid	cdna library	(14ETL)
	Oryza sativa	cdna clone	14ETL--02-C19,	mrna	sequence.

CF276855.1 GI:33654241
 CF276855.1
 EST.
 Oryza sativa
 Oryza sativa

SOURCE	ORGANISM
Oryza sativa	Oryza sativa
Oryza sativa	Oryza sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CONTACT: NAMU B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
source 1. .24
Location/Qualifiers

```

FEATURES
    source
1. .24
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="14ETL--02-C19"
    /tissue_type="leaf"
    /dev_stage="14 days after
    /lab_host="E.coli DH10B"
    /clone_lib="Rice etiolat
    (14ETL)"
    /note="Vector: pCR4-TOPO
    with oligoribonucleotide
    RT-PCR."

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Query Match	1.2%;	Score 20.4;	DB 1;	Length 24;
Best Local Similarity	95.5%;	Pred. No. 1.4e+02;		
Matches 21: Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 1734 ACACAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 22

RESULT 131					
CF301561/c					
LOCUS	CF301561	24 bp	mRNA	linear	EST 15-AUG-2003
DEFINITION	7LEAF--06-H15.b1	Rice leaf	plasmid	cdna library II	(7LEAF) Oryza

Db	24	AAAAAAAAAAAAAAAAAAAAA	3
RESULT 134	AZ328848	24 bp DNA linear	GSS 29-SEP-2000
LOCUS	1M0052M17R	Mouse 10kb plasmid UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0052M17 R, genomic survey sequence.		
ACCESSION	AZ328848		
VERSION	AZ328848.1	GI:10388979	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0052 row: M column: 17 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 24.		
FEATURES	Location/Qualifiers		
source	1. .24		
	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UUGC1M0052M17"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	1.2%;	Score 20.4;	DB 1; Length 24;
Best Local Similarity	95.5%;	Pred. No. 1.4e+02;	
Matches	21; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
QY	1734	ACAAAAAAAAAAAAAAAAAAAAA	1755
Db	1	AAAAAAAAAAAAAAAAAAAAA	22

RESULT 135	AZ363562	24 bp DNA linear	GSS 02-OCT-2000
LOCUS	1M0109G10F	Mouse 10kb plasmid UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0109G10 F, genomic survey sequence.		
ACCESSION	AZ363562		
VERSION	AZ363562.1	GI:10477262	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0109 row: G column: 10 Seq primer: CGTTGTAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 24.		
FEATURES	Location/Qualifiers		
source	1. .24		
	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UUGC1M0109G10"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	1.2%;	Score 20.4;	DB 1; Length 24;
Best Local Similarity	95.5%;	Pred. No. 1.4e+02;	
Matches	21; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
QY	1734	ACAAAAAAAAAAAAAAAAAAAAA	1755
Db	1	AAAAAAAAAAAAAAAAAAAAA	22

```

RESULT 136
AZ386491
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

FEATURES
source
    24 bp DNA linear GSS 02-OCT-2000
    1M0145D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
    clone UUGC1M0145D02 R, genomic survey sequence.
    AZ386491
    AZ386491
    GSS.
    AZ386491.1 GI:10500191
    Mus musculus (house mouse)
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1 (bases 1 to 24)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0145 row: D column: 02
    Seq primer: CACACAGGAAACAGCTATGACC
    Class: plasmid ends
    High quality sequence stop: 24.
    Location/Qualifiers
        1..24
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0145D02"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

```

```
Query Match          1.2%; Score 20.4; DB 1; Length 24;  
Best Local Similarity 95.5%; Pred. No. 1.4e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
 |||
db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 138

```

RESULT_137
AZ390642/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

```

```
Query Match      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Best Local Similarity 95.5%;   Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

LOCUS	AZ438069	24 bp	DNA	linear	GSS 03-OCT-2000
DEFINITION	IM0228A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0228A10 F, genomic survey sequence.				
ACCESSION	AZ438069				
VERSION	AZ438069.1	GI:10562178			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 24)				
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0228 row: A column: 10 Seq primer: CGTTGTAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 24.				

```

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734  ACAAACAAAAAAAAAAAAAAAAAAAA 1755
          |
Db      1      AAAAAAAAAAAAAAAAAAAAAA 22

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RESULT 139
AZ459280/C

LOCUS	AZ459280	24 bp	DNA	linear	GSS 04-OCT-2000
DEFINITION	IM0264A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0264A05.F, genomic survey sequence.				
ACCESSION	AZ459280				
VERSION	AZ459280.1 GI:10617405				
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0264 row: A column: 05 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 24.				
FEATURES	Location/Qualifiers				
source	1..24				

Query Match	1.2%;	Score 20.4;	DB 1;	Length 24;
Best Local Similarity	95.5%;	Pred. No. 1.4e+02;		
Matches 21;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;

RESULT 140			
AZ644621/c			
LOCUS	AZ644621	24 bp	DNA
			linear
			GSS 14-DEC-2000

DEFINITION 1M0508F12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0508F12 R, genomic survey sequence.

ACCESSION AZ644621
VERSION AZ644621.1 GI:11773331
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0508 row: F column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0508F12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | | |
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 141
AZ812579
LOCUS AZ812579
DEFINITION 2M0079A23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

24 bp DNA linear GSS 20-FEB-2001

clone UUGC2M0079A23 F, genomic survey sequence.

ACCESSION AZ812579
VERSION AZ812579.1 GI:12981965
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0079 row: A column: 23
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0079A23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | | |
Db 3 AAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 142
AZ834990
LOCUS AZ834990
DEFINITION 2M0129A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

24 bp DNA linear GSS 20-FEB-2001

GSS.
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0266 row: H column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

Location/Qualifiers
1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0266H05"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adaptors complementary to the insert adaptors and
chemically competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 24;

Best Local Similarity 95.5%; Pred. No. 1.4e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1734	ACAAAAA	AAAAAAAAAAAAA	1755
Db	25	AAAAA	AAAAAAAAAAAAA	4
RESULT 158				
CF317714/c				
LOCUS	CF317714	25 bp	mRNA	linear
DEFINITION	HD--07-I03_g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--07-I03, mRNA sequence.			
ACCESSION	CF317714			
VERSION	CF317714.1	GI:33689475		
KEYWORDS	EST.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.			
AUTHORS	1 (bases 1 to 25)			
TITLE	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.			
JOURNAL	Large-scale Sequencing Analysis of Rice ESTs			
COMMENT	Unpublished (2003)			
FEATURES	Contact: Nahm B.H.			
source	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University			
	Yongin, Kyeonggi, Korea			
	Tel: 82 31 330 6193			
	Fax: 82 31 321 6355			
	Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.			
	Location/Qualifiers			
	1..25			
	/organism="Oryza sativa"			
	/mol_type="mRNA"			
	/cultivar="Nackdong"			
	/db_xref="taxon:4530"			
	/clone="HD--07-I03"			
	/tissue_type="callus"			
	/dev_stage="proliferated callus on 2N6 media for 2 weeks"			
	/lab_host="E.coli DH10B"			
	/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"			
	/note="Vector: PCR4-TOPO; Site.1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."			
Query Match	1.2%;	Score 20.4;	DB 1;	Length 25;
Best Local Similarity	95.5%;	Pred. No. 1.5e+02;		
Matches	21;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
QY	1734	ACAAAAA	AAAAAAAAAAAAA	1755
Db	25	AAAAA	AAAAAAAAAAAAA	4
RESULT 159				
CF319073/c				
LOCUS	CF319073	25 bp	mRNA	linear
DEFINITION	HD--09-H05_g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-H05, mRNA sequence.			
ACCESSION	CF319073			
VERSION	CF319073.1	GI:33690834		
KEYWORDS	EST.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.			
AUTHORS	1 (bases 1 to 25)			
	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,			


```

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | |
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 161
CF638767
LOCUS
DEFINITION CF638767 25 bp mRNA linear EST 02-OCT-2003
sequence.
ACCESSION CF638767
VERSION CF638767.1 GI:37402758
KEYWORDS EST.
SOURCE Ustilago maydis
ORGANISM Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
1 (bases 1 to 25)
Nugent,K.G., Choffe,K. and Saville,B.J.
Gene Expression during Ustilago maydis Diploid Filamentous Growth:
EST Library Creation and Analyses
EST Unpublished (2003)
JOURNAL Contact: Barry J. Saville
COMMENT Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utm.utoronto.ca
Plate: UTM-UM-D126/7-006-UTM row: 05 column: G
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
High quality sequence stop: 25.
Location/Qualifiers
1. .25
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."

FEATURES
source
1. .25
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."

Query Match      1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 22

RESULT 162
N33150/c
LOCUS
DEFINITION N33150 25 bp mRNA linear EST 10-JAN-1996
YY06901.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone
IMAGE:270480 3' similar to gb:D29805 N-ACETYLACTOSAMINE SYNTHASE
(HUMAN) ;, mRNA sequence.
ACCESSION N33150
VERSION N33150.1 GI:1153549
KEYWORDS EST.
SOURCE Homo sapiens (human)

```


University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: B column: 06
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.

FEATURES

1. .25

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150B06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
Query Match      1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 168	AZ609234/c	LOCUS	AZ609234	25 bp	linear	GSS 13-DEC-2000
DEFINITION	1M0433H19R Mouse 10kb plasmid UUC1m library Mus musculus genomic clone UUC1M0433H19 R, genomic survey sequence.	ACCESSION	AZ609234			
VERSION	AZ609234.1	KEYWORDS	GI:11731424			
SOURCE	GSS.	ORGANISM	Mus musculus (house mouse)			
REFERENCE	Mus musculus		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 25)		Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		Unpublished (2000)			
JOURNAL	Contact: Robert B. Weiss		University of Utah Genome Center			
COMMENT						

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0433 row: H column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.

Query Match	1.2%;	Score 20.4;	DB 1;	Length 25;
Best Local Similarity	95.5%;	Pred. No. 1.5e+02;		
Matches 21: Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

RESULT	169
AZ623157/c	
LOCUS	AZ623157 25 bp DNA linear GSS 13-DEC-2000
DEFINITION	IM0460L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0460L02 R, genomic survey sequence.
ACCESSION	AZ623157
VERSION	AZ623157.1 GI:11745347
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0113 row: M column: 21
Seq primer: CGTTCTAAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 25

FEATURES source

```

1: 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0113M21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```
Query Match      1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

RESULT	172
AZ949287	
LOCUS	AZ949287
DEFINITION	2M0212O08R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0212O08 R, genomic survey sequence.
	linear GSS 27-APR-2001

REFERENCE

1 (bases 1 to 25)

AUTHORS

Dunn, D., Aovagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Mannamalai, S., Muchera, J., Kogentia, G., Steirognathin, Mallikarjuna, Nalland, P.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0212 row: 0 column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25

FEATURES

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0212008"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match	1.2%;	Score 20.4;	DB 1;	Length 25;
Best Local Similarity	95.5%;	Pred. No. 1.5e+02;		
Matches 21: Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

RESULT 173					
AZ980407/C					
LOCUS	AZ980407	25 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	2M0257M19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0257M19 F. genomic survey sequence.				

ORGANISM	SOURCE	ECO.
Mus musculus	Mus musculus (house mouse)	
Mus musculus		

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.

orientation:
SP6-Sali-CCACGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1754
|||
Db 22 TAAAAA 1

RESULT 179
CF278359/c
LOCUS
DEFINITION 14ETL--04-D22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--04-D22, mRNA sequence.
ACCESSION CF278359
VERSION CF278359.1 GI:33655745
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnahm@gbio.com, bnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-P01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAA 1755
|||
Db 26 AAAAAA 5

RESULT 180
CF282426
LOCUS
DEFINITION 14ETL--09-P01.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-P01, mRNA sequence.
ACCESSION CF282426
VERSION CF282426.1 GI:33659813

KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnahm@gbio.com, bnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-P01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAA 1755
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Db 1 AAAAAA 22

RESULT 181
CF296851/c
LOCUS
DEFINITION 30DGS--07-G13.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--07-G13, mRNA sequence.
ACCESSION CF296851
VERSION CF296851.1 GI:33665884
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnahm@gbio.com, bnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"

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/db_xref="taxon:4530"
/clone="30DGS--07-G13"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 26 AAAAAAA 5

RESULT 182
CF297087
LOCUS 30DGS--07-L18.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sativa cDNA clone 30DGS--07-L18, mRNA sequence.
ACCESSION CF297087
VERSION CF297087.1 GI:33666120
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--07-L18"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 1 AAAAAAA 22

RESULT 183
CF299701/c
LOCUS 7LEAF--03-N03.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-N03, mRNA sequence.

```

```

ACCESSION CF299701
VERSION CF299701.1 GI:33671462
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-N03"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 26 AAAAAAA 5

RESULT 184
CF302874/c
LOCUS 7LEAF--08-M19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--08-M19, mRNA sequence.
ACCESSION CF302874
VERSION CF302874.1 GI:33674635
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..26
/organism="Oryza sativa"
/mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--08-M19"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 185
CF311369/c
LOCUS
DEFINITION
ABF--06-J01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-J01, mRNA sequence.
ACCESSION
VERSION
CF311369
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--06-J01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 186
CF311369/c
LOCUS
DEFINITION
ABF--06-J01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-J01, mRNA sequence.
ACCESSION
VERSION
CF311369
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..26
/organism="Oryza sativa"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 186
```

```

CF331439/c
LOCUS
DEFINITION
NACL--07-J02.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-J02, mRNA sequence.
ACCESSION
VERSION
CF331439
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--07-J02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 187
CF336199/c
LOCUS
DEFINITION
JMT--06-C18.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--06-C18, mRNA sequence.
ACCESSION
VERSION
CF336199
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES source Location/Qualifiers
1. .26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--06-C18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 26 ACACAAAAA 5

RESULT 188
AZ359871 26 bp DNA linear GSS 02-OCT-2000
LOCUS
DEFINITION
1M0102H23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0102H23 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: H column: 23
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES source Location/Qualifiers
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0102H23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 1 AAAAAAA 22

RESULT 189
AZ376664

LOCUS
DEFINITION
1M0130E08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0130E08 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0130 row: E column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0130 row: E column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES source Location/Qualifiers
1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0130E08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a


```
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 27)
JOURNAL      NIH-MGC http://mgc.nci.nih.gov/.
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: Edge Biosystems
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Plate: LLCM0029 row: M column: 16
              Seq primer: -21M13 forward primer (ABI).
              Location/Qualifiers
                1..27
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:2847159"
                  /tissue_type="Burkitt lymphoma"
                  /cell_line="MGC4"
                  /clone_lib="NIH_MGC_3"
                  /note="Organ: Lymph; Vector: pOTB7a; Library prepared by
                  Edge Biosystems."

Query Match      1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 27 bp mRNA linear EST 14-AUG-2003
Db 1 AAAAAAAAAA 1755
   |||||
   |||||

RESULT 201
CF291968/c
LOCUS      14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-J21, mRNA sequence.
ACCESSION  CF291968
VERSION     CF291968.1 GI:33661001
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 27)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
  1..27
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="14ROOT--02-J21"
    /tissue_type="root"

REFERENCE    1 (bases 1 to 27)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
                1..27
                  /organism="Oryza sativa"
                  /mol_type="mRNA"
                  /cultivar="Nackdong"
                  /db_xref="taxon:4530"
                  /clone="14ROOT--02-J21"
                  /tissue_type="root"

FEATURES     source
             1..27
               /dev_stage="14 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice root plasmid cDNA library (14ROOT)"
               /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

Query Match      1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 27 bp mRNA linear EST 15-AUG-2003
Db 27 AAAAAAAAAA 1755
   |||||
   |||||

RESULT 202
CF310560/c
LOCUS      ABF--05-E14.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--05-E14, mRNA sequence.
ACCESSION  CF310560
VERSION     CF310560.1 GI:33682321
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 27)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
  1..27
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="ABF--05-E14"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

FEATURES     source
             1..27
               /dev_stage="14 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="ABF3-overexpressing transgenic rice plasmid
               cDNA library (ABF)"
               /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
               for 2hrs. Oligo-capped mRNA was reverse transcribed and
               then used for PCR. mRNA was prepared from ABA-responsive
               element binding transcription factor 3 overexpression
               line."

Query Match      1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1754
Db 22 TTCAAAAAA 1
   |||||
   |||||

RESULT 203
CF329725/c
LOCUS      NACL--05-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--05-C12, mRNA sequence.
ACCESSION  CF329725
VERSION     CF329725.1
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 27)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
  1..27
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="14ROOT--02-J21"
    /tissue_type="root"
```


ACCESSION CF329725
VERSION CF329725.1 GI:33807665
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-C12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 204
CF330557/c
LOCUS NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-F04, mRNA sequence.
ACCESSION CF330557
VERSION CF330557.1 GI:33809352
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..27
/organism="Oryza sativa"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-F04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 205
CF335229/c
LOCUS JMT--04-N08.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--04-N08, mRNA sequence.
ACCESSION CF335229
VERSION CF335229.1 GI:33818810
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--04-N08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 206
N34459/c

Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

Location/Qualifiers
 1..27
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="355b06"

Query Match 1.2%; Score 20.4; DB 1; Length 27;
 Best Local Similarity 95.5%; Pred. No. 1.5e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACANAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 221

CF317378/c

LOCUS CF317378 25 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--07-A21.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--07-A21, mRNA sequence.

ACCESSION

CF317378

VERSION

CF317378.1 GI:33689139

KEYWORDS

EST.

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
 1..25
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD--07-A21"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 1.2%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 1.5e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1726 TCGAGTTTACAAAAAAAAAAAAA 1750

Db 25 TCAAGTTCAAAAAAAAAAAAAA 1

RESULT 222

CC883604/c

LOCUS

DEFINITION

CC883604

SALK_095121.17.80.n Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_095121.17.80.n, genomic

survey sequence.

CC883604

CC883604.1 GI:33359960

GSS.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 25)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated intron of At2g45650.

Class: TDNA tagged.

Location/Qualifiers

1..25

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_095121.17.80.n"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

Query Match 1.2%; Score 20.2; DB 1; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.5e+02;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAAAAAAAAAAAAAAAAA 1755

Db 25 TTTAAAAAAAAAAAAAAAAACAAA 1

RESULT 223

AW334823/c

LOCUS

DEFINITION

AW334823

S39F5 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

AW334823

AW334823.1 GI:6831180

EST.

Pneumocystis carinii

Pneumocystis carinii

Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;

Pneumocystidaceae; Pneumocystis.

1 (bases 1 to 20)

Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,

Edman, J.C., Kovacs, J. and Cushion, M.

Expressed sequence tags from Pneumocystis carinii

Unpublished (2000)

Contact: Staben C

School of Biological Sciences

University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES

source

1. .20
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 224

CF280913

LOCUS 20 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-M07.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-M07, mRNA sequence.

ACCESSION CF280913

VERSION CF280913.1 GI:33658299

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .20
/organism="Oryza sativa"
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/clone="14ETL--07-M07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 225

CF282035

LOCUS 20 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-F19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-F19, mRNA sequence.

ACCESSION CF282035

VERSION CF282035.1 GI:33659422

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 20)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

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Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-F19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 226

CF282414

LOCUS 20 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-O19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-O19, mRNA sequence.

ACCESSION CF282414

VERSION CF282414.1 GI:33659801

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 20)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

```
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/clone="14ETL--09-O19"
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/clone_lib="Rice etiolated leaf plasmid cDNA library
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 227
CF299822/c
LOCUS 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-P22, mRNA sequence.
ACCESSION CF299822
VERSION 1 GI:33671583
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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FEATURES
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 228
CF301720/c
LOCUS 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-L01, mRNA sequence.
ACCESSION CF301720
VERSION 1 GI:33673481
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 229
CF302027/c
LOCUS 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-C16, mRNA sequence.
ACCESSION CF302027
VERSION 1 GI:33673788
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
```


Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 230

CF310604

LOCUS
DEFINITION
ABF--05-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--05-F14, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .20
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--05-F14"
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 231

CF313067

LOCUS
DEFINITION
CF313067 20 bp mRNA linear EST 15-AUG-2003
HD--01-B02.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-B02, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 232

CF313569/c

LOCUS
DEFINITION
CF313569 20 bp mRNA linear EST 15-AUG-2003
HD--01-L22.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-L22, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
CF313569.1 GI:33685330
EST.


```
RESULT 235
CF328565
LOCUS      CF328565                20 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--03-I14.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-I14, mRNA sequence.
ACCESSION  CF328565
VERSION    CF328565.1 GI:33805376
KEYWORDS  EST.
SOURCE    Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice callus plasmid cDNA library (NACL)"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

          Query Match      1.1%; Score 20; DB 1; Length 20;
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          Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
          |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 236
CF333173/c
LOCUS      CF333173                20 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION JMT--01-P11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--01-P11, mRNA sequence.
ACCESSION  CF333173
VERSION    CF333173.1 GI:33814617
KEYWORDS  EST.
SOURCE    Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea

          Query Match      1.1%; Score 20; DB 1; Length 20;
          Best Local Similarity 100.0%; Pred. No. 1.4e+02;
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QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
          |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 237
CF334170/c
LOCUS      CF334170                20 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION JMT--03-F17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-F17, mRNA sequence.
ACCESSION  CF334170
VERSION    CF334170.1 GI:33816671
KEYWORDS  EST.
SOURCE    Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice callus plasmid cDNA library (NACL)"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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            RT-PCR."

          Query Match      1.1%; Score 20; DB 1; Length 20;
          Best Local Similarity 100.0%; Pred. No. 1.4e+02;
          Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db      20 AAAAAAAAAAAAAAAAAAAAAA 1
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```
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            prepared from Arabidopsis Jasmonate Carboxyl
            methyltransferase overexpression line."

          Query Match      1.1%; Score 20; DB 1; Length 20;
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QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
          |||||
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 237
CF334170/c
LOCUS      CF334170                20 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION JMT--03-F17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-F17, mRNA sequence.
ACCESSION  CF334170
VERSION    CF334170.1 GI:33816671
KEYWORDS  EST.
SOURCE    Oryza sativa
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            prepared from Arabidopsis Jasmonate Carboxyl
            methyltransferase overexpression line."

          Query Match      1.1%; Score 20; DB 1; Length 20;
          Best Local Similarity 100.0%; Pred. No. 1.4e+02;
          Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
          |||||
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1
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/db_xref="taxon:9606"
/db_xref="IMAGE:77095"
/sex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5'
GAATTCGGCAGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTT 3'"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 241
AZ307671/c
LOCUS
DEFINITION
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1M0009M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0009M20 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: M column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
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inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

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Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 243
AZ341530
LOCUS
DEFINITION
AZ341530
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ341530 20 bp DNA linear GSS 29-SEP-2000
1M0073N21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0073N21 R, genomic survey sequence.
GSS.
AZ341530.1 GI:10417873
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: N column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20

FEATURES
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 244
AZ343031
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ343031 20 bp DNA linear GSS 29-SEP-2000
1M0076F13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0076F13 F, genomic survey sequence.
GSS.
AZ343031.1 GI:10420861
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: F column: 13
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20

FEATURES
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/mol_type="genomic DNA"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 245
AZ351273
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ351273 20 bp DNA linear GSS 29-SEP-2000
1M0089B18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089B18 F, genomic survey sequence.
AZ351273
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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University of Utah Genome Center
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606.
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: B column: 18
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

FEATURES
source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGC1M0089B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 246
AZ357623
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ357623 20 bp DNA linear GSS 02-OCT-2000
1M0099A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099A20 F, genomic survey sequence.
AZ357623
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: A column: 20
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Class: plasmid ends
High quality sequence stop: 20.

Location/Qualifiers
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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FEATURES
source
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/organism="Mus musculus"
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    1736 AAAAAAAAAAAAAAAAAAAAAA 1755 .
       |||
Db     1 AAAAAAAAAAAAAAAAAAAAAA 20

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RESULT 247	AZ369734	LOCUS	AZ369734	20 bp	DNA	linear	GSS 02-OCT-2000
DEFINITION			1M0120024F	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
				clone	UUGC1M0120024 F,	genomic survey	sequence.

RESULTS	248
AZ386573	
LOCUS	
DEFINITION	AZ386573 20 bp DNA linear GSS 02-OCT-2000 IM0145C11R Mouse 10kb plasmid UUGClm library Mus musculus genomic clone UUGClm0145C11 R, genomic survey sequence.

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class. plasmid ends
High quality sequence stop: 20.
FEATURES             Location/Qualifiers
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         /organism="Mus musculus"
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         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="UUGC1M0120024"
         /sex="Male"
         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
         /clone_lib="Mouse 10kb plasmid UUGC1M library"
         /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to

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FEATURES
  source
    magm query sequence stop: 20.
    Location/Qualifiers
      1. .20
        /organism="Mus musculus"
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        /clone="UUGC1M0145C11"
        /sex="Male"
        /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
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        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel

```

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Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 249
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LOCUS AZ396481 20 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0161K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0161K02 F, genomic survey sequence.

ACCESSION AZ396481
VERSION AZ396481.1 GI:10511553
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0161 row: K column: 02
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source Location/Qualifiers
1. .20
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/strain="C57BL/6J"
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/clone="UUGC1M0161K02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 250
AZ442328
LOCUS AZ442328 20 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0236B11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0236B11 F, genomic survey sequence.

ACCESSION AZ442328
VERSION AZ442328.1 GI:10566341
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0236 row: B column: 11
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0236B11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 255
AZ514729
LOCUS
DEFINITION
AZ514729 1M0361E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0361E11 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
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Contact: Robert B. Weiss
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84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: E column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 256
AZ579178
LOCUS
DEFINITION
AZ579178 1M0363F11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0363F11 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: F column: 11
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match		1.1%;	Score 20;	DB 1;	Length 20;		
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Matches		20;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		
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RESULT 257							
AZ581208		20 bp	DNA	linear	GSS.13-DEC-2000		
LOCUS							
DEFINITION							
IM0369P15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic							
clone UUGC1M0369P15 R, genomic survey sequence.							
ACCESSION							
AZ581208							
VERSION							
AZ581208.1 GI:11695991							
KEYWORDS							
GSS.							
SOURCE							
Mus musculus (house mouse)							
ORGANISM							
Mus musculus							
REFERENCE							
AUTHORS							
1 (bases 1 to 20)							
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,							
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,							
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von							
Niederhausern,A. and Wright,D.,Weiss,R.							
TITLE							
Mouse whole genome scaffolding with paired end reads from 10kb							
plasmid inserts							
JOURNAL							
COMMENT							
Unpublished (2000)							
Contact: Robert B. Weiss							
University of Utah Genome Center							
University of Utah							
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT							
84112, USA							
Tel: 801 585 5606							
Fax: 801 585 7177							
Email: ddunn@genetics.utah.edu							
Insert Length: 10000 Std Error: 0.00							
Plate: 0369 row: P column: 15							
Seq primer: CACACAGGAAACAGCTATGACC							
Class: plasmid ends							
High quality sequence stop: 20.							
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source							
1. .20							
/organism="Mus musculus"							
/mol_type="genomic DNA"							
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/clone_lib="Mouse 10kb plasmid UUGC1M library"							
/note="Vector: PWD42nv; Purified genomic DNA from M.							
musculus C57BL/6J (male) was obtained from the Jackson							
Laboratory Mouse DNA Resource							
(http://www.jax.org/resources/documents/dnares/). The DNA							
was hydrodynamically sheared by repeated passage through a							
0.005 inch orifice at constant velocity. The sheared DNA							
was blunt end-repaired with T4 DNA polymerase and T4							
polynucleotide kinase. Adaptor oligonucleotides were							
ligated to the blunt ends in high molar excess. The							
adaptored DNA was purified and size-selected for a 9.5 to							
10.5 kb range using preparative agarose gel							
electrophoresis. Vector DNA was prepared from a derivative							
of pWD42 (gi 4732114 gb AF129072.1), a copy-number							
inducible derivative of plasmid R1. The vector was ligated							
with adaptors complementary to the insert adaptors and							
purified. The sheared, adaptored mouse DNA was annealed to							
adaptored vector DNA, and transformed into							
chemically-competent E. coli XL10-Gold (Stratagene) cells							
and selected for ampicillin resistance."							
<hr/>							
Query Match		1.1%;	Score 20;	DB 1;	Length 20;		
Best Local Similarity		100.0%;	Pred. No. 1.4e+02;				
Matches		20;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		

Query Match		1.1%;	Score 20;	DB 1;	Length 20;		
Best Local Similarity		100.0%;	Pred. No. 1.4e+02;				
Matches		20;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		
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QY	1736	AAAAAAAAAAAAAAAAAAAAA	1755				
Db	1	AAAAAAAAAAAAAAAAAAAAA	20				
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RESULT 258							
AZ588011		20 bp	DNA	linear	GSS.13-DEC-2000		
LOCUS							
DEFINITION							
IM0396A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic							
clone UUGC1M0396A13 F, genomic survey sequence.							
ACCESSION							
AZ588011							
VERSION							
AZ588011.1 GI:11710297							
KEYWORDS							
GSS.							
SOURCE							
Mus musculus (house mouse)							
ORGANISM							
Mus musculus							
REFERENCE							
AUTHORS							
1 (bases 1 to 20)							
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,							
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,							
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von							
Niederhausern,A. and Wright,D.,Weiss,R.							
TITLE							
Mouse whole genome scaffolding with paired end reads from 10kb							
plasmid inserts							
JOURNAL							
COMMENT							
Unpublished (2000)							
Contact: Robert B. Weiss							
University of Utah Genome Center							
University of Utah							
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT							
84112, USA							
Tel: 801 585 5606							
Fax: 801 585 7177							
Email: ddunn@genetics.utah.edu							
Insert Length: 10000 Std Error: 0.00							
Plate: 0396 row: A column: 13							
Seq primer: CGTTGTAACGACGCGCCAGT							
Class: plasmid ends							
High quality sequence stop: 20.							
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"							
/clone_lib="Mouse 10kb plasmid UUGC1M library"							
/note="Vector: PWD42nv; Purified genomic DNA from M.							
musculus C57BL/6J (male) was obtained from the Jackson							
Laboratory Mouse DNA Resource							
(http://www.jax.org/resources/documents/dnares/). The DNA							
was hydrodynamically sheared by repeated passage through a							
0.005 inch orifice at constant velocity. The sheared DNA							
was blunt end-repaired with T4 DNA polymerase and T4							
polynucleotide kinase. Adaptor oligonucleotides were							
ligated to the blunt ends in high molar excess. The							
adaptored DNA was purified and size-selected for a 9.5 to							
10.5 kb range using preparative agarose gel							
electrophoresis. Vector DNA was prepared from a derivative							
of pWD42 (gi 4732114 gb AF129072.1), a copy-number							
inducible derivative of plasmid R1. The vector was ligated							
with adaptors complementary to the insert adaptors and							
purified. The sheared, adaptored mouse DNA was annealed to							
adaptored vector DNA, and transformed into							
chemically-competent E. coli XL10-Gold (Stratagene) cells							
and selected for ampicillin resistance."							
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Query Match		1.1%;	Score 20;	DB 1;	Length 20;		

Db 1 ||||| 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 263
AZ645829/c
LOCUS
DEFINITION
AZ645829 20 bp DNA linear GSS 14-DEC-2000
1M0511D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0511D03 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: D column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511D03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 264
AZ650271
LOCUS
DEFINITION
AZ650271 20 bp DNA linear GSS 14-DEC-2000
1M0520C21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0520C21 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: C column: 21
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0520C21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 265
AZ760838 20 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
1M0554A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0554A24 R, genomic survey sequence.
ACCESSION
AZ760838
VERSION
AZ760838.1 GI:12869112
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
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plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0554A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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electrophoresis. Vector DNA was prepared from a derivative
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inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 266
AZ764504 20 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
1M0560M02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560M02 R, genomic survey sequence.
ACCESSION
AZ764504
VERSION
AZ764504.1 GI:12879535
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
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plasmid inserts
JOURNAL
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COMMENT
Contact: Robert B. Weiss
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: M column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560M02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 267
AZ765211/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AZ765211 20 bp DNA linear GSS 16-FEB-2001
1M0562H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0562H04 F, genomic survey sequence.
AZ765211
GSS.
AZ765211.1 GI:12880970
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0562 row: H column: 04
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	AAAAAAAAAAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAA
D _b	20 AAAAAAAAAAAAAAAAAA	1 AAAAAAAAAAAAAAAAAA

RESULT 268

AZ772091
LOCUS 20 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0574A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0574A13 R, genomic survey sequence.
ACCESSION AZ772091
VERSION AZ772091
KEYWORDS GSS.
SOURCE AZ772091.1 GI:12895040
ORGANISM Mus musculus (house mouse)
REFERENCE Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
TITLE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
COMMENT Unpublished (2000)
CONTACT Contact: Robert B. Weiss
UNIVERSITY University of Utah Genome Center
UNIVERSITY University of Utah
RM. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
TEL: 801 585 5606
FAX: 801 585 7177
EMAIL: ddunn@genetics.utah.edu
INSERT LENGTH: 10000 Std Error: 0.00
PLATE: 0574 row: A column: 13
SEQ PRIMER: CACACAGGAAACAGCTATGACC
CLASS: plasmid ends
HIGH QUALITY SEQUENCE STOP: 20.
LOCATION/QUALIFIERS
1. 20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0574A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY, 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 269
AZ779425/C

LOCUS AZ779425 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0015M18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0015M18 R, genomic survey sequence.
ACCESSION AZ779425
VERSION AZ779425.1 GI:12910066
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0015 row: M column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0015M18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 270
AZ784041 20 bp DNA linear GSS 16-FEB-2001
LOCUS AZ784041

DEFINITION 2M0026B21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0026B21 F, genomic survey sequence.
ACCESSION AZ784041
VERSION AZ784041.1 GI:12919375
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: B column: 21
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0026B21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 271
AZ793467/c 20 bp DNA linear GSS 16-FEB-2001
LOCUS AZ793467
DEFINITION 2M0046C16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

VERSION AZ805163.1 GI:12965890

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0066 row: L column: 14 Seq primer: CGTTGTAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 20.

FEATURES Location/Qualifiers

source 1. .20 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0066L14" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755 |||||

Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 274

AZ80521

LOCUS AZ80521 20 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0068C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0068C08 R, genomic survey sequence.

ACCESSION AZ80521

VERSION AZ80521.1 GI:12969953

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0068 row: C column: 08 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 20.

FEATURES Location/Qualifiers

source 1. .20 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0068C08" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755 |||||

Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 275

AZ806585

LOCUS AZ806585 20 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0068C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0068C15 R, genomic survey sequence.

ACCESSION AZ806585

VERSION AZ806585.1 GI:12970081

KEYWORDS GSS.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0076 row: I column: 20

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES
source

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0076I20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1755
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAA 20

RESULT 278

AZ813908

LOCUS AZ813908 20 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0081F21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0081F21 F, genomic survey sequence.

ACCESSION AZ813908

VERSION AZ813908.1 GI:12983804

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0081 row: F column: 21

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

Location/Qualifiers

source

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/organism="Mus musculus"

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0081F21"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1755
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAA 20

RESULT 279

AZ817323

LOCUS AZ817323

DEFINITION 2M0086C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0086C20 R, genomic survey sequence.

ACCESSION AZ817323

VERSION AZ817323.1 GI:12987327

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: C column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E.coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 280
AZ817414
LOCUS AZ817414 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0086K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0086K08 R, genomic survey sequence.
ACCESSION AZ817414
VERSION AZ817414.1 GI:12987238
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: K column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E.coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 281
AZ817467
LOCUS AZ817467 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0086J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0086J15 R, genomic survey sequence.
ACCESSION AZ817467
VERSION AZ817467.1 GI:12987291
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: J column: 15
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source

Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086J15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 282
AZ817608/c
LOCUS AZ817608 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0087K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0087K08 F, genomic survey sequence.
ACCESSION AZ817608
VERSION AZ817608.1 GI:12987516
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: K column: 08
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source

Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0087K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
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electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 283
AZ818489/c
LOCUS AZ818489 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0088K01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0088K01 R, genomic survey sequence.
ACCESSION AZ818489
VERSION AZ818489.1 GI:12988397
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0088 row: K column: 01
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0088K01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 284
AZ818816/c
LOCUS 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0089M05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0089M05 F, genomic survey sequence.
ACCESSION AZ818816
VERSION AZ818816.1 GI:12988724
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: M column: 05
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0089M05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 285
AZ837491
LOCUS 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0132K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0132K13 R, genomic survey sequence.
ACCESSION AZ837491
VERSION AZ837491.1 GI:13007399
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

```

JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0139 row: H column: 16
             Seq primer: CGTTGTAAACGACGCGCCAGT
             Class: plasmid ends
             High quality sequence stop: 20.

FEATURES     Location/Qualifiers
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             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC2M0139H16"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGC1M library"
             /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
         |||||||||||||||||||
Db       1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 287
AZ841558/c
LOCUS
DEFINITION 2M0139A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0139A10 R, genomic survey sequence.
ACCESSION  AZ841558
VERSION     AZ841558.1 GI:13011466
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)

JOURNAL

```

```

JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0132 row: K column: 13
             Seq primer: CACACAGGAACAGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 20.

FEATURES     Location/Qualifiers
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             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC2M0132K13"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGC1M library"
             /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db       1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 286
AZ841342
LOCUS
DEFINITION 2M0139H16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0139H16 F, genomic survey sequence.
ACCESSION  AZ841342
VERSION     AZ841342.1 GI:13011250
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)

JOURNAL

```

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: A column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0139A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 288

AZ858052

LOCUS

DEFINITION 2M0163003F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0163003 F, genomic survey sequence.

ACCESSION AZ858052

VERSION AZ858052.1 GI:13050813

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

JOURNAL

COMMENT

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0163 row: O column: 03

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0163003"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0193 row: G column: 23
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0193G23"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 290
AZ949180/c
LOCUS
DEFINITION
AZ949180 2M0212102R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0212102 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: I column: 02
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0212102"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 291
AZ963973/c
LOCUS
DEFINITION
AZ963973 2M0233J01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0233J01 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: J column: 01
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0233J01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 292
AL048777
LOCUS AL048777 21 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp566N053 r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION AL048777
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 21)
TITLE Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
JOURNAL EST (Koehrer, et al.)
COMMENT Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
1. .21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566N053"

/tissue type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 293
BX556006/c
LOCUS BX556006 21 bp mRNA linear EST 10-OCT-2003
DEFINITION BX556006 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse24c09_plc, mRNA sequence.
ACCESSION BX556006
VERSION BX556006.1 GI:33379965
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
AUTHORS 1 (bases 1 to 21)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxtun, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.
Location/Qualifiers
1. .21
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse24c09_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 294
BX58161/c

LOCUS BX558161 21 bp mRNA linear EST 10-OCT-2003
DEFINITION BX558161 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse37a05_plc, mRNA sequence.
ACCESSION BX558161
VERSION BX558161.1 GI:33429302
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix gic are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source Location/Qualifiers
1..21
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse37a05_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1753
|||||
Db 21 ACACAAAAA 2

RESULT 295
CF276638/c 21 bp mRNA linear EST 14-AUG-2003
LOCUS 14ETL--01-N19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa cDNA clone 14ETL--01-N19, mRNA sequence.
ACCESSION CF276638
VERSION CF276638.1 GI:33654024
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1..21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--01-N19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA 1755
|||||
Db 20 AAAAAA 1

RESULT 296
CF282216 21 bp mRNA linear EST 14-AUG-2003
LOCUS 14ETL--09-K01.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa cDNA clone 14ETL--09-K01, mRNA sequence.
ACCESSION CF282216
VERSION CF282216.1 GI:33659603
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1..21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-K01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
1 AAAAAAAAAAAAAAAAAAAAAA 20

Db

RESULT 297
CF292703/c

LOCUS
DEFINITION 30DGS--01-K01.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--01-K01, mRNA sequence.

ACCESSION
VERSION CF292703.1 GI:33661736
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--01-K01"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--01-K01"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
1 AAAAAAAAAAAAAAAAAAAAAA 20

Db

RESULT 298
CF295642/c

LOCUS
DEFINITION 30DGS--05-K20.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--05-K20, mRNA sequence.

ACCESSION
VERSION CF295642.1 GI:33664675
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
1 AAAAAAAAAAAAAAAAAAAAAA 20

Db

RESULT 299
CF297615

LOCUS
DEFINITION 30DGS--08-J10.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--08-J10, mRNA sequence.

ACCESSION
VERSION CF297615.1 GI:33666648
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
1 AAAAAAAAAAAAAAAAAAAAAA 20

Db

RESULT 299
CF297615

LOCUS
DEFINITION 30DGS--08-J10.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--08-J10, mRNA sequence.

ACCESSION
VERSION CF297615.1 GI:33666648
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 21)
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FEATURES
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1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 AAAAAAAAAAAAAAAAAAAAAA 20

Db

RESULT 299
CF297615

LOCUS
DEFINITION 30DGS--08-J10.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--08-J10, mRNA sequence.

ACCESSION
VERSION CF297615.1 GI:33666648
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
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FEATURES
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1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
1 AAAAAAAAAAAAAAAAAAAAAA 20

Db

RESULT 299
CF297615

LOCUS
DEFINITION 30DGS--08-J10.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--08-J10, mRNA sequence.

ACCESSION
VERSION CF297615.1 GI:33666648
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 300
CF298322/c
LOCUS      21 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-K14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-K14, mRNA sequence.
ACCESSION  CF298322
VERSION     CF298322.1 GI:33670083
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 302
CF312715
LOCUS      21 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-J10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-J10, mRNA sequence.
ACCESSION  CF312715
VERSION     CF312715.1 GI:33684476
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 301
CF300809/c
LOCUS      21 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-G20, mRNA sequence.
ACCESSION  CF300809
VERSION     CF300809.1 GI:33672570
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 303
CF316073/c
LOCUS
DEFINITION HD--05-D16.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-D16, mRNA sequence.
ACCESSION CF316073
VERSION CF316073.1 GI:33687834
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Unpublished (2003)
Contact: Nahm B.H.
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 AAAAAAAAAAAAAAAAAA 2

RESULT 304
CF318152/c
LOCUS
DEFINITION HD--08-C11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-C11, mRNA sequence.
ACCESSION CF318152
VERSION CF318152.1 GI:33689913
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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FEATURES
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Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 AAAAAAAAAAAAAAAAAA 2

RESULT 305
CF326952/c
LOCUS
DEFINITION NACL--01-D20.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-D20, mRNA sequence.
ACCESSION CF326952
VERSION CF326952.1 GI:33802159
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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FEATURES
source
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library (JMT) Oryza sativa cDNA clone JMT--01-K14, mRNA sequence.

CF332956

CF332956.1 GI:33814150

EST.

Oryza sativa

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

REFERENCE

AUTHORS

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COMMENT

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FEATURES

Location/Qualifiers

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/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

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Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 308

CF338057

LOCUS

DEFINITION

JMT--08-M03.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--08-M03, mRNA sequence.

ACCESSION

CF338057

VERSION

CF338057.1 GI:33824485

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

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COMMENT

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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

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/cultivar="Nackdong"

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Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 307

CF332956/c

LOCUS

DEFINITION

JMT--01-K14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-K14, mRNA sequence.

ACCESSION

CF332956

VERSION

CF332956.1 GI:33814150

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

REFERENCE

AUTHORS

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TITLE

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COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..21

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--01-N18"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 306

CF327391

LOCUS

DEFINITION

NACL--01-N18.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-N18, mRNA sequence.

ACCESSION

CF327391

VERSION

CF327391.1 GI:33803041

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..21

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--01-N18"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 307

CF332956/c

LOCUS

DEFINITION

JMT--01-K14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-K14, mRNA sequence.

ACCESSION

CF332956

VERSION

CF332956.1 GI:33814150

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..21

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--01-N18"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus

Db	1	AAAAAAAAAAAAAAAAAAAAA	20
RESULT 311	AZ350611	21 bp	DNA linear GSS 29-SEP-2000
LOCUS	1M0088C14F	Mouse 10kb plasmid UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0088C14 F, genomic survey sequence.		
ACCESSION	AZ350611		
VERSION	AZ350611.1	GI:10429848	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0088 row: C column: 14 Seq primer: CGTTGTAAACGACGCGCCAGT Class: plasmid ends High quality sequence stop: 21.		
FEATURES	Location/Qualifiers		
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	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
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	/clone="UUGC1M0088C14"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	1.1%;	Score 20;	DB 1; Length 21;
Best Local Similarity	100.0%;	Pred. No. 1.5e+02;	
Matches	20;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1736	AAAAAAAAAAAAAAAAAAAAA	1755
Db	1	AAAAAAAAAAAAAAAAAAAAA	20

RESULT 312	AZ386711	21 bp	DNA linear GSS 02-OCT-2000
LOCUS	1M0145O16R	Mouse 10kb plasmid UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0145O16 R, genomic survey sequence.		
ACCESSION	AZ386711		
VERSION	AZ386711.1	GI:10500411	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0145 row: O column: 16 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 21.		
FEATURES	Location/Qualifiers		
source	1. .21		
	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UUGC1M0145O16"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	1.1%;	Score 20;	DB 1; Length 21;
Best Local Similarity	100.0%;	Pred. No. 1.5e+02;	
Matches	20;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1736	AAAAAAAAAAAAAAAAAAAAA	1755
Db	1	AAAAAAAAAAAAAAAAAAAAA	20

RESULT 313

AZ386794

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AZ386794

1M0145022R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0145022 R, genomic survey sequence.

AZ386794

AZ386794.1 GI:10500494

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isalam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0145 row: 0 column: 22

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

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/mol_type="genomic DNA"

/strain="C57Bl/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0145022"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match          1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
db 1 AAAAAAAAAAAAAAAAAAAAAA 20

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RESULT 315

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RESULT 314
AZ389287
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

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Query Match      1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736  AAAAAAAAAAAAAAAAAAAAAA 1755
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Db      1  AAAAAAAAAAAAAAAAAAAAAA 20

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AZ389687
LOCUS
DEFINITION
1M0150B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0150B10 R, genomic survey sequence.
ACCESSION
AZ389687
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: B column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 316
AZ406936/c

AZ406936
LOCUS
DEFINITION
1M0176E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0176E24 F, genomic survey sequence.
ACCESSION
AZ406936
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0176 row: E column: 24
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 317
AZ412739/c
LOCUS
AZ412739
21 bp DNA linear GSS 03-OCT-2000

ACCESSION AZ415029
VERSION AZ415029.1 GI:10539042
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0189 row: M column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0189M07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 320
AZ461824
LOCUS AZ461824 21 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0267B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0267B23 R, genomic survey sequence.
ACCESSION AZ461824

VERSION AZ461824.1 GI:10619949
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: B column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGC1M0267B23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 321
AZ465890/c
LOCUS AZ465890 21 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0276F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0276F07 F, genomic survey sequence.
ACCESSION AZ465890
VERSION AZ465890.1 GI:10624015

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
GSS.
Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: F column: 07
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21
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/clone="UUGC1M0276F07"
/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2
RESULT 322
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LOCUS
DEFINITION
1M0436N02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0436N02 R, genomic survey sequence.
AZ611116
ACCESSION
AZ611116.1 GI:11733306
KEYWORDS
GSS.

```


ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0437 row: E column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
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/clone="UUGC1M0437E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 324
AZ615628/c
LOCUS
DEFINITION
1M044M19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M044M19 R, genomic survey sequence.
ACCESSION
AZ615628
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0444 row: M column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0444M19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 325
AZ627843/c
LOCUS
DEFINITION
1M0474H03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474H03 F, genomic survey sequence.
ACCESSION
AZ627843
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0534 row: B column: 07
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0534B07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 328
AZ766552
LOCUS
DEFINITION
AZ766552 21 bp DNA linear GSS 16-FEB-2001
1M0564O11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0564O11 F, genomic survey sequence.
ACCESSION
AZ766552
VERSION
AZ766552.1 GI:12883741
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE
JOURNAL
COMMENT
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: O column: 11
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
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/clone="UUGC1M0564O11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 329
AZ769976
LOCUS
DEFINITION
AZ769976 21 bp DNA linear GSS 16-FEB-2001
1M0571L11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0571L11 F, genomic survey sequence.
ACCESSION
AZ769976
VERSION
AZ769976.1 GI:12890681
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

TITLE
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: L column: 11
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 330
AZ793486/c
LOCUS
DEFINITION 2M0046G18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0046G18 R, genomic survey sequence.

ACCESSION
VERSION AZ793486.1 GI:12938487
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: G column: 18
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 331
AZ799327
LOCUS
DEFINITION 2M0056C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0056C09 R, genomic survey sequence.

ACCESSION
VERSION AZ799327.1 GI:12950331
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: C column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC2M0056C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 332

AZ810054

LOCUS 21 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0074E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0074E19 F, genomic survey sequence.

ACCESSION AZ810054

VERSION AZ810054.1 GI:12976935

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: E column: 19
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0074E19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 333

AZ815424

LOCUS 21 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0083H11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0083H11 R, genomic survey sequence.

ACCESSION AZ815424

VERSION AZ815424.1 GI:12985332

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

```
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0083 row: H column: 11
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 21.
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              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC2M0083H11"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."

Query Match      1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 334
AZ819181
LOCUS AZ819181 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0089110R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0089110 R, genomic survey sequence.
ACCESSION AZ819181
VERSION AZ819181.1 GI:12989089
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
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JOURNAL Unpublished (2000)

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COMMENT Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0089 row: I column: 10
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 21.
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              /mol_type="genomic DNA"
              /strain="C57BL/6J"
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              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
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              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."

Query Match      1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 335
AZ832198
LOCUS AZ832198 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0112P20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0112P20 F, genomic survey sequence.
ACCESSION AZ832198
VERSION AZ832198.1 GI:13002106
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
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JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
```


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Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: P column: 20
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0112P20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 336
AZ843603
LOCUS AZ843603 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0142I06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0142I06 R, genomic survey sequence.
ACCESSION AZ843603
VERSION AZ843603.1 GI:13013511
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: I column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source

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/strain="C57BL/6J"
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/clone="UUGC2M0142I06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 337
AZ960063
LOCUS AZ960063 21 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0228A01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0228A01 F, genomic survey sequence.
ACCESSION AZ960063
VERSION AZ960063.1 GI:13831290
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0228 row: A column: 01
Seq primer: CGTTGTAACGACGCCGAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0228A01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 338

BH000837

LOCUS

DEFINITION BH000837 21 bp DNA linear GSS 27-APR-2001
2M0288020R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0288020 R, genomic survey sequence.

ACCESSION BH000837

VERSION BH000837.1

KEYWORDS GI:13872063

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: O column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288020"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 339

CF282024/c

LOCUS

DEFINITION

CF282024

CF282024

CF282024.1

GI:33659411

EST.

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 22)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

CF282024 22 bp mRNA linear EST 14-AUG-2003
14ETL--09-F13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-F13, mRNA sequence.

CF282024

CF282024.1

GI:33659411

EST.

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 22)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

```
FEATURES
  source
    Location/Qualifiers
      1. .22
        /organism="Oryza sativa"
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        /tissue_type="leaf"
        /dev_stage="14 days after germination"
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Query Match      1.1%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 22 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 340
AZ82374487
LOCUS
DEFINITION
  AZ374487 1M0127H16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0127H16 F, genomic survey sequence.
ACCESSION
  AZ374487
VERSION
  AZ374487.1 GI:10488187
KEYWORDS
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SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 22)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
TITLE
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  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0127 row: H column: 16
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 22.
  Location/Qualifiers
    1. .22
      /organism="Mus musculus"
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      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA

FEATURES
  source
    Location/Qualifiers
      1. .22
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0127H16"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA

0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 342
BH000233
LOCUS
DEFINITION
2M0287L21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0287L21 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0287 row: L column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0287L21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 343
AL048745
LOCUS
DEFINITION
DKFZp566K213_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566K213, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 23)

REFERENCE
AUTHORS
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
JOURNAL
COMMENT
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1. .23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566K213"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMPLI; Site_1: NotI; Site_2: Sali"

Query Match 1.1%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 4 CAAAAAAAAAAAAAAAAAAAAA 23

RESULT 344
AL048776
LOCUS
DEFINITION
AL048776 DKFZp566N213_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566N213, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
REFERENCE
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     1 (bases 1 to 23)
JOURNAL   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
COMMENT   EST (Koehrer, et al.)
          Unpublished (1999)
          Contact: MIPS
          MIPS
          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source    Location/Qualifiers
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            /db_xref="taxon:9606"
            /clone="DKFZp566N213"
            /tissue_type="kidney"
            /dev_stage="fetal"
            /lab_host="Xl-2blue"
            /clone_lib="566 (synonym: hfk2)"
            /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      1.1%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 4 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 345
CF334077/c 23 bp mRNA linear EST 18-AUG-2003
LOCUS      JMT--03-D17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-D17, mRNA sequence.
ACCESSION  CF334077
VERSION    CF334077.1 GI:33816466
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 23)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source    Location/Qualifiers
          1..23
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="JMT--03-D17"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="AtJMT-overexpressing transgenic rice plasmid
            cDNA library (JMT)"
            /note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
            was reverse transcribed and then used for PCR. mRNA was
            prepared from Arabidopsis Jasmoinate Carboxyl
            methyltransferase overexpression line."

Query Match      1.1%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 23 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 346
AZ621676 23 bp DNA linear GSS 13-DEC-2000
LOCUS      1M0455J07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0455J07 F, genomic survey sequence.
ACCESSION  AZ621676
VERSION    AZ621676.1 GI:11743962
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 23)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
           Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
           Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
           Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
           University of Utah Genome Center
           University of Utah
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0455 row: J column: 07
           Seq primer: CGTTGTAAACGACGCGCCAGT
           Class: plasmid ends
           High quality sequence stop: 23.

FEATURES
source    Location/Qualifiers
          1..23
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            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0455J07"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptored DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptored mouse DNA was annealed to
            adaptored vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      1.1%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@qgbio.com, bhnahm@bio.myongji.ac.kr

```
Query Match          1.1%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT	350
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LOCUS	26 bp DNA linear GSS 05-OCT-2000
DEFINITION	IM0313H11F Mouse 10kb plasmid UUGC1m library Mus musculus genomic clone UUGC1M0313H11 F, genomic survey sequence.
ACCESSION	AZ485624
VERSION	AZ485624.1 GI:10651606
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0313H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      1.1%; Score 20; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736  AAAAAAAAAAAAAAAAAAAAAA 1755
          |||||
Db      1  AAAAAAAAAAAAAAAAAAAAAA 20

```

RESULT 351	TA321G11P	26 bp	DNA	linear	GSS 13-DEC-2000
LOCUS	TA321G11P	T. brucei sheared genomic DNA clone 321g11, forward sequence,			
DEFINITION	TA321G11P	genomic survey sequence.			
ACCESSION	AL492371				
VERSION	AL492371.1	GI:11867375			
KEYWORDS	GSS.				
SOURCE	Trypanosoma brucei				
ORGANISM	Trypanosoma brucei				
	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.				
REFERENCE	1 (bases 1 to 26)				
AUTHORS	Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk				
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).				
	Email: nelsayed@tigr.org				
	Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ .				

FEATURES	source
High quality sequence stop: 26.	
Location/Qualifiers	
1..26	
/organism="Mus musculus"	
/mol type="genomic DNA"	

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0016 row: B column: 10
 Seq primer: CGTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES

source
 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0016B10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19.8; DB 1; Length 24;
 Best Local Similarity 91.3%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1753
 ||| |||||
 Db 2 TTTTAAAAA 24

RESULT 355
 AZ486788/c 24 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0315122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0315122 F, genomic survey sequence.

ACCESSION AZ486788
 VERSION AZ486788.1 GI:10653906
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)

REFERENCE 1 (bases 1 to 24)
 AUTHORS Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: I column: 22
 Seq primer: CGTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES

source
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0315I22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19.8; DB 1; Length 24;
 Best Local Similarity 91.3%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
 ||| |||||
 Db 23 TAAATAAAAA 1

RESULT 356
 AZ607198 24 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0429G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0429G03 R, genomic survey sequence.

ACCESSION AZ607198
 VERSION AZ607198.1 GI:11729388
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)

REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: G column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0429G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 1 TAAATAAAAA 23

RESULT 357
CF319499/c
LOCUS CF319499 25 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-A10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--10-A10, mRNA sequence.

ACCESSION CF319499
VERSION CF319499.1 GI:33691260
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 25)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .25
/organism="Oryza sativa"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--10-A10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.1%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1753
Db 23 TTTGCTAAAAA 1

RESULT 358
CNS00BGV/c
LOCUS CNS00BGV 26 bp DNA linear GSS 04-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR23F05 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL057060
VERSION AL057060.1 GI:4937627
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 26)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
1. .26
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR23F05"
/clone_lib="RPCI-98"
/note="end : TET3"

Query Match 1.1%; Score 19.6; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA 1754
Db :||||| 1

```

Db      21  SAAAAAAAAAAAAAAAAAAAAA 2

RESULT 359
CF276747/c
LOCUS   21 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION
Oryza sativa cDNA clone 14ETL--02-A06, mRNA sequence.
ACCESSION
CF276747
VERSION
CF276747.1 GI:33654133
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--02-A06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734  ACACAAAAAAAAAAAAAAAAAAAA 1754
         |||||||
Db      21  ACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 360
AZ493766
LOCUS   21 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION
1M0328C11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0328C11 R, genomic survey sequence.
ACCESSION
AZ493766
VERSION
AZ493766.1 GI:10667750
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
AUTHORS
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)

Db      21  SAAAAAAAAAAAAAAAAAAAAA 2

RESULT 359
CF276747/c
LOCUS   21 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION
Oryza sativa cDNA clone 14ETL--02-A06, mRNA sequence.
ACCESSION
CF276747
VERSION
CF276747.1 GI:33654133
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--02-A06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734  ACACAAAAAAAAAAAAAAAAAAAA 1754
         |||||||
Db      21  ACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 360
AZ493766
LOCUS   21 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION
1M0328C11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0328C11 R, genomic survey sequence.
ACCESSION
AZ493766
VERSION
AZ493766.1 GI:10667750
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
AUTHORS
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0328 row: C column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0328C11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734  ACACAAAAAAAAAAAAAAAAAAAA 1754
         |||||||
Db      1  ATAAAAAAAAAAAAAAAAAAAAAA 21

RESULT 361
BX556059/c
LOCUS   22 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION
BX556059 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse24f09_plc, mRNA sequence.
ACCESSION
BX556059
VERSION
BX556059.1 GI:33380008
KEYWORDS
EST.
SOURCE
Glossina morsitans morsitans
ORGANISM
Glossina morsitans morsitans
REFERENCE
AUTHORS
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL
Genome Biol. 4 (10), R63 (2003)
MEDLINE
22881942

```


SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
TITLE Homo sapiens CB library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute in Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
Location/Qualifiers
FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBFBIB11"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digest"

Query Match 1.1%; Score 19.4; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 4 ANAAAAA 25

RESULT 365
T49097/c
LOCUS T49097 25 bp mRNA linear EST 06-FEB-1995
DEFINITION Yb08h08.s1 Stragatene placenta (#937225) Homo sapiens cDNA clone IMAGE:70623 3' similar to gb:X62744 CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN (HUMAN), mRNA sequence.
ACCESSION T49097.1 GI:650957
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 25)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevisan,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Other ESTs: yb08h08.r1
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High qality sequence starts: 1
High qality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:491520"
/db_xref="taxon:9606"
/clone="IMAGE:70623"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene placenta (#937225)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match 1.1%; Score 19.4; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1751
Db 21 TTTAAAAA 1

RESULT 366
BQ588729
LOCUS BQ588729 19 bp mRNA linear EST 06-DEC-2002
DEFINITION S013713-024-014-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris cDNA clone 024-014-B24 3-PRIME, mRNA sequence.
ACCESSION BQ588729
VERSION BQ588729.1 GI:26118312
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 19)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 14 row: B column: 24
Seq primer: T7; GTAATACGACTCACTATAGGC.
Location/Qualifiers
FEATURES
source
1..19
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:187281"
/db_xref="taxon:161934"
/clone="024-014-B24"


```
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
Db      1 AAAAAAAAAAAAAAAAAA 19

RESULT 367
CB174047/c
LOCUS
DEFINITION
OR_2032F05 010529.Y1 Adult mouse olfactory epithelium library Mus
musculus cDNA clone 2032F05 5', mRNA sequence.
ACCESSION
CB174047
VERSION
CB174047.1 GI:37592676
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS
Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priddy, L., Ross, J.A.,
Walker, M., Williams, E.M. and Trask, B.J.
TITLE
Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and
unequal expression levels
JOURNAL
Genome Biol. 4 (11), R71.1-R71.15 (2003)
COMMENT
Contact: Young JM
Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org
Seq primer: M13 Reverse.

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2032F05"
/tissue_type="Olfactory and respiratory epithelium"
/dev_stage="Adult"
/clone_lib="Adult mouse olfactory epithelium library"
/note="Organ: Olfactory turbinates; Vector:
LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by Leslie Voshall. mRNA was prepared from
the olfactory and respiratory epithelium of an adult
mouse. Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdaZAPII-XR vector."

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
Db      1 AAAAAAAAAAAAAAAAAA 19

/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
Db      1 AAAAAAAAAAAAAAAAAA 19

RESULT 367
CB174047/c
LOCUS
DEFINITION
OR_2032F05 010529.Y1 Adult mouse olfactory epithelium library Mus
musculus cDNA clone 2032F05 5', mRNA sequence.
ACCESSION
CB174047
VERSION
CB174047.1 GI:37592676
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS
Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priddy, L., Ross, J.A.,
Walker, M., Williams, E.M. and Trask, B.J.
TITLE
Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and
unequal expression levels
JOURNAL
Genome Biol. 4 (11), R71.1-R71.15 (2003)
COMMENT
Contact: Young JM
Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org
Seq primer: M13 Reverse.

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2032F05"
/tissue_type="Olfactory and respiratory epithelium"
/dev_stage="Adult"
/clone_lib="Adult mouse olfactory epithelium library"
/note="Organ: Olfactory turbinates; Vector:
LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by Leslie Voshall. mRNA was prepared from
the olfactory and respiratory epithelium of an adult
mouse. Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdaZAPII-XR vector."

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
Db      1 AAAAAAAAAAAAAAAAAA 19
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Db      19 AAAAAAAAAAAAAAAAAA 1

RESULT 368
CF279008/c
LOCUS
DEFINITION
CF279008
14ETL--05-C13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-C13, mRNA sequence.
ACCESSION
CF279008
VERSION
CF279008.1 GI:33656394
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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FEATURES
source
1..19
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--05-C13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
Db      19 AAAAAAAAAAAAAAAAAA 1

RESULT 369
CF291089/c
LOCUS
DEFINITION
CF291089
14ROOT--01-G03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-G03, mRNA sequence.
ACCESSION
CF291089
VERSION
CF291089.1 GI:33660122
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
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```

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FEATURES

source

Location/Qualifiers
1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="root"
/dev_stage="14 days after germination"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 370

CF291090

LOCUS

DEFINITION 14ROOT--01-G03.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-G03, mRNA sequence.

ACCESSION

VERSION CF291090.1 GI:33660123

KEYWORDS

SOURCE EST.

ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
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Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .19
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="14ROOT--01-G03"
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/dev_stage="14 days after germination"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 371

CF298396/c

LOCUS

DEFINITION 7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-M05, mRNA sequence.

ACCESSION

VERSION CF298396.1 GI:33670157

KEYWORDS

SOURCE EST.

ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

COMMENT

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Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .19
/organism="Oryza sativa"
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/clone="7LEAF--01-M05"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753

Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 372

CF299598/c

LOCUS

DEFINITION 7LEAF--03-K23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-K23, mRNA sequence.

ACCESSION

VERSION CF299598.1 GI:33671359

KEYWORDS

SOURCE EST.

ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

COMMENT

Unpublished (2003)
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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 373

CF302327/c

LOCUS

DEFINITION 7LEAF--07-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-L24, mRNA sequence.

ACCESSION CF302327

VERSION CF302327.1 GI:33674088

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Unpublished (2003)
Contact: Nahm B.H.

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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FEATURES

source

1. .19
/organism="Oryza sativa"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 374

CF302456/c

LOCUS

DEFINITION 7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-P22, mRNA sequence.

ACCESSION CF302456

VERSION CF302456.1 GI:33674217

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .19
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/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
|||||
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 375

CF304589/c

LOCUS

DEFINITION ABF1--05-G10.g1 ABF3-overexpressing transgenic rice lambda phage
cDNA library (ABF1) Oryza sativa cDNA clone ABF1--05-G10, mRNA
sequence.

ACCESSION CF304589

VERSION CF304589.1 GI:33676350

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

```
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source  Location/Qualifiers
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/organism="Oryza sativa"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_lib="ABF3-overexpressing transgenic rice lambda
phage CDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 376
CF309801/c
LOCUS 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--04-C04.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa CDNA clone ABF--04-C04, mRNA sequence.
ACCESSION CF309801.1 GI:33681562
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source  Location/Qualifiers
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 376
CF309801/c
LOCUS 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--04-F15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa CDNA clone ABF--04-F15, mRNA sequence.
ACCESSION CF309943
VERSION CF309943.1 GI:33681704
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source  Location/Qualifiers
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 376
CF309943
LOCUS 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--04-F15.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa CDNA clone ABF--06-L18, mRNA sequence.
ACCESSION CF311496/c
LOCUS 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-L18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa CDNA clone ABF--06-L18, mRNA sequence.
ACCESSION CF311496
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VERSION      CF311496.1  GI:33683257
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..19
            /organism="Oryza sativa"
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            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="ABF3-overexpressing transgenic rice plasmid
            cDNA library (ABF)"
            /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
            for 2hrs. Oligo-capped mRNA was reverse transcribed and
            then used for PCR. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
      |||||
Db      19 AAAAAAAAAAAAAAAAAA 1

RESULT 379
CF311513/c
LOCUS      CF311513
DEFINITION ABF--06-M03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-M03, mRNA sequence.
ACCESSION  CF311513
VERSION     CF311513.1  GI:33683274
KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
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            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="ABF3-overexpressing transgenic rice plasmid
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            for 2hrs. Oligo-capped mRNA was reverse transcribed and
            then used for PCR. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
      |||||
Db      19 AAAAAAAAAAAAAAAAAA 1

RESULT 379
CF311513/c
LOCUS      CF311513
DEFINITION ABF--06-M03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-M03, mRNA sequence.
ACCESSION  CF311513
VERSION     CF311513.1  GI:33683274
KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            /organism="Oryza sativa"
            /mol_type="mRNA"
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            /db_xref="taxon:4530"
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            /lab_host="E.coli DH10B"
            /clone_lib="ABF3-overexpressing transgenic rice plasmid
            cDNA library (ABF)"
            /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
            for 2hrs. Oligo-capped mRNA was reverse transcribed and
            then used for PCR. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
      |||||
Db      19 AAAAAAAAAAAAAAAAAA 1

RESULT 380
CF312403
LOCUS      CF312403
DEFINITION ABF--08-C07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-C07, mRNA sequence.
ACCESSION  CF312403
VERSION     CF312403.1  GI:33684164
KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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            /clone_lib="ABF3-overexpressing transgenic rice plasmid
            cDNA library (ABF)"
            /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
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            element binding transcription factor 3 overexpression
            line."

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1754
      |||||
Db      19 AAAAAAAAAAAAAAAAAA 1
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Db      ||||| 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 381
CF315299/c
LOCUS
DEFINITION HD--04-C17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
ACCESSION CF315299
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 382
CF316480/c
LOCUS
DEFINITION HD--05-M14.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
ACCESSION CF316480
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 382
CF316480/c
LOCUS
DEFINITION HD--05-M14.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
ACCESSION CF316480
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
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cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 383
CF318788
LOCUS
DEFINITION HD--09-A23.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
ACCESSION CF318788
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736  AAAAAAAAAAAAAAAAAAAAAA 1754
          |||
Db      1      AAAAAAAAAAAAAAAAAAAAAA 19
          |||

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RESULT 384	CF329986	LOCUS	CF329986	19 bp	mrna	linear	EST 18-AUG-2003
DEFINITION	NACL--05-I09.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-I09, mRNA sequence.						

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

CONTACT: JUNGIL LEE
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

FEATURES

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1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	1.1%	Score 19;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 1.8e+02;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
         |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAA 19

```

RESULT	385
CF332063/C	
LOCUS	
DEFINITION	CF332063 19 bp mRNA linear EST 18-AUG-2003 NACL--08-G19.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-G19, mRNA sequence.

SOURCE	ORGANISM	Oryza sativa	Oryza sativa
		Oryza sativa	Oryza sativa

SOURCE	ORGANISM	ORYZA SATIVA	ORYZA SATIVA
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DATA ANALYSIS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Orzveae; Orvza.

REFERENCE 1 (bases 1 to 19)

REFERENCE	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

[illegible]

FEATURES

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/mol_type="mRNA"
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RT-PCR."

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Best Local Similarity	100.0%;	Pred. No. 1.8e+02;		

QY 1736 AAAAAAAAAAAAAAAAAA 1754

[illegible]

RESULT 386

REF ID: A633507

LOCUS

LOCUS	JMT-02-G23.g1	15 bp	mRNA	ES1 18-AUG-2000
DEFINITION	AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT-02-G23, mRNA sequence.			

ACCESSION
CF333507

RECESSION
VERSION
CF333507.1
GI:33815309

KEYWORDS

KEYWORDS EST.
SOURCE Orvza sativa

SOURCE	OLYZA SATIVA
ORGANISM	ORYZA SATIVA

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

REFERENCE	AUTHORS	TITLE
1 (Cases 1 to 19)	Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.	Large-scale Sequencing Analysis of Rice ESTs

CONTACT: NAMU B.R.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 330 6355

Email: brianm@apple.com; brianm@apple.com; brianm@apple.com

FEATURES

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1. .19
/organism="Oryza sativa"
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/tissue_type="leaf"
/dev_stage="14 days after

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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 387
CF333753 19 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--02-M08.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-M08, mRNA sequence.
CF333753
ACCESSION CF333753.1 GI:33815809
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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methyltransferase overexpression line."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 388
CF334014/c 19 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--03-C09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-C09, mRNA sequence.

ACCESSION CF334014
VERSION CF334014.1 GI:33816333
KEYWORDS
SOURCE
ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .19
Location/Qualifiers

/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 389

AZ307313 19 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0008H20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0008H20 R, genomic survey sequence.
ACCESSION AZ307313.1 GI:10346192
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: H column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0008H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 390

AZ310079/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ310079 19 bp DNA linear GSS 29-SEP-2000
1M0018K17R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0018K17 R, genomic survey sequence.

AZ310079 GI:10351709
GSS.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: K column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0018K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 391

AZ310105/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ310105 19 bp DNA linear GSS 29-SEP-2000
1M0018E21R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0018E21 R, genomic survey sequence.

AZ310105 GI:10351761
GSS.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0018 row: E column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0018E21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 392
AZ317743
LOCUS
DEFINITION
AZ317743
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ317743 19 bp DNA linear GSS 29-SEP-2000
1M0036B18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0036B18 R, genomic survey sequence.
AZ317743
AZ317743.1 GI:10366848
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0036 row: B column: 18

Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0036B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 393
AZ340311/c
LOCUS
DEFINITION
AZ340311
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ340311 19 bp DNA linear GSS 29-SEP-2000
1M0072H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0072H15 F, genomic survey sequence.
AZ340311
AZ340311.1 GI:10415441
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0072 row: H column: 15
Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0072H15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 1.1%; Score 19; DB 1; Length 19;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1736 AAAAAAAAAAAAAAAA 1754

|||||||

Db

19 AAAAAAAAAAAAAAAA 1

RESULT 394

AZ350519/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

19 bp

DNA

linear

GSS 29-SEP-2000

IM008A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M008A10 F; genomic survey sequence.

AZ350519

AZ350519.1 GI:10429756

GSS.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0088 row: A column: 10

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M008A10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 1.1%; Score 19; DB 1; Length 19;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1736 AAAAAAAAAAAAAAAA 1754

|||||||

Db

19 AAAAAAAAAAAAAAAA 1

RESULT 395

AZ364226

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

19 bp

DNA

linear

GSS 02-OCT-2000

IM0110B24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0110B24 F; genomic survey sequence.

AZ364226

AZ364226.1 GI:10477926

GSS.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

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Unpublished (2000)

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0110 row: B column: 24

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0110B24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 396
AZ365696 19 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0112A07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0112A07 R, genomic survey sequence.
ACCESSION AZ365696
VERSION AZ365696.1 GI:10479396
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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University of Utah
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: A column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19

source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0112A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 397
AZ374409 19 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0127D10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0127D10 F, genomic survey sequence.
ACCESSION AZ374409
VERSION AZ374409.1 GI:10488109
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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JOURNAL Unpublished (2000)
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University of Utah
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: D column: 10
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19


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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0127D10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1736 AAAAAAAAAAAAAAAAAA 1754
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Db       1 AAAAAAAAAAAAAAAAAA 19
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RESULT 398
AZ374619
LOCUS      AZ374619      19 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION IM0127F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0127F04 R, genomic survey sequence.
ACCESSION  AZ374619
VERSION     AZ374619.1 GI:10488319
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT     Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0127 row: F column: 04
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
            Location/Qualifiers
                1..19
                    /organism="Mus musculus"
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FEATURES
source
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0127F04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1736 AAAAAAAAAAAAAAAAAA 1754
          |||||
Db       1 AAAAAAAAAAAAAAAAAA 19
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RESULT 399
AZ385952
LOCUS      AZ385952      19 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION IM0144L10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0144L10 R, genomic survey sequence.
ACCESSION  AZ385952
VERSION     AZ385952.1 GI:10499652
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT     Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0144 row: L column: 10
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
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                1..19
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
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FEATURES
source
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/strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0144L10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

RESULT	400
AZ391509	
LOCUS	
DEFINITION	AZ391509 1M0153K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0153K08 R, genomic survey sequence.
	19 bp DNA linear GSS 03-OCT-2000

FEATURES
source

/db_xref="taxon:10090"
/clone="UUGC1M0153K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAAAAAAA 1754
D_b 1 AAAAAAAAAAAAAAAAAA 19

RESULT	401
AZ410050	
LOCUS	
DEFINITION	AZ410050 1M0182P04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0182P04 F, genomic survey sequence.
	19 bp DNA linear GSS 03-OCT-2000

FEATURES
source

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/clone="UUGC1M0182P04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1736 AAAAAAAAAAAAAAAAAA 1754
          |||||||
Db       1 AAAAAAAAAAAAAAAAAA 19
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RESULT 402
AZ414413
LOCUS      19 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION 1M0188O13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0188O13 R, genomic survey sequence.
```

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ACCESSION  AZ414413
VERSION     AZ414413.1  GI:10538426
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```

```
JOURNAL     Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0188 row: 0 column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
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FEATURES     source
            Location/Qualifiers
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0188O13"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1736 AAAAAAAAAAAAAAAAAA 1754
          |||||||
Db       1 AAAAAAAAAAAAAAAAAA 19
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RESULT 403
AZ422604
LOCUS      19 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION 1M0201B21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0201B21 F, genomic survey sequence.
```

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ACCESSION  AZ422604
VERSION     AZ422604.1  GI:10546617
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```

```
JOURNAL     Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0201 row: B column: 21
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
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FEATURES     source
            Location/Qualifiers
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0201B21"
                /sex="Male"
```


/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 406
AZ442365/c
LOCUS
DEFINITION
AZ442365
1M0236C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0236C13 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
AZ442365.1 GI:10566378

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mus whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0236 row: C column: 13
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0236C13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 407
AZ453930/c

LOCUS
DEFINITION
AZ453930
1M0255G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0255G11 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
AZ453930.1 GI:10612055

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0255 row: G column: 11

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0255G11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 410
AZ476576/c
LOCUS
DEFINITION
AZ476576 19 bp DNA linear GSS 04-OCT-2000
1M0295F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0295F04 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: F column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0295F04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 411
AZ486786/c
LOCUS
DEFINITION
AZ486786 19 bp DNA linear GSS 05-OCT-2000
1M0315D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315D21 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: D column: 21
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 414
AZ579119
LOCUS
DEFINITION
AZ579119 19 bp DNA linear GSS 13-DEC-2000
1M0363M16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0363M16 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
AZ579119.1 GI:11693580

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH

RM. 308, BIOMEDICAL POLYMERS RESEARCH BLDG., 20 S. 2030 E., SLC, UT

84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

INSERT LENGTH: 10000 Std Error: 0.00

PLATE: 0363 row: M column: 16

SEQ PRIMER: CGTTGTAAACGACGCCAGT

CLASS: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0363M16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 415

AZ583970

LOCUS

DEFINITION
AZ583970 19 bp DNA linear GSS 13-DEC-2000
1M0388M11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0388M11 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
AZ583970.1 GI:11704386

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH

RM. 308, BIOMEDICAL POLYMERS RESEARCH BLDG., 20 S. 2030 E., SLC, UT

84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

INSERT LENGTH: 10000 Std Error: 0.00

PLATE: 0388 row: M column: 11

SEQ PRIMER: CGTTGTAAACGACGCCAGT

CLASS: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0388M11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 418
AZ616154/c
LOCUS
DEFINITION
1M0445P16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0445P16 R, genomic survey sequence.
ACCESSION
AZ616154
VERSION
AZ616154.1 GI:11738344
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0445 row: P column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/clone="UUGC1M0445P16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 419
AZ627844/c
LOCUS
DEFINITION
1M0474J05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474J05 F, genomic survey sequence.
ACCESSION
AZ627844
VERSION
AZ627844.1 GI:11750130
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0445 row: P column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
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/db_xref="taxon:10090"
/clone="UUGC1M0474J05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

FEATURES
source

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0474J05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 426
AZ764497
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AZ764497 19 bp DNA linear GSS 16-FEB-2001
1M0560H03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560H03 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AZ764497.1 GI:12879521
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: H column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 427
AZ764522
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AZ764522 19 bp DNA linear GSS 16-FEB-2001
1M0560B16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560B16 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AZ764522.1 GI:12879571
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: E column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0560B16"
/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
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Db      1 AAAAAAAAAAAAAAAAAAAAAA 19

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RESULT 428	AZ764534	19 bp	DNA	linear	GSS 16-FEB-2001
AZ764534	LOCUS	1M0560P14R	Mouse 10kb plasmid UUGC1M library	Mus musculus genomic	
DEFINITION		clone UUGC1M0560P14 R,	genomic survey sequence.		
ACCESSION	AZ764534	GI:12879595			
VERSION					
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	- 1 (bases 1 to 19)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA				

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FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 429
AZ770387
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AZ770387 19 bp DNA linear GSS 16-FEB-2001
IM0571L23R Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0571L23 R, genomic survey sequence.
AZ770387
AZ770387.1 GI:12891520
GSS.
Mus musculus (house mouse)
Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: L column: 23
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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/clone="UGCLM0571L23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 430
AZ778858 19 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0014O20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0014O20 F, genomic survey sequence.
ACCESSION AZ778858
VERSION AZ778858.1 GI:12908925
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: O column: 20
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES source
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0014O20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 431
AZ779901 19 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0016E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0016E16 R, genomic survey sequence.
ACCESSION AZ779901
VERSION AZ779901.1 GI:12911024
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: E column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES source
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC2M0016E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754

[illegible]

RESULT 434	AZ788058	19 bp	DNA	linear	GSS 16-FEB-2001
LOCUS	2M0034124R	Mouse 10kb plasmid	UUGC1M	library	Mus musculus genomic
DEFINITION	clone UUGC2M0034124 R,	genomic survey	sequence.		
ACCESSION	AZ788058				
VERSION	AZ788058.1	GI:12927475			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0034 row: I column: 24 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19.				
FEATURES	Location/Qualifiers				
source	1. .19				

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Query Match      1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
| | | | | | | | | | | | | |
db 19 AAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 436

RESULT 435
AZ789590/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AZ789590
2M0037G06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0037G06 R, genomic survey sequence.
AZ789590
AZ789590.1 GI:12930573
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: G column: 06
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037G06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match          1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No. 1.8e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1736 AAAAAAAAAAAAAAAAAA 1754
| | | | | | | | | | | | |
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 436

AZ792713/c	19 bp DNA linear	GSS 16-FEB-2001
LOCUS		
DEFINITION	2M0045C22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0045C22 F, genomic survey sequence.	
ACCESSION	AZ792713	
VERSION	AZ792713.1	GI:12936930
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 19)	
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss	
	University of Utah Genome Center	
	University of Utah	
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	
	Tel: 801 585 5606	
	Fax: 801 585 7177	
	Email: ddunn@genetics.utah.edu	
	Insert Length: 10000	Std Error: 0.00
	Plate: 0045	row: C column: 22
	Seq primer: CGTTGTAAACGACGGCCAGT	
	Class: plasmid ends	
	High quality sequence stop: 19.	

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Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
      |||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 437
AZ795403

LOCUS	AZ795403	19 bp	DNA	linear	GSS 16-FEB-2000
DEFINITION	2M0049C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0049C12 R, genomic survey sequence.				
ACCESSION	AZ795403				
VERSION	AZ795403.1	GI:12942392			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 19) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0049 row: C column: 12 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers				
FEATURES					

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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1754      -
Db      1 AAAAAAAAAAAAAAAAAA 19

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RESULT 438			
AZ801970/c			
LOCUS	AZ801970	19 bp	DNA
			linear
			GSS 16-FEB-2001

ACCESSION AZ841581
VERSION AZ841581.1 GI:13011489
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: G column: 08
Seq primer: CACACAGGAAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
1..19
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/mol_type="genomic DNA"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 441
AZ841622
LOCUS AZ841622 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0139A16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0139A16 R, genomic survey sequence.
ACCESSION AZ841622

VERSION AZ841622.1 GI:13011530
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: A column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 442
AZ861896
LOCUS AZ861896 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0168P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0168P10 R, genomic survey sequence.
ACCESSION AZ861896
VERSION AZ861896.1 GI:13058674

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished. (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0168 row: P column: 10
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 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. 19
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0168P10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1m library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gll4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
source

Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
 Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 443
 AZ936798
 LOCUS
 DEFINITION
 clone UUGC2M0193L10 R, genomic survey sequence.
 AZ936798
 accession
 version
 keywords

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
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JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: E column: 21
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0267E21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 445
BH000498
LOCUS BH000498 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0288I21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0288I21 F, genomic survey sequence.
ACCESSION BH000498
VERSION BH000498.1 GI:13871724
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: I column: 21
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288I21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 446
AL587572/c
LOCUS AL587572 20 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587572 BP Chicken Brain Library Gallus gallus cDNA clone
R05059B11, mRNA sequence.
ACCESSION AL587572
VERSION AL587572.1 GI:13192606
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Murray,F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
CGGCCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetechn (*6854-

Seq primer: M13F.

Location/Qualifiers

1. .20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetechn (*6854-1)"

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
|||||
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 447

AL587727/C

LOCUS

DEFINITION AL587727 BP Chicken Brain Library Gallus gallus cDNA clone
ROS061D01, mRNA sequence.

AL587727 1 GI:13192761

EST.

KEYWORDS Gallus gallus (chicken)

SOURCE Gallus gallus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases 1 to 20)

Murray,F.

BP Chicken Brain Library

Unpublished (2001)

Contact: Frazer Murray

Dept. Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 440 0434

Email: frazer.murray@bbsrc.ac.uk

CGGCCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetechn (*6854-

Seq primer: M13F.

Location/Qualifiers

1. .20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"

FEATURES
source

/clone="ROS061D01"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetechn (*6854-1)"

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
|||||
Db 20 CAAAAAAAAAAAAAAAAA 2

RESULT 448

CF282002/C

LOCUS

DEFINITION CF282002 20 bp mRNA linear EST 14-AUG-2003
14ETL--09-F01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

CF282002 1 GI:33659389

EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .20

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ETL--09-F01"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
|||||
Db 20 CAAAAAAAAAAAAAAAAA 2

RESULT 449

CF316662/C

LOCUS

CF316662 20 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--06-A20.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--06-A20, mRNA sequence.
ACCESSION CF316662
VERSION CF316662.1 GI:33688423
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--06-A20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1753
|||||
Db 19 CAAAAA...AAAAA 1

RESULT 450
CF318278/c
LOCUS
DEFINITION HD--08-F13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--08-F13, mRNA sequence.
ACCESSION CF318278
VERSION CF318278.1 GI:33690039
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..20
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--08-F13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA...AAAAA 1754
|||||
Db 20 AAAAAA...AAAAA 2

RESULT 451
CF320843/c
LOCUS
DEFINITION HD--11-O01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--11-O01, mRNA sequence.
ACCESSION CF320843
VERSION CF320843.1 GI:33692604
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..20
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--11-O01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;


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QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 454
AZ638704
LOCUS AZ638704 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0498E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0498E13 R, genomic survey sequence.
ACCESSION AZ638704
VERSION AZ638704.1 GI:11760894
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 row: E column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0498E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
RESULT 455
AZ821905
LOCUS AZ821905 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0094D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0094D20 R, genomic survey sequence.
ACCESSION AZ821905
VERSION AZ821905.1 GI:12991813
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0094D20"
/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 AAAAAAAAAAAAAAAAAAAAAA 1753
|||||
```

Db 2 CAAAAAAAAAAAAAAAAAAAA 20

RESULT 456
AZ858419 20 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0163003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0163003 R, genomic survey sequence.
ACCESSION AZ858419
VERSION AZ858419.1 GI:13051545
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: 0 column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163003"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAA 1754
Db 2 AAAAAAAAAAAAAAAAAAAAA 20

RESULT 457
AL587702/c 21 bp mRNA linear EST 02-MAR-2001
LOCUS AL587702 BP Chicken Brain Library Gallus gallus cDNA clone
DEFINITION ROS060H09, mRNA sequence.
ACCESSION AL587702
VERSION AL587702.1 GI:13192736
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Murray, F.
BP Chicken Brain Library
Unpublished (2001)
JOURNAL
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
FEATURES
source
1. .21
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS060H09"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
5' TCGACTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAA 2

RESULT 458
CF302218/c 21 bp mRNA linear EST 15-AUG-2003
LOCUS CF302218 7LEAF--07-I17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--07-I17, mRNA sequence.
ACCESSION CF302218
VERSION CF302218.1 GI:33673979
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-07-I17"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 459

CF314260/c

LOCUS

DEFINITION HD--02-L11.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--02-L11, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--02-L11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 460

AL048750

LOCUS

DEFINITION DKFP566L123_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFP566L123, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 22)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP566L123"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMPI; Site_1: NotI; Site_2: SalI"

Query Match 1.1%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
|||||
Db 4 CAAAAAAAAAAAAAAAAAAAAA 22

RESULT 461

CF328832/c

LOCUS

DEFINITION NACL--03-020.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-020, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 22)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers
1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-020"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1753
|||||
Db 19 CAAAAA...AAAAA 1

RESULT 462

AZ309907/c

LOCUS AZ309907 22 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0017N14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0017N14 F, genomic survey sequence.

ACCESSION AZ309907

VERSION AZ309907.1 GI:10351367

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0017 row: N column: 14

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

FEATURES
source

Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0017N14"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA...AAAAA 1754
|||||
Db 19 AAAAAA...AAAAA 1

RESULT 463

AL587621/c

LOCUS

DEFINITION AL587621 BP Chicken Brain Library Gallus gallus linear EST 02-MAR-2001
ROS059H07, mRNA sequence.

ACCESSION AL587621

VERSION AL587621.1 GI:13192655

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM

Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BP Chicken Brain Library

Unpublished (2001)

Contact: Frazer Murray

Dept. Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 440 0434

Email: frazer.murray@bbsrc.ac.uk

CGGCCGCTTTT...TTTTTTT 3' Poly A RNA purchased from Clonetechn

(*6854-

Seq primer: M13F.

Location/Qualifiers

1. .23

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="ROS059H07"

/tissue_type="Brain"

/dev_stage="Unknown"

/lab_host="DH10B"

/clone_lib="BP Chicken Brain Library"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned

unidirectionally. Primer: Oligo dT. 5' adaptor sequence:

5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'

GCGGCCGCTTTT...TTTTTTT 3' Poly A RNA purchased from

Clonetechn (*6854-1)"

Query Match

Best Local Similarity 95.0%; Pred. No. 2e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAA...AAAAA 1755
|||||

Db	23	AAAAAAAAAAAAAAAAAANA	4
RESULT 464	AZ764496		
LOCUS	1M0560H02R	Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560H02 R, genomic survey sequence.	
DEFINITION	clone UUGC1M0560H02 R, genomic survey sequence.		
ACCESSION	AZ764496		
VERSION	AZ764496.1	GI:12879519	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1	(bases 1 to 24)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0560 row: H column: 02 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 24.		
FEATURES	source		
	1. .24		
	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UUGC1M0560H02"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	1.1%;	Score 19;	DB 1; Length 24;
Best Local Similarity	100.0%;	Pred. No. 2.1e+02;	
Matches	19;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1736	AAAAAAAAAAAAAAAAAAAA	1754
Db	1	AAAAAAAAAAAAAAAAAAAA	19

RESULT 465	AZ764513		
LOCUS	1M0560D11R	Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560D11 R, genomic survey sequence.	
DEFINITION	clone UUGC1M0560D11 R, genomic survey sequence.		
ACCESSION	AZ764513		
VERSION	AZ764513.1	GI:12879553	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1	(bases 1 to 24)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0560 row: D column: 11 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 24.		
FEATURES	source		
	1. .24		
	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UUGC1M0560D11"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	1.1%;	Score 19;	DB 1; Length 24;
Best Local Similarity	100.0%;	Pred. No. 2.1e+02;	
Matches	19;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1736	AAAAAAAAAAAAAAAAAAAA	1754
Db	1	AAAAAAAAAAAAAAAAAAAA	19

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RESULT 466
AZ774476
LOCUS
DEFINITION
  AZ774476      25 bp  DNA      linear      GSS 16-FEB-2001
  2M0004A01F Mouse 10kb plasmid UUGClm library Mus musculus genomic
  clone UUGC2M0004A01 F, genomic survey sequence.
ACCESSION
  AZ774476
VERSION
  AZ774476.1 GI:12899965
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 25)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0004 row: A column: 01
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 25.
FEATURES
  source
    1..25
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0004A01"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGClm library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

```

```

Query Match      1.1%; Score 19; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
      |||||
Db 1 AAAAAAAAAAAAAAAAAA 19

```

```

RESULT 467
CF298427/c
LOCUS
DEFINITION
  CF298427      22 bp  mRNA      linear      EST 15-AUG-2003
  7LEAF--01-M24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa cDNA clone 7LEAF--01-M24, mRNA sequence.
ACCESSION
  CF298427
VERSION
  CF298427.1 GI:33670188
KEYWORDS
  EST.
SOURCE
  Oryza sativa
ORGANISM
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
  1 (bases 1 to 22)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

FEATURES
  source
    1..22
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultur="Nackdong"
    /db_xref="taxon:4530"
    /clone="7LEAF--01-M24"
    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

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Query Match      1.1%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1733 TACAAAAA 1754
      |||||
Db 22 TAAAAACAAAAA 1

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```

RESULT 468
TA303G05P
LOCUS
DEFINITION
  TA303G05P      22 bp  DNA      linear      GSS 13-DEC-2000
  T. brucei sheared genomic DNA clone 303g05, forward sequence,
  genomic survey sequence.
ACCESSION
  AL497383
VERSION
  AL497383.1 GI:11865504
KEYWORDS
  GSS.
SOURCE
  Trypanosoma brucei
ORGANISM
  Trypanosoma brucei
  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  Trypanosoma.
REFERENCE
  1 (bases 1 to 22)
  Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
  Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
  Melville, S.E., Rajandream, M.A. and Barrell, B.G.
  Direct Submission
  Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
  project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
  Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
  nh@sanger.ac.uk
  Constructed at the Institute for Genomic Research (TIGR),
  Rockville, MD. Genomic DNA isolated from a cloned population of
  Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

```

to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source

1. .22
Location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="303g05"

Query Match 1.1%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 ACNAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAGAAAAAAAAAAAA 22

RESULT 469
BX550903/c

LOCUS BX550903 23 bp mRNA linear EST 10-OCT-2003
DEFINITION BX550903 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tsel15e01_q1c, mRNA sequence.

ACCESSION BX550903
VERSION BX550903.1 GI:33374645
KEYWORDS EST.

SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 23)

AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198

COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

FEATURES
source

1. .23
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tsel15e01_q1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 1.1%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAAAAAAAAAAAAAAAAA 1752
Db 22 TTTTAAAAAAAAAAAAAAAAAAAA 1

RESULT 470
CF279593/c

LOCUS CF279593 23 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--05-P06.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--05-P06, mRNA sequence.

ACCESSION CF279593
VERSION CF279593.1 GI:33656979
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 23)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .23
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--05-P06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 ACNAAAAAAAAAAAAAAAAAAAA 1755
Db 22 AAAAGAAAAAAAAAAAAAAAAAAAA 1

RESULT 471
CF333801/c

LOCUS CF333801 23 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-N11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-N11, mRNA sequence.

ACCESSION CF333801
VERSION CF333801.1 GI:33815910
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 23)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
Location/Qualifiers
1. .23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-N11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1753
Db 23 TTA 2

RESULT 472
AZ330773
LOCUS AZ330773 23 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0056O08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0056O08 F, genomic survey sequence.
ACCESSION AZ330773
VERSION AZ330773.1 GI:10392809
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: 0 column: 08
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES source
Location/Qualifiers
1. .23
/organism="Mus musculus"

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0056O08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1729 AGTTTACAAAAA 1750
Db 2 ATTTTCAAAAAA 23

RESULT 473
AZ382013
LOCUS AZ382013 23 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0138M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0138M14 R, genomic survey sequence.
ACCESSION AZ382013
VERSION AZ382013.1 GI:10495713
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0138 row: M column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES source
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 GGGGGAAGAGGAAAAA 45
|||||
Db 3 GGGGGAAGAAAAA 24

RESULT 487

TA12F02Q
LOCUS T. brucei sheared genomic DNA clone 12f02, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL451366
VERSION AL451366.1 GI:11833388
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei

Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 25)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

source
1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="12f02"

Query Match 1.1%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTACAAAAA 1752
|||||
Db 4 TTTTAAAAA 25

RESULT 488

CF308984/c
LOCUS ABF--03-A01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--03-A01, mRNA sequence.
ACCESSION CF308984

VERSION CF308984.1 GI:33680745

KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--03-A01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAA 1755
|||||
Db 20 AAAAAA 1

RESULT 489

AZ375620
LOCUS AZ375620
DEFINITION 1M0129A08F Mouse 10kb plasmid UUGC1m library Mus musculus genomic
clone UUGC1M0129A08 F, genomic survey sequence.

ACCESSION AZ375620
VERSION AZ375620.1 GI:10489320
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: A column: 08
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0129A08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0129A08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAATAAAAAAAAAAAAAA 20

RESULT 490

AZ486787/c

LOCUS

DEFINITION IM0315D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315D23 F, genomic survey sequence.

ACCESSION AZ486787

VERSION AZ486787.1 GI:10653904

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: D column: 23
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 491

AZ579122

LOCUS

DEFINITION IM0363G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0363G19 F, genomic survey sequence.

ACCESSION AZ579122

VERSION AZ579122.1 GI:11693583

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

FEATURES	Class: plasmid ends	
	High quality sequence stop: 20.	
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	/organism="Mus musculus"	
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	/clone="UUGC2M0150P21"	
	/sex="Male"	
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	
	/clone_lib="Mouse 10kb plasmid UUGC1m library"	
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptedore DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptedore mouse DNA was annealed to adaptedore vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
	Query Match 1.0%; Score 18.4; DB 1; Length 20;	
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	Db 1 TTA 1751	
	RESULT 494	
	AZ949997	
	LOCUS	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	REFERENCE	
	AUTHORS	
	TITLE	
	JOURNAL	
	COMMENT	
	Contact: Robert B. Weiss	
	University of Utah	
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	
	84112, USA	
	Tel: 801 585 5606	
	Fax: 801 585 7177	
	Email: ddunn@genetics.utah.edu	
	Insert Length: 10000 Std Error: 0.00	
	Plate: 0213 row: D column: 24	
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	Class: plasmid ends	
	20 bp DNA linear GSS 27-APR-2001	
	2M0213D24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic	
	clone UUGC2M0213D24 R, genomic survey sequence.	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	REFERENCE	
	AUTHORS	
	TITLE	
	JOURNAL	
	COMMENT	
	Contact: Robert B. Weiss	
	University of Utah	
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	
	84112, USA	
	Tel: 801 585 5606	
	Fax: 801 585 7177	
	Email: ddunn@genetics.utah.edu	
	Insert Length: 10000 Std Error: 0.00	
	Plate: 0213 row: D column: 24	
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	Class: plasmid ends	
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	BX548564 Glossina morsitans morsitans adult infected gut Glossina	
	morsitans morsitans cDNA clone Tse101g03_plc, mRNA sequence.	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	REFERENCE	
	AUTHORS	
	TITLE	
	JOURNAL	
	MEDLINE	
	PUBMED	
	COMMENT	
	Contact: Hall N	
	Pathogen Sequencing Unit	
	The Sanger Institute The Wellcome Trust Genome Campus	
	Hinxtion, Cambridge, CB10 1SA, UK	
	Request for clones, please contact: Mike Lehane	
	Prof. M.J. Lehane	
	School of Biological Sciences,	
	University of Wales,	
	Bangor LL57 2UW	
	All clones with suffix q1c are reverse primer reads starting at 5'	
	end of the cDNA all plc reads are from	
	1. .20	
	/organism="Mus musculus"	
	/mol_type="genomic DNA"	
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	/sex="Female"	
	/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"	
	/clone_lib="Mouse 10kb plasmid UUGC2M library"	
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptedore DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptedore mouse DNA was annealed to adaptedore vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
	Query Match 1.0%; Score 18.4; DB 1; Length 20;	
	Best Local Similarity 95.0%; Pred. No. 2.2e+02;	
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
	Qy 1736 AAAAAA 1755	
	Db 1 AAAAAA 1755	
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	BX548564/c	
	LOCUS	
	DEFINITION	
	ACCESSION	
	VERSION	
	KEYWORDS	
	SOURCE	
	ORGANISM	
	REFERENCE	
	AUTHORS	
	TITLE	
	JOURNAL	
	MEDLINE	
	PUBMED	
	COMMENT	
	Contact: Hall N	
	Pathogen Sequencing Unit	
	The Sanger Institute The Wellcome Trust Genome Campus	
	Hinxtion, Cambridge, CB10 1SA, UK	
	Request for clones, please contact: Mike Lehane	
	Prof. M.J. Lehane	
	School of Biological Sciences,	
	University of Wales,	
	Bangor LL57 2UW	
	All clones with suffix q1c are reverse primer reads starting at 5'	
	end of the cDNA all plc reads are from	

```
the 3' end.
FEATURES             Location/Qualifiers
     source           1..21
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                     /mol_type="mRNA"
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                     /tissue_type="adult infected gut"
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                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

Query Match          1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAGAAAA 2

RESULT 496
BX564412/c          21 bp mRNA linear EST 10-OCT-2003
LOCUS               BX564412 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION          morsitans morsitans cDNA clone Tse71e10_plc, mRNA sequence.
ACCESSION           BX564412
VERSION             BX564412.1 GI:33431592
KEYWORDS
SOURCE
ORGANISM            Glossina morsitans morsitans
                    Glossina morsitans morsitans
                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                    Hippoboscidae; Glossinidae; Glossina.
REFERENCE           1 (bases 1 to 21)
AUTHORS             Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
                    Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE              Adult midgut expressed sequence tags from the tsetse fly Glossina
                    morsitans morsitans and expression analysis of putative immune
                    response genes
JOURNAL             Genome Biol. 4 (10), R63 (2003)
MEDLINE            22881942
PubMed             14519198
COMMENT            Contact: Hall N
                    Pathogen Sequencing Unit
                    The Sanger Institute The Wellcome Trust Genome Campus
                    Hinxton, Cambridge, CB10 1SA, UK
                    Request for clones, please contact: Mike Lehane
                    Prof. M.J.Lehane
                    School of Biological Sciences,
                    University of Wales,
                    Bangor LL57 2UW
                    All clones with suffix q1c are reverse primer reads starting at 5'
                    end of the cDNA all plc reads are from
                    the 3' end.

FEATURES             Location/Qualifiers
     source           1..21
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                     /tissue_type="adult infected gut"
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                     T.brucei"

Query Match          1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 20 TTCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 497
CF296213/c          21 bp mRNA linear EST 14-AUG-2003
LOCUS               CF296213 30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION          sativa cDNA clone 30DGS--06-H19, mRNA sequence.
ACCESSION           CF296213
VERSION             CF296213.1 GI:33665246
KEYWORDS            EST.
SOURCE              Oryza sativa
ORGANISM            Oryza sativa
                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE           1 (bases 1 to 21)
AUTHORS             Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE              Large-scale Sequencing Analysis of Rice ESTs
JOURNAL             Unpublished (2003)
COMMENT            Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 330 6193
                    Fax: 82 31 321 6355
                    Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAACAAAAAAAAAAAA 2

RESULT 498
CF333393/c          21 bp mRNA linear EST 18-AUG-2003
LOCUS               CF333393 JMT--02-E09.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION          library (JMT) Oryza sativa cDNA clone JMT--02-E09, mRNA sequence.
ACCESSION           CF333393
VERSION             CF333393.1 GI:33815062
KEYWORDS            EST.
SOURCE              Oryza sativa
ORGANISM            Oryza sativa
                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE           1 (bases 1 to 21)
AUTHORS             Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE              Large-scale Sequencing Analysis of Rice ESTs
JOURNAL             Unpublished (2003)
```

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source Location/Qualifiers
1. .21
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACACAAAAA 1753
Db 20 ACCAAAAA 1

RESULT 499
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LOCUS 1M0035J02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0035J02 R, genomic survey sequence.

ACCESSION AZ317208.1 GI:10365804
VERSION AZ317208.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: J column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAA 1755
Db 21 AAAAGAAAAA 2

RESULT 500
AZ486776/c 21 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0315M10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0315M10 F, genomic survey sequence.

ACCESSION AZ486776.1 GI:10653882
VERSION AZ486776.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: M column: 10
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES source Location/Qualifiers
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/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 21 AAAAAATAAAAAAAAAAAAAA 2

RESULT 501
AZ610868/c
LOCUS
DEFINITION
AZ610868 21 bp DNA linear GSS 13-DEC-2000
IM0436G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0436G12 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0436 row: G column: 12
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAAAAAAAAAAAAAA 1750
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Db 20 TTTAAAAAAAAAAAAAAAAA 1

RESULT 502
AZ764492

LOCUS
DEFINITION
AZ764492 21 bp DNA linear GSS 16-FEB-2001
IM0560D04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560D04 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: D column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
1. .21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560D04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1750
Db 2 TTTAAAAA 21

RESULT 503
AZ822825 21 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0096I20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0096I20 F, genomic survey sequence.

ACCESSION AZ822825
VERSION AZ822825.1 GI:12992733
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0096 row: I column: 20

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0096I20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAA 1755
Db 1 AAAAAA 20

RESULT 504

AZ853429

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0156D09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 505
CF291486/c
LOCUS
DEFINITION
14ROOT--01-021.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-021, mRNA sequence.
ACCESSION
CF291486
VERSION
CF291486.1 GI:33660519
KEYWORDS
EST.
SOURCE
Oryza sativa

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-021"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.0%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1753
|||

Db 20 ACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 506
CF311534/c
LOCUS

DEFINITION
CF311534
ACCESSION
CF311534
VERSION
CF311534.1 GI:33683295
KEYWORDS
EST.
SOURCE
Oryza sativa

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--06-M14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 1.0%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAAAAAAAAAAAAAAAA 1751
|||||
Db 20 TCACAAAAAAAAAAAAAAAAAAAA 1

RESULT 507
CF337747/c
LOCUS

DEFINITION
CF337747
ACCESSION
CF337747.1 GI:33823871
VERSION
CF337747
KEYWORDS
EST.
SOURCE
Oryza sativa

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 24)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

CF337747 24 bp mRNA linear EST 18-AUG-2003
JMT--08-F05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--08-F05, mRNA sequence.

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT-08-F05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.Coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.0%; Score 18.4; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1750
Db 20 TATACAAAAA 1

RESULT 508

AZ626101/c

LOCUS

DEFINITION AZ626101 24 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0466J07 F, genomic survey sequence.

ACCESSION AZ626101

VERSION AZ626101.1 GI:11748291

KEYWORDS

SOURCE

ORGANISM Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0466 row: J column: 07

Seq primer: CGTTGTAAACGACGCCACT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1. .24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0466J07"

FEATURES

source

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0542D04"

/sex="Male"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.0%; Score 18.4; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAA 1755

Db 24 AAAAAA 5

RESULT 509

AZ662734

LOCUS

DEFINITION AZ662734 23 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0542D04 F, genomic survey sequence.

ACCESSION AZ662734

VERSION AZ662734.1 GI:11799880

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0542 row: D column: 04

Seq primer: CGTTGTAAACGACGCCACT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0542D04"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 TTTCACAAAAA 1753
| | | | |
Db 1 TCTACTAAATAA 23

RESULT 510
BQ582676/c

LOCUS BQ582676 18 bp mRNA linear EST 06-DEC-2002
DEFINITION E012281-024-007-P18-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris
CDNA clone 024-007-P18 5-PRIME, mRNA sequence.

ACCESSION BQ582676
VERSION BQ582676.1 GI:26112253
KEYWORDS EST.

SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 7 row: P column: 18

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

Location/Qualifiers
1. .18
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:184018"
/db_xref="taxon:161934"
/clone="024-007-P18"
/tissue_type="inflorescence"
/lab_host="EMDH10B"

FEATURES
source

/clone_lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA 1753
| | | | |
Db 18 AAAAAA 1

RESULT 511
BQ590027/c

LOCUS BQ590027 18 bp mRNA linear EST 06-DEC-2002
DEFINITION E012844-024-019-E24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-E24 3-PRIME, mRNA sequence.

ACCESSION BQ590027
VERSION BQ590027.1 GI:26119610
KEYWORDS EST.

SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 19 row: E column: 24
Seq primer: T7; GTAATACGACTCACTATAGGGC.

Location/Qualifiers
1. .18
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:190095"
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/clone="024-019-E24"
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/lab_host="EMDH10B"

Seq primer: T7; GTAATACGACTCACTATAGGGC.

FEATURES
source

1. .18
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
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/db_xref="taxon:161934"
/clone="024-019-E24"
/tissue_type="storage root"
/lab_host="EMDH10B"

SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

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Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 512
CF277873/c
LOCUS      18 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 14ETL--03-J04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--03-J04, mRNA sequence.
ACCESSION  CF277873
VERSION     CF277873.1 GI:33655259
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            Location/Qualifiers
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                /organism="Oryza sativa"
                /mol_type="mRNA"
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                /db_xref="taxon:4530"
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                /lab_host="E.coli DH10B"
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                /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 513
CF297446/c
LOCUS      18 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 30DGS--08-F02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--08-F02, mRNA sequence.
ACCESSION  CF297446
VERSION     CF297446.1 GI:33666479
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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                /tissue_type="leaf"
                /dev_stage="30 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 514
CF299027/c
LOCUS      18 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--02-N14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-N14, mRNA sequence.
ACCESSION  CF299027
VERSION     CF299027.1 GI:33670788
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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                /clone="7LEAF--02-N14"
                /tissue_type="leaf"
                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1753
      |||||||
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 515
CF299674/c
LOCUS      18 bp mRNA linear EST 15-AUG-2003
DEFINITION      7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-M14, mRNA sequence.
ACCESSION      CF299674
VERSION      CF299674.1 GI:33671435
KEYWORDS
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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      /lab_host="E.coli DH10B"
      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1753
      |||||||
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 516
CF301325/c
LOCUS      18 bp mRNA linear EST 15-AUG-2003
DEFINITION      7LEAF--06-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-C12, mRNA sequence.
ACCESSION      CF301325
VERSION      CF301325.1 GI:33673086
KEYWORDS
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

```
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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      1..18
      /organism="Oryza sativa"
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      /lab_host="E.coli DH10B"
      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1753
      |||||||
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 517
CF301760/c
LOCUS      18 bp mRNA linear EST 15-AUG-2003
DEFINITION      7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-L22, mRNA sequence.
ACCESSION      CF301760
VERSION      CF301760.1 GI:33673521
KEYWORDS
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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      /lab_host="E.coli DH10B"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 518
CF291665/c
LOCUS
DEFINITION 14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-D01, mRNA sequence.
ACCESSION CF291665
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-D01"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAA 1

RESULT 519
CF293167/c
LOCUS
DEFINITION 30DGS--02-E02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--02-E02, mRNA sequence.
ACCESSION CF293167
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 520
CF309821/c
LOCUS
DEFINITION ABF--04-C17.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--04-C17, mRNA sequence.
ACCESSION CF309821
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .19
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="14ROOT--02-D01"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 19 AAAAAAAAAAAAAAAAAA 2
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 520
CF309821/c
LOCUS
DEFINITION ABF--04-C17.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--04-C17, mRNA sequence.
ACCESSION CF309821
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .19
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/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 524
AL587759/c
LOCUS
DEFINITION AL587759 BP Chicken Brain Library Gallus gallus cDNA clone
ROS061G06, mRNA sequence.
ACCESSION AL587759
VERSION AL587759.1 GI:13192793
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 20)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
Location/Qualifiers
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/clone="ROS061G06"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"
Query Match 1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 19 AAAAAAAAAAAAAAAAAA 2

Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 525
CA853586/c
LOCUS
DEFINITION CA853586 B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
B09H12 5', mRNA sequence.
ACCESSION CA853586
VERSION CA853586.1 GI:33390391
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 20)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ba.ars.usda.gov.
Location/Qualifiers
1. .20
/organism="Glycine max"
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/clone="B09H12"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."
Query Match 1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 526
AZ345856/c
LOCUS
DEFINITION AZ345856 1M0080G17R Mouse 10kb plasmid UUGClM library Mus musculus genomic
clone UUGClM0080G17 R, genomic survey sequence.
ACCESSION AZ345856
VERSION AZ345856.1 GI:10425093
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080G17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 527
AZ370699/c
LOCUS AZ370699 20 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0121N17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0121N17 R, genomic survey sequence.
ACCESSION AZ370699
VERSION AZ370699.1 GI:10484399
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0121 row: N column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0121N17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 528
AZ843648
LOCUS AZ843648 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0142B07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0142B07 R, genomic survey sequence.
ACCESSION AZ843648
VERSION AZ843648.1 GI:13013556
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0142 row: B column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0142B07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 529

TA211D06P/c

LOCUS

DEFINITION T. brucei sheared genomic DNA clone 211d06, forward sequence,
genomic survey sequence.

ACCESSION AL478564

VERSION AL478564.1 GI:11844523

KEYWORDS GSS.

SOURCE

ORGANISM

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 22)

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

Location/Qualifiers
1..22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="211d06"

Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1752

Db 18 CAAAAAAAAAAAAAAAAA 1

RESULT 530

TA231E08Q

LOCUS

DEFINITION T. brucei sheared genomic DNA clone 231e08, reverse sequence,
genomic survey sequence.

ACCESSION AL480935

VERSION AL480935.1 GI:11846704

KEYWORDS GSS.

SOURCE

ORGANISM

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 22)

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

1..22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="231e08"

Query Match 1.0%; Score 18; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 531
TA386H07Q/c 22 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 386h07, reverse sequence,
genomic survey sequence.
ACCESSION AL498291
VERSION AL498291.1 GI:11874013
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1. .22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="386h07"

Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 532
AW334124/c 23 bp mRNA linear EST 31-JAN-2000
LOCUS
DEFINITION S30G5 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AW334124
VERSION AW334124.1 GI:6830481
KEYWORDS EST.
SOURCE Pneumocystis carinii
ORGANISM Pneumocystis carinii
REFERENCE 1 (bases 1 to 23)
AUTHORS Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
Edman, J.C., Kovacs, J. and Cushion, M.
TITLE Expressed sequence tags from Pneumocystis carinii
JOURNAL Unpublished (2000)
COMMENT Contact: Staben C
School of Biological Sciences

University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES
source
1. .23
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 1.0%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 23 AAAAAAAAAAAAAAAAAA 6

RESULT 533
CF293321
LOCUS
DEFINITION 30DGS--02-H12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--02-H12, mRNA sequence.
ACCESSION CF293321
VERSION CF293321.1 GI:33662354
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--02-H12"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 6 AAAAAAAAAAAAAAAAAA 23

RESULT 534
AZ764519 24 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0560P11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0560P11 R, genomic survey sequence.
ACCESSION AZ764519
VERSION AZ764519.1 GI:12879566
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: p column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
source
1. .24
Location/Qualifiers
/organism="Mus musculus"
/mol_type="Genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560P11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 535
AL048772 21 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp566N143_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION DKFZp566N143, mRNA sequence.
ACCESSION AL048772
VERSION AL048772.1 GI:4727843
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1. .21
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566N143"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="XL-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1730 GTTTACAAAAAAAAAAAAA 1750
Db 1 GGTAAAAAAAAAAAAA 21

RESULT 536
AW335179/c
LOCUS AW335179 23 bp mRNA linear EST 31-JAN-2000
DEFINITION S44B4 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AW335179
VERSION AW335179.1 GI:6831798
KEYWORDS EST.
SOURCE Pneumocystis carinii
ORGANISM Pneumocystis carinii
REFERENCE Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
AUTHORS Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 23)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
JOURNAL Contact: Staben C
COMMENT School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
FEATURES
source
1. .23
Location/Qualifiers
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"

/lab_host="E. coli"
/clone_lib="AGS-1"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/project/Pneumocystis/"

Query Match 1.0%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1751
Db 21 TTTTGA 1

RESULT 537
AW248747/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW248747 19 bp mRNA linear EST 07-JAN-2000
2821119.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821119 3',
mRNA sequence.

AW248747
AW248747.1 GI:6591740
EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2821119.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality

Scores: PHRED from University of Washington Genome Center

Trimming: cross match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

<http://www.genome.washington.edu> Low Quality Sequence: 7 contiguous

PHRED high quality bases following vector sequence. Very Low

Quality Sequence: Trace file contained 19 contiguous distinct peaks

following vector sequence. Polyadenylation: Based upon the presence

of a XhoI site followed by a run of 14 or more T residues at the

beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCMS row: P column: 16

High quality sequence stop: 7.

Location/Qualifiers

1. .19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:2821119"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC 7"

/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAA 1754
Db 19 AAAAAA 1

RESULT 538
CF291899/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. .19

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ROOT--02-108"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAA 1754
Db 19 AAAAAA 1

RESULT 539
CF292072/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-M03"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAACA 1

RESULT 540

CF292144/c

LOCUS 14ROOT--02-N17.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-N17, mRNA sequence.

ACCESSION CF292144.1 GI:33661177

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-N17"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAACA 1

RESULT 541

CF310688

LOCUS ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--05-H18, mRNA sequence.

ACCESSION CF310688

VERSION CF310688.1 GI:33682449

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--05-H18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754

Db 1 AAAAAAAAAAAAAAAAAAACA 19

RESULT 542

CF319596/c

LOCUS HD--10-C14.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.

ACCESSION CF319596

VERSION CF319596.1 GI:33691357

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HD-10-C14"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match

Best Local Similarity 1.0%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1750

19 TTTCAAAAA 1

RESULT 543

CF329136/c

LOCUS

DEFINITION NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--04-F15, mRNA sequence.

CF329136

CF329136.1 GI:33806509

EST.

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--04-F15"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 1.0%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAA 1754

19 AAAGAAAAA 1

RESULT 544

AZ345795

LOCUS

DEFINITION 1M0080H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0080H09 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: H column: 09

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0080H09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1750
Db 1 TTA 19

RESULT 545
AZ363907/c

LOCUS
DEFINITION
AZ363907 19 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0109113 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 row: I column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0109113"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAA 1754
Db 19 AAAAAA 1

RESULT 546
AZ447251/c

LOCUS
DEFINITION
AZ447251 19 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0244J19 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: J column: 19
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244J19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAGAAAAAAAAA 1

RESULT 549
AZ645841/c
LOCUS
DEFINITION
AZ645841 19 bp DNA linear GSS 14-DEC-2000
IM0511G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0511G04 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: G column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511G04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAGAAAAAAAAA 1

RESULT 550
AZ650252

LOCUS
DEFINITION
AZ650252 19 bp DNA linear GSS 14-DEC-2000
IM0520N17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0520N17 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: N column: 17
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGC1M0520N17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

and selected for ampicillin resistance."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 551
AZ650575 19 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0520P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0520P13 R, genomic survey sequence.
ACCESSION AZ650575
VERSION AZ650575.1 GI:11785200
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: P column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0520P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAAAAAAAAAAAA 1750
|||||
Db 1 TTAACAAAAAAAAAAAAAAAAA 19

RESULT 552
AZ654747/c 19 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0529F08 F, genomic survey sequence.
ACCESSION AZ654747
VERSION AZ654747.1 GI:11791893
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
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COMMENT Contact: Robert B. Weiss
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: F column: 08
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
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/organism="Mus musculus"
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
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Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 553
CF282165/c
LOCUS
DEFINITION
20 bp mRNA linear EST 14-AUG-2003
Oryza sativa cDNA clone 14ETL--09-I22, mRNA sequence.
CF282165
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-I22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAAAAAAAAAAAAAA 1749
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Db 19 TTTCACAAAAAAAAAAAAAAAA 1

RESULT 554
CF330490/c
LOCUS
DEFINITION
20 bp mRNA linear EST 18-AUG-2003
NACL--06-D16.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--06-D16, mRNA sequence.
CF330490
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)

AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

TITLE
JOURNAL
COMMENT

FEATURES
source
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-D16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAAAAAAAAAAAA 1750
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Db 19 TTCCAAAAAAAAAAAAAAAA 1

RESULT 555
CF333052/c
LOCUS
DEFINITION
20 bp mRNA linear EST 18-AUG-2003
JMT--01-M17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--01-M17, mRNA sequence.
CF333052
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--01-M17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
DB 20 AAAAAAAAAAAAAAAAAACA 2

RESULT 556

CF3119625 21 bp mRNA linear EST 15-AUG-2003
LOCUS HD--10-D06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--10-D06, mRNA sequence.

ACCESSION CF3119625.1 GI:33691386
VERSION
KEYWORDS
SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 21)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

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/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HD--10-D06"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAAAAAAAAAAAAAA 1751
|||||
DB 3 TATAAAAAAAAAAAAAAAAAA 21

RESULT 557

CF330439 21 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--06-C12, mRNA sequence.

ACCESSION CF330439

VERSION CF330439.1 GI:33809110

KEYWORDS EST.

SOURCE

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 21)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..21

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--06-C12"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAAAAAAAAA 1750
|||||
DB 19 TTATAAAAAAAAAAAAAA 1

RESULT 558

AZ308846/c
LOCUS 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0012H15F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0012H15 F, genomic survey sequence.

ACCESSION AZ308846

VERSION AZ308846.1 GI:10349246

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0012 row: H column: 15

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 21.
FEATURES
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Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
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Db 21 AAAAAAAAAACAAAAA 3

RESULT 559
AZ627840/c
LOCUS
DEFINITION
IM0474B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0474B05 F, genomic survey sequence.
ACCESSION
AZ627840
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
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JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: B column: 05
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474B05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 21 AAAAAAAAAACAAAAA 3

RESULT 560
CF302435
LOCUS
DEFINITION
7LEAF--07-O22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-O22, mRNA sequence.
ACCESSION
CF302435
VERSION
CF302435.1 GI:33674196
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-O22"
/tissue_type="leaf"
/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 17.4; DB 1; Length 22;
Best Local Similarity 94.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1751
|||
Db 4 TAGAAAAA 22

RESULT 561
AL048695
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL048695. 23 bp mRNA linear EST 04-SEP-2003
DKFZp566D063_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566D063, mRNA sequence.
AL048695
AL048695.1 GI:4727766
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 23)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566D063"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMPl; Site 1: NotI; Site 2: SalI"

Query Match 1.0%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA 1753
|||
Db 5 CAAAAA 23

RESULT 562
BQ590647/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

BQ590647 23 bp mRNA linear EST 06-DEC-2002
S015086-024-018-P17-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-P17 5-PRIME, mRNA sequence.
BQ590647
BQ590647.1 GI:26120230
EST.
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 23)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Plate: 18 row: P column: 17
Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES
Location/Qualifiers
1..23
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189468"
/db_xref="taxon:161934"
/clone="024-018-P17"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAA 1754
|||||
Db 21 AAAAAA 3

RESULT 563
BX560037/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

BX560037 23 bp mRNA linear EST 10-OCT-2003
BX560037 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse47e08_plc, mRNA sequence.
BX560037
BX560037.1 GI:33368052
EST.
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 23)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)

JOURNAL
MEDLINE
PUBMED
COMMENT

22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane

School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.

FEATURES
source

Location/Qualifiers
1. .23
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse47e08_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 1.0%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1749

Db 19 TTTAGAAAAA 1

RESULT 564
BQ591193/c

LOCUS
DEFINITION BQ591193 22 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-017-D14-T7 MP12-ADIS-024-storage root Beta vulgaris

ACCESSION BQ591193

VERSION BQ591193.1

KEYWORDS GI:26120776

SOURCE EST.

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 22)

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL 22362189

MEDLINE 12472698

PUBMED

COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 22 Std Error: 0.00

Plate: 17 row: D column: 14

Seq primer: T7; GTAATACGACTCATTATAGGC.

FEATURES
source

Location/Qualifiers
1. .22
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188927"
/db_xref="taxon:161934"
/clone="024-017-D14"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1734 ACAAAAAA 1755

Db 22 ACATATTAAAAA 1

RESULT 565
CF297521/c

LOCUS
DEFINITION CF297521 22 bp mRNA linear EST 14-AUG-2003
30DGS--08-H01.91 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--08-H01, mRNA sequence.

ACCESSION CF297521

VERSION CF297521.1

KEYWORDS GI:33666554

SOURCE EST.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 22)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--08-H01"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1728 GAGTTTACAAAAA 1749

Db 22 GGGTTTGA 1

RESULT 566
AZ442146/c

LOCUS
DEFINITION AZ442146 22 bp DNA linear GSS 03-OCT-2000
1M0234B16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0234B16 R, genomic survey sequence.

ACCESSION AZ442146

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VERSION      AZ442146.1  GI:10566159
KEYWORDS
SOURCE      GSS.
ORGANISM    Mus musculus (house mouse)
            Mus musculus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 22)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0234 row: B column: 16
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
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            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0234B16"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gil4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
Query Match      1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
        | | | | | | | | | | | | | | | |
DB      22 AAAAAAAAAACCAAAAAAAAAAAAA 1

RESULT 567
TA110B07P/C
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 110b07, forward sequence,
            genomic survey sequence.
ACCESSION AL464946
VERSION   AL464946.1 GI:11877920

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Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189432"
/db_xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/Note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1752
Db      17 AAAAAAAAAAAAAAAAAA 1

RESULT 570
CF290854/c
LOCUS      CF290854      17 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION      14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-A21, mRNA sequence.
ACCESSION      CF290854
VERSION      CF290854.1 GI:33659887
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/Note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1752
Db      17 AAAAAAAAAAAAAAAAAA 1

RESULT 571
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Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
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line)"
/db_xref="GABI:189432"
/db_xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/Note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1752
Db      1 AAAAAAAAAAAAAAAAAA 17

RESULT 569
BQ591177/c
LOCUS      BQ591177      17 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION      BQ591177
cDNA clone 024-017-B22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
BQ591177
ACCESSION      BQ591177.1 GI:26120760
VERSION      BQ591177.1 GI:26120760
KEYWORDS      EST.
SOURCE      Beta vulgaris
ORGANISM      Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED      12472698
COMMENT      Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: B column: 22
Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
1. .17
/organism="Beta vulgaris"
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189432"
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/clone="024-017-B22"

FEATURES
source
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CF295807/c
LOCUS       CF295807               17 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION  30DGS--05-O12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-O12, mRNA sequence.
ACCESSION   CF295807
VERSION     CF295807.1  GI:33664840
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--05-O12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     QUERY MATCH      1.0%; Score 17; DB 1; Length 17;
     BEST LOCAL SIMIL 100.0%; Pred. No. 2.8e+02;
     MATCHES          17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAAAAAA 1751
Db      17 CAAAAAAAAAAAAAAAAA 1

RESULT 572
CF298589/c
LOCUS       CF298589               17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION  7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A18, mRNA sequence.
ACCESSION   CF298589
VERSION     CF298589.1  GI:33670350
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--05-O12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     QUERY MATCH      1.0%; Score 17; DB 1; Length 17;
     BEST LOCAL SIMIL 100.0%; Pred. No. 2.8e+02;
     MATCHES          17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAAAAAA 1751
Db      17 CAAAAAAAAAAAAAAAAA 1

RESULT 572
CF298589/c
LOCUS       CF298589               17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION  7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A18, mRNA sequence.
ACCESSION   CF298589
VERSION     CF298589.1  GI:33670350
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..17
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-A18"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     QUERY MATCH      1.0%; Score 17; DB 1; Length 17;
     BEST LOCAL SIMIL 100.0%; Pred. No. 2.8e+02;
     MATCHES          17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAAAAAA 1751
Db      17 CAAAAAAAAAAAAAAAAA 1

RESULT 573
CF299639/c
LOCUS       CF299639               17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION  7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L20, mRNA sequence.
ACCESSION   CF299639
VERSION     CF299639.1  GI:33671400
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-L20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     QUERY MATCH      1.0%; Score 17; DB 1; Length 17;
     BEST LOCAL SIMIL 100.0%; Pred. No. 2.8e+02;
     MATCHES          17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1752
Db      17 AAAAAAAAAAAAAAAAAA 1

RESULT 573
CF299639/c
LOCUS       CF299639               17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION  7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L20, mRNA sequence.
ACCESSION   CF299639
VERSION     CF299639.1  GI:33671400
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..17
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-L20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     QUERY MATCH      1.0%; Score 17; DB 1; Length 17;
     BEST LOCAL SIMIL 100.0%; Pred. No. 2.8e+02;
     MATCHES          17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAAAAAA 1751
Db      17 CAAAAAAAAAAAAAAAAA 1

RESULT 573
CF299639/c
LOCUS       CF299639               17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION  7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-L20, mRNA sequence.
ACCESSION   CF299639
VERSION     CF299639.1  GI:33671400
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-L20"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

     QUERY MATCH      1.0%; Score 17; DB 1; Length 17;
     BEST LOCAL SIMIL 100.0%; Pred. No. 2.8e+02;
     MATCHES          17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAAAAAA 1751
Db      17 CAAAAAAAAAAAAAAAAA 1
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RESULT 574
CF310219/c
LOCUS
DEFINITION ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--04-M02, mRNA sequence.
ACCESSION CF310219
VERSION CF310219.1 GI:33681980
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--04-M02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 575
CF334566/c
LOCUS
DEFINITION JMT--03-O13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-O13, mRNA sequence.
ACCESSION CF334566
VERSION CF334566.1 GI:33817460
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-O13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 576
AL048754
LOCUS
DEFINITION DKFZp566L173_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
AL048754
ACCESSION AL048754
VERSION AL048754.1 GI:4727825
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehler, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566L173"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAA 1751
Db 2 CAAAAAAAAAAAAAAAAA 18
RESULT 577
CF301057/c
LOCUS
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CF301057/c 18 bp mRNA linear EST 15-AUG-2003

DEFINITION 7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M05, mRNA sequence.
ACCESSION CF301057
VERSION CF301057.1 GI:33672818
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-M05"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
|||||
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 578
CF301151/c
LOCUS 7LEAF--05-M05.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--05-M05, mRNA sequence.
ACCESSION CF301151
VERSION CF301151.1 GI:33672912
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .18

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-M05"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
|||||
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 579

CF320418/c

LOCUS CF320418 18 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--11-E22.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--11-E22, mRNA sequence.
ACCESSION CF320418
VERSION CF320418.1 GI:33692179
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--11-E22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
|||||
Db 18 AAAAAAAAAAAAAAAAAA 2


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RESULT 580
CF327587/c
LOCUS
DEFINITION NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-C04, mRNA sequence.
ACCESSION CF327587
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..19
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="NACL--02-C04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 1.0%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAA 1751
|||||
Db 17 CAAAAAAAAAAAAAAAAA 1

RESULT 581
AZ853220
LOCUS
DEFINITION AZ853220 19 bp DNA linear GSS 21-FEB-2001
2M0156J15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0156J15 F, genomic survey sequence.
ACCESSION AZ853220
VERSION AZ853220.1 GI:13041116
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
```

```
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: J column: 15
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0156J15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 1.0%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1752
|||||
Db 3 AAAAAAAAAAAAAAAAAA 19

RESULT 582
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LOCUS
DEFINITION CF298018 20 bp mRNA linear EST 15-AUG-2003
7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-D19, mRNA sequence.
ACCESSION CF298018
VERSION CF298018.1 GI:33669779
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
```

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES
  source
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        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:4530"
        /clone="7LEAF--01-D19"
        /tissue_type="leaf"
        /dev_stage="7 days after germination"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
        /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1751
Db 17 CAAAAAAAAAAAAAAAAA 1

RESULT 583
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LOCUS 7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--01-H23, mRNA sequence.
ACCESSION CF298207
VERSION CF298207.1 GI:33669968
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
  source
    Location/Qualifiers
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        /lab_host="E.coli DH10B"
        /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
        /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      1.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1751
Db 18 CAAAAAAAAAAAAAAAAA 2

RESULT 585
AZ818055
LOCUS 2M0087B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0087B23 R, genomic survey sequence.
ACCESSION AZ818055
VERSION AZ818055.1 GI:12987963
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

Query Match      1.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAAAAA 17
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RESULT 584
CF319428/c
LOCUS CF319428
DEFINITION HD--09-O20.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-O20, mRNA sequence.
ACCESSION CF319428
VERSION CF319428.1 GI:33691189
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="Oryza sativa"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:4530"
        /clone="HD--09-O20"
        /tissue_type="callus"
        /dev_stage="proliferated callus on 2N6 media for 2 weeks"
        /lab_host="E.coli DH10B"
        /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
        /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      1.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1751
Db 18 CAAAAAAAAAAAAAAAAA 2

RESULT 585
AZ818055
LOCUS 2M0087B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0087B23 R, genomic survey sequence.
ACCESSION AZ818055
VERSION AZ818055.1 GI:12987963
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE
JOURNAL
```

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: B column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0087B23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
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Db 4 AAAAAAAAAAAAAAAAAA 20

RESULT 586
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LOCUS AZ943299 21 bp DNA linear GSS 26-APR-2001
DEFINITION 2M0203K21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0203K21 R, genomic survey sequence.

ACCESSION AZ943299
VERSION AZ943299.1 GI:13807290
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: K column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0203K21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
|||||
Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 587
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LOCUS AZ310057 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0018A15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0018A15 R, genomic survey sequence.

ACCESSION AZ310057
VERSION AZ310057.1 GI:10351664
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: A column: 15
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

source

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/strain="C57BL/6J"
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/clone="UUGC1M0018A15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1751
Db 17 CAAAAA1

RESULT 588

CF299570/c

LOCUS 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-K09, mRNA sequence.

ACCESSION CF299570
VERSION CF299570.1 GI:33671331
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)

REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .20
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1733 TACAAAAA1752
Db 20 TAGTAAAAA1

RESULT 589

CF300961/c

LOCUS 20 bp mRNA linear EST 15-AUG-2003

DEFINITION 7LEAF--05-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--05-K03, mRNA sequence.

ACCESSION CF300961
VERSION CF300961.1 GI:33672722
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)

REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .20
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-K03"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAA1755
Db 20 AAAGGAAAAA1

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RESULT 590
CF301101/c
LOCUS
DEFINITION
7LEAF--05-N04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-N04, mRNA sequence.
ACCESSION
CF301101
VERSION
CF301101.1 GI:33672862
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
source
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-N04"
/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1753
Db 20 AGAAGAAAAA 1
RESULT 591
AZ343730/c
LOCUS
DEFINITION
1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0077E20 F, genomic survey sequence.
ACCESSION
AZ343730
VERSION
AZ343730.1 GI:10422288
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: E column: 20
Seq primer: CGTTGTAAACACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0077E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1753
Db 20 AGAAGAAAAA 1
RESULT 592
AZ633741
LOCUS
DEFINITION
AZ633741 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0489G12 F, genomic survey sequence.
ACCESSION
AZ633741
VERSION
AZ633741.1 GI:11755931
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
```


Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0489 row: G column: 12

Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0489G12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAACCAA 20

RESULT 593

AW248782/c

LOCUS AW248782 21 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821017.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821017 3', mRNA sequence.

ACCESSION AW248782

VERSION AW248782.1 GI:6591775

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 21)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other_ESTs: 2821017.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 21 contiguous PHRED high quality bases followed by vector sequence. Very Low Quality Sequence: Trace file contained 21 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM5 row: L column: 10

High quality sequence stop: 21.

FEATURES

source

Location/Qualifiers
1. .21
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2821017"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
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Db 21 AAAAAAAAAATTAATAAAAAA 2

RESULT 594

CF293087/c

LOCUS

DEFINITION

CF293087

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1. .21

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="30DGS--02-C07"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTATCAAAAAAAAAAAAAA 1750
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Db 20 TTGTCAAAAAAAAAAAAA 1

RESULT 595
CF319122/c
LOCUS
DEFINITION HD--09-I07.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-I07, mRNA sequence.
ACCESSION CF319122
VERSION CF319122.1 GI:33690883
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-I07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 ACAAACAAAAAAAAAAAAA 1753
||| ||||| ||||| |||||
Db 20 ACGAAACAAAAAAAAATAAA 1

RESULT 596
AZ597932/c
LOCUS
DEFINITION IM0514117F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION 1M0412D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0412D23 F, genomic survey sequence.
ACCESSION AZ597932
VERSION AZ597932.1 GI:11720122
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0412 row: D column: 23
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0412D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
||||| ||||| ||||| |||||
Db 21 AAAAAAAAAAGAAAAAGAAAA 2

RESULT 597
AZ647578/c
LOCUS
DEFINITION 1M0514117F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0514I17 F, genomic survey sequence.

ACCESSION AZ647578
VERSION AZ647578.1 GI:11779183
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0514 row: I column: 17
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
source Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0514I17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
||||| ||||| ||||| |||||
Db 21 AAAAAAGAAAAAGAAAAAA 2

RESULT 598
BM658677/c
LOCUS BM658677
DEFINITION L2V602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA sequence.

BM658677
BM658677.1 GI:18958948
EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS 1 (bases 1 to 18)
Adelson,D.L. and Gill,C.A.
TITLE Porcine ESTs
JOURNAL Unpublished (2002)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
FEATURES
source Location/Qualifiers
1. .18
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone_lib="CSEQFXL37 pig adrenal"
/note="Organ: adrenal gland; Vector: pBluescript SK+; Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert (5'-NNN...NNNinsert)
GCGAATTGGAGCTCCACCGCGGTGGCGCGCGGCTCGAG. Sequence 3' of the inserts (AAGAATTGATATCAAGCTTATCGATACCGTCGACCTCGAG. non-normalized library, sequenced 3' with M13R primer."

Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
||||| ||||| ||||| |||||
Db 18 AAAAAAGAAAAAGAAAAAA 1

RESULT 599
CF298591/c
LOCUS CF298591
DEFINITION 7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--02-A20, mRNA sequence.

ACCESSION CF298591
VERSION CF298591.1 GI:33670352
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
AUTHORS 1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source Location/Qualifiers
1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--02-A20"

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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1748
      |||||
DB 18 TTTAAAAA 1

RESULT 600
CF300456/c
LOCUS
DEFINITION      18 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--04-N23, mRNA sequence.
ACCESSION      CF300456
VERSION        CF300456.1 GI:33672217
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaem@gbio.com, bhnaem@bio.myongji.ac.kr.

FEATURES
source
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAA 1751
      |||||
DB 18 AGAA 1

RESULT 601
CF302409/c
LOCUS
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sativa cDNA clone 7LEAF--07-N19, mRNA sequence.
ACCESSION      CF302409
VERSION        CF302409.1 GI:33674170

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 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.9%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 3.4e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1751
 Db 18 ATAAAAA 1

RESULT 603
 CF329285/c

LOCUS 18 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--04-i22.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--04-I22, mRNA sequence.

ACCESSION CF329285
 VERSION CF329285.1 GI:33806806
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 18)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
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 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /clone="NACL--04-I22"
 /tissue_type="callus"
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 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.9%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 3.4e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1750
 Db 18 TAGAAAAA 1

RESULT 604
 CF278272/c

LOCUS 19 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa cDNA clone 14ETL--04-C01, mRNA sequence.
 ACCESSION CF278272
 VERSION CF278272.1 GI:33655658
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 19)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ETL--04-C01"
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 /clone_lib="Rice etiolated leaf plasmid cDNA library
 (14ETL)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.9%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 3.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1748
 Db 18 TTTAAAAA 1

RESULT 605
 CF298472/c

LOCUS 19 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--01-O01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--01-O01, mRNA sequence.

ACCESSION CF298472
 VERSION CF298472.1 GI:33670233
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 19)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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Best Local Similarity 94.4%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1750
Db 18 TATAAAAA 1750

RESULT 606
CF309636/c
LOCUS
DEFINITION
ABF--03-008.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--03-008, mRNA sequence.
ACCESSION
CF309636
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--01-B12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1750
Db 2 TAGAAAAA 1750

RESULT 608
CF334610/c
LOCUS
DEFINITION
JMT--03-P13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-P13, mRNA sequence.
ACCESSION
CF334610
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
```


Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-P13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
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Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 609

AZ360314

LOCUS

DEFINITION

1M0103G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0103G03 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0103 row: G column: 03

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0103G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

FEATURES

source

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
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Db 2 AAAAAAAAAAAAAAAAAA 19

RESULT 610

CF309614/c

LOCUS

DEFINITION

ABF--03-N20.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--03-N20, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .21

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--03-N20"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match

Best Local Similarity 0.9%; Score 16.4; DB 1; Length 21;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ACCESSION	CDNA clone 024-019-015 3-PRIME, mRNA sequence.	AUTHORS	Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
VERSION	BQ590207	TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
KEYWORDS	EST.	JOURNAL	Plant J. 32 (5), 845-857 (2002)
SOURCE	Beta vulgaris	MEDLINE	22362189
ORGANISM	Beta vulgaris	PUBMED	12472698
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.	COMMENT	Contact: Weisshaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weisshaar@piz-koeln.mpg.de Insert Length: 16 Std Error: 0.00 Plate: 19 row: O column: 15 Seq primer: T7; GTAATACGACTCACTATAGGCG.
AUTHORS	Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.	FEATURES	Location/Qualifiers
TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes	source	1. .16
JOURNAL	Plant J. 32 (5), 845-857 (2002)		/organism="Beta vulgaris"
MEDLINE	22362189		/mol_type="mRNA"
PUBMED	12472698		/cultivar="KWS2320 (double haploid, monogerm breeding line)"
COMMENT	Contact: Weisshaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weisshaar@piz-koeln.mpg.de Insert Length: 16 Std Error: 0.00 Plate: 19 row: O column: 15 Seq primer: T7; GTAATACGACTCACTATAGGCG.		/db_xref="GABI:189913"
FEATURES	Location/Qualifiers		/db_xref="taxon:161934"
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	/mol_type="mRNA"		/lab_host="EMDH10B"
	/cultivar="KWS2320 (double haploid, monogerm breeding line)"		/clone_lib="MPIZ-ADIS-024-storage root"
	/db_xref="GABI:189913"		/note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
	/db_xref="taxon:161934"		SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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	/lab_host="EMDH10B"		
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	/note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:		
	SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"		
Query Match	0.9%; Score 16; DB 1; Length 16;	QY	1736 AAAAAAAAAAAAAAAAAA 1751
Best Local Similarity	100.0%; Pred. No. 3.6e+02;	Db	1 AAAAAAAAAAAAAAAAAA 16
Matches	16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
		RESULT 615	
		BQ592965/c	
		LOCUS	
		DEFINITION	BQ592965 16 bp mRNA linear EST 06-DEC-2002
		ACCESSION	S013324-024-028-A01-T7 MPIZ-ADIS-024-developing root Beta vulgaris
		VERSION	CDNA clone 024-028-A01 3-PRIME, mRNA sequence.
		KEYWORDS	BQ592965
		SOURCE	BQ592965.1 GI:26122548
		ORGANISM	EST.
			Beta vulgaris
			Beta vulgaris
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
		REFERENCE	1 (bases 1 to 16)
		AUTHORS	Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
		TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
		JOURNAL	Plant J. 32 (5), 845-857 (2002)
		MEDLINE	22362189
		PUBMED	12472698
		COMMENT	Contact: Weisshaar B ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES

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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match

Best Local Similarity 100.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1751

Db 16 AAAAAAAAAAAAAAA 1

RESULT 616

BQ595717

LOCUS

DEFINITION BQ595717 16 bp mRNA linear EST 06-DEC-2002
E012692-024-022-H07-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-H07 5-PRIME, mRNA sequence.

ACCESSION BQ595717

VERSION BQ595717.1 GI:26125300

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)

AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weissshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissshaar@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 22 row: H column: 07

Seq primer: SP6; CATACGATTAGTGACACTATAG.

Location/Qualifiers

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/organism="Beta vulgaris"

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/mol_type="mRNA"
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/db_xref="taxon:161934"
/clone="024-022-H07"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match

Best Local Similarity 100.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAAAAAAAAAAAAA 16

RESULT 617

CF279325/c

LOCUS

DEFINITION CF279325 16 bp mRNA linear EST 14-AUG-2003
14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-J09, mRNA sequence.

ACCESSION CF279325

VERSION CF279325.1 GI:33656711

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .16

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ETL--05-J09"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 618
CF311057/c
LOCUS
DEFINITION ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
ACCESSION CF311057
VERSION CF311057.1 GI:33682818
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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line."

Query Match 0.9%; Score 16; DB 1; Length 16;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 619
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LOCUS
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ACCESSION CF314377
VERSION CF314377.1 GI:33686138
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (ABF)"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 16; DB 1; Length 16;
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Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 620
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ACCESSION CF315789
VERSION CF315789.1 GI:33687550
KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 16; DB 1; Length 16;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 620
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LOCUS
DEFINITION HD--04-N10.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
ACCESSION CF315789
VERSION CF315789.1 GI:33687550
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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line."

Query Match 0.9%; Score 16; DB 1; Length 16;
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Db 16 CAAAAAAAAAAAAAAAAA 1

RESULT 624
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LOCUS
DEFINITION
HD--11-D14.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
Db 16 CAAAAAAAAAAAAAAAAA 1

RESULT 624
CF320356/c
LOCUS
DEFINITION
HD--11-D14.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 625
CF327722/c
LOCUS
DEFINITION
NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-F06, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 626
CF327923/c
LOCUS
DEFINITION
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sativa cDNA clone NACL--02-J18, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
```


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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Db 16 CAAAAAAAAAAAAA 1

RESULT 627

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LOCUS
DEFINITION
NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-A10, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

CONTACT: Nahm B.H.

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Db 16 CAAAAAAAAAAAAA 1

RESULT 628

CF333386
LOCUS
DEFINITION
JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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RESULT 629

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cDNA clone 024-019-E19 3-PRIME, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 17)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.9%; Score 16; DB 1; Length 17;
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Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 630
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sativa cDNA clone 30DGS--04-E17, mRNA sequence.
ACCESSION
CF294668
VERSION
CF294668.1 GI:33663701
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 630
CF294668/c
LOCUS
DEFINITION
30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--04-E17, mRNA sequence.
ACCESSION
CF294668
VERSION
CF294668.1 GI:33663701
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1. .17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--04-E17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 632
CF295988/c
LOCUS
DEFINITION
30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--06-C17, mRNA sequence.
ACCESSION
CF295988
VERSION
CF295988.1 GI:33665021
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1. .17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--06-C17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 632
CF295988/c
LOCUS
DEFINITION
30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--06-C17, mRNA sequence.
ACCESSION
CF295988
VERSION
CF295988.1 GI:33665021
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1. .17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--06-C17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 632
CF295988/c
LOCUS
DEFINITION
30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--06-C17, mRNA sequence.
ACCESSION
CF295988
VERSION
CF295988.1 GI:33665021
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

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CF297251/c
LOCUS       CF297251                17 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION   30DGS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
              sativa cDNA clone 30DGS--07-P12, mRNA sequence.
ACCESSION    CF297251
VERSION      CF297251.1  GI:33666284
KEYWORDS     EST.
SOURCE       Oryza sativa
             Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--07-P12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA...AAAAA 1750
Db      16 CAAAAA...AAAAA 1

RESULT 633
CF298341/c
LOCUS       CF298341                17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--01-K24, mRNA sequence.
ACCESSION    CF298341
VERSION      CF298341.1  GI:33670102
KEYWORDS     EST.
SOURCE       Oryza sativa
             Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..17
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="30DGS--07-P12"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA...AAAAA 1750
Db      16 CAAAAA...AAAAA 1

RESULT 633
CF298341/c
LOCUS       CF298341                17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--01-K24, mRNA sequence.
ACCESSION    CF298341
VERSION      CF298341.1  GI:33670102
KEYWORDS     EST.
SOURCE       Oryza sativa
             Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--01-K24"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA...AAAAA 1750
Db      16 CAAAAA...AAAAA 1

RESULT 634
CF302447/c
LOCUS       CF302447                17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--07-P11, mRNA sequence.
ACCESSION    CF302447
VERSION      CF302447.1  GI:33674208
KEYWORDS     EST.
SOURCE       Oryza sativa
             Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-P11"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAA...AAAAA 1751
Db      16 AAAAAA...AAAAA 1

RESULT 635
CF302447/c
LOCUS       CF302447                17 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--07-P11, mRNA sequence.
ACCESSION    CF302447
VERSION      CF302447.1  GI:33674208
KEYWORDS     EST.
SOURCE       Oryza sativa
             Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
```

```
RESULT 635
CF313013/c
LOCUS
DEFINITION
ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-P19, mRNA sequence.
CF313013
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1.17
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="ABF--08-P19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 636
CF336950/c
LOCUS
DEFINITION
JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.
CF336950
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1.17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--08-P19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 637
CF300236/c
LOCUS
DEFINITION
7LEAF--04-I24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-I24, mRNA sequence.
CF300236
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1.19
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-I24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1.17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-D04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 637
CF300236/c
LOCUS
DEFINITION
7LEAF--04-I24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-I24, mRNA sequence.
CF300236
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1.19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-I24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/db_xref="taxon:10090"
/clone="UUGC1M0560L07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.9%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
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Db 1 AAAAAAAAAAAAAA 16

RESULT 641
CF336815/c

LOCUS

DEFINITION JMT--07-A04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-A04, mRNA sequence.

ACCESSION CF336815.1 GI:33822012
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..20

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="JMT--07-A04"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750
|||||
Db 16 CAAAAAAAAAAAAA 1

RESULT 642

CF282313

LOCUS

DEFINITION

CF282313 21 bp mRNA linear EST 14-AUG-2003

Oryza sativa cDNA clone 14ETL--09-M08, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 21)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..21

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ETL--09-M08"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750
|||||
Db 6 CAAAAAAAAAAAAA 21

RESULT 643

AZ316019

LOCUS

DEFINITION

clone UUGC1M0033C05 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

AZ316019 21 bp DNA linear GSS 29-SEP-2000

1M0033C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0033C05 R, genomic survey sequence.

Accession AZ316019

Version AZ316019.1 GI:10363426

Keywords GSS.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

source
Location/Qualifiers
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-01-G09"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
||| ||||| ||||| |||||
Db 1 AAGGAAAAAAAAAAAAAAAA 19

RESULT 646
CF329137
LOCUS
DEFINITION
NACL--04-F15.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-F15, mRNA sequence.
ACCESSION
CF329137
VERSION
CF329137.1 GI:33806511
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

source
Location/Qualifiers
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-F15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
||| ||||| ||||| |||||
Db 1 AAAGATAAAAAAAAAAAAAA 19

RESULT 647
AZ345499/c
LOCUS
DEFINITION
1M0080F06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080F06 F, genomic survey sequence.
ACCESSION
AZ345499
VERSION
AZ345499.1 GI:10424736
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: F column: 06
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
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Db 19 AAAAAAAAAAGAAAAA 1

RESULT 648

AZ509929 19 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0354A07 F, genomic survey sequence.

ACCESSION AZ509929
VERSION AZ509929.1 GI:10691245
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0354 row: A column: 07
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0354A07"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
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Db 1 AAAAAAAAAAAATTAA 19

RESULT 649

AZ611602/c 19 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0438G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0438G03 F, genomic survey sequence.

ACCESSION AZ611602
VERSION AZ611602.1 GI:11733792
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0438 row: G column: 03
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers
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/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
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Db 19 AAAAAAAAAAACCAAAA 1

RESULT 650
AZ775624 19 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0008E01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0008E01 R, genomic survey sequence.

ACCESSION AZ775624
VERSION AZ775624.1 GI:12902356
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: E column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0008E01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAA 1752
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Db 1 ACACACAAAAAAAAAAAA 19

RESULT 651
AZ786336/c

LOCUS 19 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0031H17 R, genomic survey sequence.

ACCESSION AZ786336

VERSION AZ786336.1 GI:12923992

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0031 row: H column: 17

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

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/db_xref="taxon:10090"

/clone="UUGC2M0031H17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@piz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: H column: 16
Seq primer: T7; GTAATACGACTCACTATAGGCGC.

FEATURES

source

1..17
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188932"
/clone="024-017-H16"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match

0.9%; Score 15.4; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 4.3e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAA 1750

Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 655

BQ591588/c

LOCUS

BQ591588 17 bp mRNA linear EST 06-DEC-2002
E012616-024-017-C15-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-C15 5-PRIME, mRNA sequence.

ACCESSION

BQ591588

VERSION

BQ591588.1 GI:26121171

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 17)

Herwig,R.; Schulz,B.; Weissshaar,B.; Hennig,S.; Steinfath,M.;

Drungowski,M.; Stahl,D.; Wruck,W.; Menze,A.; O'Brien,J.; Lehrach,H.

and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

PUBMED

12472698

Contact: Weissshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissshaar@piz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 17 row: C column: 15

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES

source

Location/Qualifiers

1..17

/organism="Beta vulgaris"

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/db_xref="GABI:188532"
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/clone="024-017-C15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match

0.9%; Score 15.4; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 4.3e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752

Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 656

CF276637

LOCUS

DEFINITION

CF276637

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

Kim,J.S.; Jun,K.M.; Cheong,P.J.; Kim,M.J.; Lee,T.H.; Shin,Y.C.;

Song,S.I.; Kim,J.K.; Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..17

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ETL--01-N18"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

0.9%; Score 15.4; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 4.3e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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Db 1 AAAAAACAAAAAAAAAAAAA 17

RESULT 657
CF291802/c
LOCUS 1736 AAAAAAAAAAAAAAAAAA 1752 linear EST 14-AUG-2003
DEFINITION 14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION CF291802
VERSION CF291802.1 GI:33660835
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ROOT--02-G05"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAACAAAAAAAAAAAAA 17

RESULT 658
CF299997/c
LOCUS 1736 AAAAAAAAAAAAAAAAAA 1752 linear EST 15-AUG-2003
DEFINITION 7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-D19, mRNA sequence.
ACCESSION CF299997
VERSION CF299997.1 GI:33671758
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ROOT--02-G05"
/tissue_type="root"
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAACAAAAAAAAAAAAA 17

RESULT 659
CF319075/c
LOCUS 1736 AAAAAAAAAAAAAAAAAA 1752 linear EST 15-AUG-2003
DEFINITION HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence.
ACCESSION CF319075
VERSION CF319075.1 GI:33690836
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
```

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES source
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAAAAAAAAAAA 1750
Db 17 AGAAAAAAAAAAAAAAAAAA 1

RESULT 659
CF319075/c
LOCUS 1734 ACACAAAAAAAAAAAAAA 1750 linear EST 15-AUG-2003
DEFINITION HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence.
ACCESSION CF319075
VERSION CF319075.1 GI:33690836
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES source
Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
/clone="HD--09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 4.3e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1750
 Db 17 ATAAAAAAAAAAAAAAAA 1

RESULT 660
 AA953971

LOCUS
 DEFINITION
 AA953971 19 bp mRNA linear EST 07-JUL-1998
 o088h01.s1 NCI CGAP Kid5 Homo sapiens cDNA clone IMAGE:1573297 3'
 similar to TR:Q00484 Q00484 MINI-COLLAGEN PRECURSOR ; contains
 element MSR1 repetitive element ;, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

FEATURES
 source
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:1573297"
 /tissue_type="2 pooled tumors (clear cell type)"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Kid5"
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 AACTGGAGCAATTCGGCGCGCAATATTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match 0.9%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 4.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 GCCCTCCCGGCCCC 754
 Db 2 GCCCGCCCGGCCCC 18

RESULT 661
 CF297010/c

LOCUS
 DEFINITION
 CF297010 20 bp mRNA linear EST 14-AUG-2003
 30DGS--07-J24.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 sativa cDNA clone 30DGS--07-J24, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .20
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--07-J24"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.9%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1750
 Db 17 ACCAAAAAAAAAAAAAAAA 1

RESULT 662
 AZ316368

LOCUS
 DEFINITION
 AZ316368 20 bp DNA linear GSS 29-SEP-2000
 1M0034L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0034L22 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: L column: 22
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034L22"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAATTTAA 20

RESULT 663

AZ345646

LOCUS

DEFINITION AZ345646 20 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0080K20 F, genomic survey sequence.

ACCESSION AZ345646

VERSION AZ345646.1 GI:10424883

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: K column: 20
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080K20"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1753
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Db 1 ACAAACATTAAAAAAAAAAAAA 20

RESULT 664

AZ368518

LOCUS

DEFINITION AZ368518 20 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0118G09 R, genomic survey sequence.

ACCESSION AZ368518

VERSION AZ368518.1 GI:10482218

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE

AUTHORS

1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0118 row: G column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0118G09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1733 TACAAAAA...AAAAA 1752
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Db 1 TATTAAAAA...AACAAAA 20

RESULT 665
AZ959504 20 bp DNA linear GSS 27-APR-2001
LOCUS 2M027N12F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M027N12 F, genomic survey sequence.
ACCESSION AZ959504
VERSION AZ959504.1 GI:13830731
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0227 row: N column: 12
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Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0227N12"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 25 GGGGGAAGAGGAAAAA 44
||||| | ||||| |||||
Db 1 GGGGGGGGGGAAAAA 20

RESULT 666
BE230585 15 bp mRNA linear EST 07-JUL-2000
LOCUS 99AS799 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa
DEFINITION (indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION BE230585
VERSION BE230585.1 GI:8956782
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of ESTs from Rice Seedling
JOURNAL Unpublished (1999)
COMMENT Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr.
Location/Qualifiers
1. .15
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="Milyang23"

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/db_xref="taxon:39946"
/clone="99AS799"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 667
BQ582543/c
LOCUS
DEFINITION S013300-024-007-B02-T7 MP1Z-ADIS-024-inflorescence Beta vulgaris
CDNA clone 024-007-B02 3-PRIME, mRNA sequence.
ACCESSION BQ582543
VERSION BQ582543.1 GI:26112120
KEYWORDS
SOURCE
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 7 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.
FEATURES
source
Location/Qualifiers
1..15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
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/clone="024-007-B02"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
orientation:
SP6-Sall-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match
0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 669
BQ585820/c
LOCUS
DEFINITION E012533-024-014-H17-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-014-H17 5-PRIME, mRNA sequence.
ACCESSION BQ585820
VERSION BQ585820.1 GI:26115402
KEYWORDS
SOURCE
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 14 row: H column: 17
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
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line)"
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/clone="024-014-H17"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
orientation:
SP6-Sall-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match
0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 669
BQ590410/c
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LOCUS BQ590410 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012844-024-019-M08-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-M08 3-PRIME, mRNA sequence.
ACCESSION BQ590410
VERSION BQ590410.1 GI:26119993
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R.; Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL 22362189
MEDLINE 12472698
PUBMED
COMMENT Contact: Weissshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaampiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 19 row: M column: 08
Seq primer: T7; GTAATACGACTCACTATAGGCG.
FEATURES
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/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

RESULT 670
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LOCUS S015086-024-018-L13-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-018-L13 5-PRIME, mRNA sequence.
ACCESSION BQ590656
VERSION BQ590656.1 GI:26120239
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R.; Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL 22362189
MEDLINE 12472698
PUBMED
COMMENT Contact: Weissshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaampiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 18 row: L column: 13
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES
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/db_xref="GABI:189464"
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

RESULT 671
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DEFINITION cDNA clone 024-017-N18 3-PRIME, mRNA sequence.
ACCESSION BQ591170
VERSION BQ591170.1 GI:26120753
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R.; Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL 22362189
MEDLINE 12472698
PUBMED

[illegible]

/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 674
BQ594689/c
LOCUS
DEFINITION BQ594689 15 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-024-M05-T7 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-024-M05 3-PRIME, mRNA sequence.

ACCESSION BQ594689
VERSION BQ594689.1 GI:26124272
KEYWORDS EST.

SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 15)

AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weissshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissshaar@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Plate: 24 row: M column: 05

Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES

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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="GABI:192163"
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/tissue_type="developing root"
/lab_host="EMDH10B"

/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:

SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 675
CF277319/c

LOCUS

DEFINITION

CF277319

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..15

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/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

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/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

RESULT 676

CF281923/c

LOCUS

DEFINITION

CF281923

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-D04"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 15; DB 1; Length 15;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 677
CF290920/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF290920 15 bp mRNA linear EST 14-AUG-2003
14ROOT--01-C09.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-C09, mRNA sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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FEATURES

source

1..15
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-C09"
/tissue_type="root"
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/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 678
CF291029/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF291029 15 bp mRNA linear EST 14-AUG-2003
14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-E19, mRNA sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF291029 GI:33660062
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 15)
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FEATURES

source

1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-E19"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 679
CF291103/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF291103 15 bp mRNA linear EST 14-AUG-2003
14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-G10, mRNA sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF291103 GI:33660136
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

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Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..15

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone_lib="Rice root plasmid cDNA library (14ROOT)"

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with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 0.9%; Score 15; DB 1; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

|||||

15 AAAAAAAAAAAAAA 1

RESULT 680

CF291717/c

LOCUS

14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa cDNA clone 14ROOT--02-E04, mRNA sequence.

CF291717

CF291717.1 GI:33660750

EST.

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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FEATURES

source

1..15

/organism="Oryza sativa"

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/cultivar="Nackdong"

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/tissue_type="root"

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/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 0.9%; Score 15; DB 1; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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15 AAAAAAAAAAAAAA 1

RESULT 681

CF291798/c

LOCUS

14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa cDNA clone 14ROOT--02-G02, mRNA sequence.

CF291798

CF291798.1 GI:33660831

EST.

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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FEATURES

source

1..15

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

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/tissue_type="root"

/dev_stage="14 days after germination"

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/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

|||||

15 AAAAAAAAAAAAAA 1

RESULT 682

CF292458/c

LOCUS

30DGS--01-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza

sativa cDNA clone 30DGS--01-E17, mRNA sequence.

CF292458

CF292458.1 GI:33661491

EST.

Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

RESULT 683
CF292461/c
LOCUS 15 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--01-E19, mRNA sequence.
ACCESSION CF292461
VERSION CF292461.1 GI:33661494
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"

/dev_stage="30 days after germination"
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RT-PCR."

Query Match 0.9%; Score 15; DB 1; Length 15;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

RESULT 684
CF296652/c
LOCUS 15 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--07-C02, mRNA sequence.
ACCESSION CF296652
VERSION CF296652.1 GI:33665685
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1..15
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 CAAAAAAAAAAAAA 1

RESULT 685
CF298148/c
LOCUS 15 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-G17, mRNA sequence.
ACCESSION CF298148
VERSION CF298148.1 GI:33669909
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .15

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 0.9%; Score 15; DB 1; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750

|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 686

CF298630/c

LOCUS

DEFINITION 7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--02-B23, mRNA sequence.

CF298630

CF298630.1 GI:33670391

EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .15

/organism="Oryza sativa"

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Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

RESULT 687

CF298733/c

LOCUS

DEFINITION 7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--02-E20, mRNA sequence.

CF298733

CF298733.1 GI:33670494

EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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FEATURES

source

1. .15

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

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Query Match

Best Local Similarity 100.0%; Score 15; DB 1; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

RESULT 688

CF298805/c

LOCUS

DEFINITION 7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--02-G20, mRNA sequence.

CF298805

CF298805.1 GI:33670566

15 bp mRNA linear EST 15-AUG-2003


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KEYWORDS
SOURCE   Oryza sativa
ORGANISM  Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..15
/organism="Oryza sativa"
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Query Match      0.9%; Score 15; DB 1; Length 15;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

RESULT 689
CF298889/c
LOCUS      7LEAF--02-J09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-J09, mRNA sequence.
ACCESSION  CF298889
VERSION     CF298889.1 GI:33670650
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 689
CF298889/c
LOCUS      7LEAF--02-J09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-J09, mRNA sequence.
ACCESSION  CF298889
VERSION     CF298889.1 GI:33670650
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

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Db 15 AAAAAAAAAAAAAA 1

RESULT 691
CF299608/c
LOCUS      7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-L04, mRNA sequence.
ACCESSION  CF299608
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

RESULT 690
CF299602/c
LOCUS      7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
ACCESSION  CF299602
VERSION     CF299602.1 GI:33671363
KEYWORDS   EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
      |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 691
CF299608/c
LOCUS      7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-L04, mRNA sequence.
ACCESSION  CF299608
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[illegible]

ACCESSION CF300992
VERSION CF300992.1 GI:33672753
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Query Match 0.9%; Score 15; DB 1; Length 15;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

RESULT 695
CF302034/c
LOCUS
DEFINITION 7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-C24, mRNA sequence.
ACCESSION CF302034
VERSION CF302034.1 GI:33673795
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

RESULT 696
CF302124/c
LOCUS
DEFINITION 7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-F16, mRNA sequence.
ACCESSION CF302124
VERSION CF302124.1 GI:33673885
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 697
CF302182/c
LOCUS
DEFINITION 7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

Accession: CF302182
Version: CF302182.1
Keywords: EST
Source: Oryza sativa
Organism: Oryza sativa
Reference: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
Authors: Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Title: Large-scale Sequencing Analysis of Rice ESTs
Journal: Unpublished (2003)
Comment: Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/mol_type="mRNA"
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Query Match: 0.9%; Score 15; DB 1; Length 15;
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Matches: 15; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

Result: 698
Locus: CF307923/c
Definition: ABF--01-I15.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--01-I15, mRNA sequence.
Accession: CF307923
Version: CF307923.1
Keywords: EST
Source: Oryza sativa
Organism: Oryza sativa
Reference: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
Authors: Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Title: Large-scale Sequencing Analysis of Rice ESTs
Journal: Unpublished (2003)
Comment: Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

source

1. .15
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match: 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity: 100.0%; Pred. No. 4.4e+02;
Matches: 15; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

Result: 699

Locus: CF311159/c

Definition: ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--06-E11, mRNA sequence.

Accession: CF311159

Version: CF311159.1

Keywords: EST

Source: Oryza sativa

Organism: Oryza sativa

Reference: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

Authors: Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Title: Large-scale Sequencing Analysis of Rice ESTs

Journal: Unpublished (2003)

Comment: Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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Query Match: 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity: 100.0%; Pred. No. 4.4e+02;
Matches: 15; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1736 AAAAAAAAAAAAAA 1750
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Db 15 AAAAAAAAAAAAAA 1

RESULT 700
CF311907/c
LOCUS
DEFINITION ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-G04, mRNA sequence.
ACCESSION CF311907
VERSION CF311907.1 GI:33683668
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Location/Qualifiers
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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
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Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 701
CF313319/c
LOCUS
DEFINITION HD--01-G13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.
ACCESSION CF313319
VERSION CF313319.1 GI:33685080
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 702
CF313320
LOCUS
DEFINITION HD--01-G13.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.
ACCESSION CF313320
VERSION CF313320.1 GI:33685081
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/mol_type="mRNA"
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/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 703
CF316251
LOCUS
DEFINITION HD--05-H15.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.

ACCESSION CF316251
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. 15
/organism="Oryza sativa"
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Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 704
CF318035/c
LOCUS
DEFINITION HD--07-P06.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.

ACCESSION CF318035
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--05-H15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Oryza `sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
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/organism="Oryza sativa"
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/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 705
CF327434/c
LOCUS
DEFINITION NACL--01-O18.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-O18, mRNA sequence.

ACCESSION CF327434
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1. 15
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/mol_type="mRNA"
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Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 709
 CF336202/c
 LOCUS
 DEFINITION JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-C20, mRNA sequence.
 ACCESSION CF336202
 VERSION CF336202.1 GI:33820794
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .15

/organism="Oryza sativa"
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Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 710

BQ590507/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BQ590507 16 bp mRNA linear EST 06-DEC-2002
 E012844-024-019-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris cDNA clone 024-019-M04 3-PRIME, mRNA sequence.

BQ590507.1 GI:26120090

EST.
 Beta vulgaris
 Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,J.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

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Seq primer: T7; GTAATACGACTCATATAGGC.

FEATURES

source

Location/Qualifiers
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 /cultivar="KWS2320 (double haploid, monogerm breeding line)"

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/db_xref="taxon:161934"

/clone="024-019-M04"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and orientation:

SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 711

BQ595369/c

LOCUS

DEFINITION S013317-024-022-P02-T7 MP1Z-ADIS-024-developing root Beta vulgaris cDNA clone 024-022-P02 3-PRIME, mRNA sequence.

BQ595369.1 GI:26124952

EST.

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: P column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
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line)"
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
source

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 713
CF314013/c

LOCUS CF314013 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-G01.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa clone HD--02-G01, mRNA sequence.

ACCESSION CF314013
VERSION CF314013.1 GI:33685774
KEYWORDS EST.

SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .16

FEATURES
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/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="OSHAC1-overexpressing transgenic rice plasmid
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;

CF296130 16 bp mRNA linear EST 14-AUG-2003
30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--06-F22, mRNA sequence.
CF296130
CF296130.1 GI:33665163
EST.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

RESULT 712
CF296130/c

LOCUS CF296130 16 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--06-F22, mRNA sequence.

ACCESSION CF296130
VERSION CF296130.1 GI:33665163
KEYWORDS EST.

SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 714
CF329320/c
LOCUS
DEFINITION
NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-J17, mRNA sequence.
ACCESSION
CF329320
VERSION
CF329320.1 GI:33806877
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 715
CF311499/c
LOCUS
DEFINITION
ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION
CF311499
VERSION
CF311499.1 GI:33683260
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
COMMENT
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..17
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 716
CF301359/c
LOCUS
DEFINITION
7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-D05, mRNA sequence.
ACCESSION
CF301359
VERSION
CF301359.1 GI:33673120
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..18
/organism="Oryza sativa"
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/db_xref="taxon:4530"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 717
CF309376/c
LOCUS
DEFINITION ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-I19, mRNA sequence.
ACCESSION CF309376.1 GI:33681137
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--03-I19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 718
CF329484/c
LOCUS
DEFINITION NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION CF329484.1 GI:33807207
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-N06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 719
CF329485
LOCUS
DEFINITION NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION CF329485
VERSION CF329485.1 GI:33807209
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-N06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"


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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
    |||||
Db 4 AAAAAAAAAAAAAA 18

RESULT 720
CF308042/c
LOCUS
DEFINITION ABF--01-L07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-L07, mRNA sequence.
ACCESSION CF308042
VERSION CF308042.1 GI:33679803
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--01-L07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.9%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
    |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 721
CF313751/c
LOCUS
DEFINITION HD--01-P23.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.
ACCESSION CF313751
```

```
CF313751.1 GI:33685512
EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-P23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1749
    |||||
Db 15 CAAAAAAAAAAAAA 1

RESULT 722
CF313752
LOCUS
DEFINITION HD--01-P23.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.
ACCESSION CF313752
VERSION CF313752.1 GI:33685513
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..20
```



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/organism="Oryza sativa"  
/mol_type="mRNA"  
/cultivar="Nackdong"  
/db_xref="taxon:4530"  
/clone="HD--01-P23"  
/tissue_type="callus"  
/dev_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab_host="E.coli DH10B"  
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."
```

```
Query Match      0.9%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1735 CAAAAAAAAAAAAA 1749  
Db 6 CAAAAAAAAAAAAA 20
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RESULT 723  
CF331733  
LOCUS  
DEFINITION  
NACL--07-P15.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--07-P15, mRNA sequence.
```

```
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
CF331733.1 GI:33811693  
EST.
```

```
ORGANISM  
Oryza sativa
```

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.
```

```
REFERENCE  
1 (bases 1 to 20)
```

```
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

```
TITLE  
JOURNAL  
COMMENT  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)
```

```
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355
```

```
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
```

```
FEATURES  
Location/Qualifiers
```

```
1..20
```

```
/organism="Oryza sativa"  
/mol_type="mRNA"  
/cultivar="Nackdong"  
/db_xref="taxon:4530"  
/clone="NACL--07-P15"  
/tissue_type="callus"
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/dev_stage="proliferated callus on 2N6 media for 30 days"  
/lab_host="E.coli DH10B"  
/clone_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."
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```
Query Match      0.9%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAAA 1750  
Db 1 AAAAAAAAAAAAAA 15
```

```
RESULT 724  
AW246505/c
```

```
LOCUS  
DEFINITION
```

```
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
Homo sapiens (human)
```

```
ORGANISM  
Homo sapiens
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE  
1 (bases 1 to 18)
```

```
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NIH-MGC http://mgc.nci.nih.gov/.
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National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)
```

```
Other_ESTs: 2821585.5prime  
Contact: Robert Strausberg, Ph.D.
```

```
Email: cgapbs@mail.nih.gov
```

```
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:
```

```
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector
```

```
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
```

```
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 18
```

```
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 18 contiguous distinct
```

```
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues
```

```
at the beginning of the sequence, this cDNA insert was  
polyadenylated.
```

```
Plate: L1CM7 row: D column: 2
```

```
High quality sequence stop: 18.
```

```
FEATURES  
Location/Qualifiers
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source
```

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1..18
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/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="IMAGE:2821585"  
/tissue_type="small cell carcinoma"  
/cell_line="MGC3"  
/lab_host="DH10B (phage-resistant)"  
/clone_lib="NIH_MGC_7"
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```
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally
```

```
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average
```

```
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of
```

```
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
Query Match      0.8%; Score 14.8; DB 1; Length 18;
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```
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
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```
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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Qy 1736 AAAAAAAAAAAAAA 1753
```

```
|||||
```

```
Db 18 AATAAAGAAAAA 1
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```
RESULT 725  
CF309858
```

```
LOCUS  
DEFINITION
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```
CF309858  
ABF--04-D16.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--04-D16, mRNA sequence.
```

```
ACCESSION  
CF309858
```

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VERSION      CF309858.1  GI:33681619
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoidae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT      Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--04-D16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAA 1753
        |||||
Db      2 AAAAAAAAAAAAAAAAAACATA 19

RESULT 726
AZ775540
LOCUS      AZ775540      19 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION 2M0008H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0008H15 F, genomic survey sequence.
ACCESSION  AZ775540
VERSION     AZ775540.1  GI:12902183
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: H column: 15
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0008H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      861 AGGAAGAGGAGGAGGAGG 878
        |||||
Db      1 AGGAGGAGGAGGAGGAGG 18

RESULT 727
AI954491
LOCUS      AI954491      43 bp      mRNA      linear      EST 09-MAR-2000
DEFINITION wx83d04.x1 NCI_CGAP Ov38 Homo sapiens cDNA clone IMAGE:2550247 3'
similar to SW:TRI6_HUMAN Q15654 THYROID RECEPTOR INTERACTING
PROTEIN 6 ;, mRNA sequence.
ACCESSION  AI954491
VERSION     AI954491.1  GI:5746801
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 43)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL
COMMENT      Unpublished (1997)
               Contact: Robert Strausberg, Ph.D.
               Email: cgaps-r@mail.nih.gov
               Tissue Procurement: Jeff Struewing, M.D., Michael R. Emmert-Buck,
               M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA
               Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA
               Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
```

Trace considered overall poor quality
Insert Length: 1014 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2550247"
/tissue_type="normal epithelium"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ov38"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."

Query Match 0.8%; Score 14.8; DB 1; Length 43;
Best Local Similarity 64.7%; Pred. No. 6.2e+02;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 680 TGGCACACCCAGTACGGGGCTGCGGCCACCCAG 713
|||||
Db 2 TGGCTACGCACTACGGCCCCACCGCACCCGAG 35

RESULT 728
AW246490/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW246490 16 bp mRNA linear EST 07-JAN-2000
2821591.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821591 3',
mRNA sequence.
AW246490
AW246490.1 GI:6589483
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821591.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
<http://www.llnl.gov/bhrp/image/image.html> Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu/LowQuality> Sequence: 12
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM7 row: D column: 8
High quality sequence stop: 12.
Location/Qualifiers
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821591"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1730 GTTTACAAAAA 1745
|||||
Db 16 GTTTCAAAAA 1

RESULT 729
CF312586/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF312586 16 bp mRNA linear EST 15-AUG-2003
ABF--08-G13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-G13, mRNA sequence.
CF312586
CF312586.1 GI:33684347
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 16)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaem@gbio.com, bhnaem@bio.myongji.ac.kr.
Location/Qualifiers
1. .16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--08-G13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

FEATURES
source

Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1746
|||||
Db 16 TTTAAAAA 1

RESULT 730
CF317778/c

LOCUS CF317778 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-J13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--07-J13, mRNA sequence.

ACCESSION CF317778
VERSION CF317778.1 GI:33689539
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1..16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--07-J13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db 16 AAAAAAAAAAACAA 1

RESULT 731
AW247165/c
LOCUS AW247165 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2819675.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819675 3', mRNA sequence.

ACCESSION AW247165
VERSION AW247165.1 GI:6590158
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819675.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 17 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence.
Plate: LLCM2 row: D column: 12
High quality sequence stop: 17.

FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819675"
/tissue_type="small cell carcinoma"
/cell_line="WGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 732
AU102453/c
LOCUS AU102453 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU102453 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS11875, mRNA sequence.

ACCESSION AU102453
VERSION AU102453.1 GI:13551973
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS11875"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 0.8%; Score 14.2; DB 1; Length 50;
Best Local Similarity 70.4%; Pred. No. 6.4e+02;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 531 GCCCCGCCACCTCTCGCTACCGCAC 557
Db 49 GCCTTCAACCCCTCTTCGTCGCCGCAC 23

RESULT 733
BQ586422/c
LOCUS
DEFINITION BQ586422 14 bp mRNA linear EST 06-DEC-2002
024-013-002 3-PRIME, mRNA sequence.
ACCESSION BQ586422
VERSION BQ586422.1 GI:26116004
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 13 row: 0 column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.
FEATURES
source
1..14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:186441"
/db_xref="taxon:161934"
/clone="024-013-002"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 734
BQ587890/c
LOCUS
DEFINITION BQ587890 14 bp mRNA linear EST 06-DEC-2002
S013302-024-009-B02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
024-009-B02 3-PRIME, mRNA sequence.
ACCESSION BQ587890
VERSION BQ587890.1 GI:26117472
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 9 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.
FEATURES
source
1..14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:184980"
/db_xref="taxon:161934"
/clone="024-009-B02"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 735
BQ589191/c
LOCUS
DEFINITION BQ589191 14 bp mRNA linear EST 06-DEC-2002
S014009-024-015-I20-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-015-I20 3-PRIME, mRNA sequence.
ACCESSION BQ589191

VERSION BQ589191.1 GI:26118774
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 15 row: 1 column: 20
Seq primer: T7; GTAATACGACTCACTATAGGC.
Location/Qualifiers
1. .14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:187878"
/db_xref="taxon:161934"
/clone="024-015-120"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 736
BQ590242/c
LOCUS
DEFINITION E012840-024-019-E16-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-019-E16 5-PRIME, mRNA sequence.
ACCESSION BQ590242
VERSION BQ590242.1 GI:26119825
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 19 row: E column: 16
Seq primer: SP6; CATACGATTAGTGCACACTATAG.
Location/Qualifiers
1. .14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189878"
/db_xref="taxon:161934"
/clone="024-019-E16"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 737
BQ590261/c
LOCUS
DEFINITION BQ590261 14 bp mRNA linear EST 06-DEC-2002
E012844-024-019-K14-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-019-K14 3-PRIME, mRNA sequence.
ACCESSION BQ590261
VERSION BQ590261.1 GI:26119844
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
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Db 14 AAAAAAAAAAAAAA 1

RESULT 740
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LOCUS
DEFINITION E012715-024-017-B04-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-B04 3-PRIME, mRNA sequence.
ACCESSION BQ591207
VERSION BQ591207.1 GI:26120790
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188904"
/db_xref="taxon:161934"
/clone="024-017-B04"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;

QY 1736 AAAAAAAAAAAAAA 1749
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Db 14 AAAAAAAAAAAAAA 1

RESULT 740
BQ591482/c
LOCUS
DEFINITION E012715-024-017-B04-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-B04 3-PRIME, mRNA sequence.
ACCESSION BQ591482
VERSION BQ591482.1 GI:26120963
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: B column: 04
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Location/Qualifiers
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/clone="024-017-B15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
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Db 14 AAAAAAAAAAAAAA 1

RESULT 741
BQ591380/c
LOCUS
DEFINITION E012714-024-017-B15-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-B15 3-PRIME, mRNA sequence.
ACCESSION BQ591380
VERSION BQ591380.1 GI:26120963
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: B column: 15
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1. .14
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/db_xref="GABI:188734"
/db_xref="taxon:161934"
/clone="024-017-B15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 14 AAAAAAAAAAAAAA 1

RESULT 742
BQ591482/c
LOCUS
DEFINITION E012714-024-017-B15-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-B15 3-PRIME, mRNA sequence.
ACCESSION BQ591482
VERSION BQ591482.1 GI:26120963
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: B column: 15
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1. .14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188734"
/db_xref="taxon:161934"
/clone="024-017-B15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 14 AAAAAAAAAAAAAA 1

RESULT 742
BQ591482/c
LOCUS
DEFINITION E012714-024-017-B15-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-B15 3-PRIME, mRNA sequence.
ACCESSION BQ591482
VERSION BQ591482.1 GI:26120963
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

DEFINITION E012713-024-017-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-M04 3-PRIME, mRNA sequence.
ACCESSION BQ591482
VERSION BQ591482.1 GI:26121065
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: M column: 04
Seq primer: T7; GTATACGACTCACTATAGGCG.
FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188633"
/db_xref="taxon:161934"
/clone="024-017-M04"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
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Db 14 AAAAAAAAAAAAAA 1

RESULT 743
BQ593052/c
LOCUS BQ593052
DEFINITION E012375-024-028-C03-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
CDNA clone 024-028-C03 5-PRIME, mRNA sequence.
ACCESSION BQ593052
VERSION BQ593052.1 GI:26122635
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 28 row: C column: 03
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
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Location/Qualifiers
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line)"
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/clone="024-028-C03"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
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Db 14 AAAAAAAAAAAAAA 1

RESULT 744
CF277935/c
LOCUS CF277935
DEFINITION 14ETL--03-K11.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--03-K11, mRNA sequence.
ACCESSION CF277935
VERSION CF277935.1 GI:33655321
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

FEATURES		Fax: 82 31 321 6355		Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.			
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		/tissue_type="leaf"					
		/dev_stage="14 days after germination"					
		/lab_host="E.coli DH10B"					
		/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"					
		/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."					
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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/organism="Oryza sativa"
/mol_type="mRNA"
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/clone_lib="Rice etiolated leaf plasmid cDNA library
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 748

CF279992/c
LOCUS
DEFINITION
14ETL--06-I01.b1 14 bp mRNA linear EST 14-AUG-2003
Oryza sativa cDNA clone 14ETL--06-I01, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Yongin, Kyeonggi, Korea
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--06-I01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 749

CF281958/c
LOCUS
DEFINITION
14ETL--09-D24.b1 14 bp mRNA linear EST 14-AUG-2003
Oryza sativa cDNA clone 14ETL--09-D24, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-D24"
/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

Best Local Similarity 100.0%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 750

CF282350/c
LOCUS
DEFINITION
14ETL--09-N05.b1 14 bp mRNA linear EST 14-AUG-2003
Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

REFERENCE

AUTHORS

TITLE
JOURNAL
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
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(14ETL)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 751
CF294449/c

LOCUS
DEFINITION
30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--03-P15, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF294449
CF294449.1 GI:33663482
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
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/clone="30DGS--03-P15"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 752
CF295570/c

LOCUS
DEFINITION
30DGS--05-J06.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--05-J06, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF295570
CF295570.1 GI:33664603
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--05-J06"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 753
CF296120/c

LOCUS
DEFINITION
30DGS--06-F17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--06-F17, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF296120
CF296120.1 GI:33665153
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--06-F17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 754

CF297969/c
LOCUS 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-C16, mRNA sequence.

ACCESSION CF297969
VERSION CF297969.1 GI:33669730

KEYWORDS

EST.

SOURCE

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

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FEATURES

source
Location/Qualifiers
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-C16"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 755

CF298109/c
LOCUS 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-F19, mRNA sequence.

ACCESSION CF298109
VERSION CF298109.1 GI:33669870

KEYWORDS

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT

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FEATURES

source
Location/Qualifiers
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-F19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 756

CF299368/c
LOCUS 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-F21, mRNA sequence.

ACCESSION CF299368
VERSION CF299368.1 GI:33671129

KEYWORDS

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
AUTHORS Ehrhartoidae; Oryzae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-F21"
/tissue_type="leaf"
/dev_stage="7 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 757
CF300542/c
LOCUS 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION CF300542
VERSION CF300542.1 GI:33672303
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 758
CF301020/c
LOCUS 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
ACCESSION CF301020
VERSION CF301020.1 GI:33672781
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 759
CF301083/c
LOCUS 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M19, mRNA sequence.
ACCESSION CF301083
VERSION CF301083.1 GI:33672844
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS 1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-M19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 760

CF301380/c

LOCUS

DEFINITION 7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--06-D16, mRNA sequence.

ACCESSION CF301380.1 GI:33673141

VERSION EST.

KEYWORDS

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..14
/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
/clone="7LEAF--06-D16"
/tissue_type="leaf"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

|||||

Db 14 AAAAAAAAAAAAAA 1

RESULT 761

CF302675/c

LOCUS

DEFINITION 7LEAF--08-G18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--08-G18, mRNA sequence.

ACCESSION CF302675

VERSION CF302675.1 GI:33674436

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

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FEATURES

source

1..14
/organism="Oryza sativa"
/mol_type="mRNA"
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

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Db 14 AAAAAAAAAAAAAA 1

RESULT 762

CF302846/c

LOCUS

DEFINITION 7LEAF--08-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--08-M05, mRNA sequence.

ACCESSION CF302846

VERSION CF302846.1 GI:33674607

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

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JOURNAL

Unpublished (2003)

COMMENT

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FEATURES

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1. .14
/organism="Oryza sativa"
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/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 763

CF308006/c

LOCUS

DEFINITION ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--01-K10, mRNA sequence.

ACCESSION

VERSION CF308006.1 GI:33679767

KEYWORDS

SOURCE EST.

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

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FEATURES

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1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
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/dev_stage="14 days after germination"

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/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 764

CF308220/c

LOCUS

DEFINITION ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.

ACCESSION

VERSION CF308220.1 GI:33679981

KEYWORDS

SOURCE EST.

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

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FEATURES

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1. .14
/organism="Oryza sativa"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 765

CF308445/c

LOCUS

14 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.

ACCESSION CF308445

VERSION CF308445.1 GI:33680206

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

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/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 766

CF308918/c

LOCUS

DEFINITION ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--02-O16, mRNA sequence.

ACCESSION CF308918

VERSION CF308918.1 GI:33680679

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 767

CF310714/c

LOCUS

DEFINITION ABF--05-I11.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--05-I11, mRNA sequence.

ACCESSION CF310714

VERSION CF310714.1 GI:33682475

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Location/Qualifiers

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/organism="Oryza sativa"

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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
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Db 14 AAAAAAAAAAAAAA 1

RESULT 768
CF311201/c
LOCUS
DEFINITION ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-F09, mRNA sequence.
ACCESSION CF311201
VERSION CF311201.1 GI:33682962
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
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/clone="ABF--06-F09"
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cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
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Db 14 AAAAAAAAAAAAAA 1

RESULT 769
CF311813/c
LOCUS
DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.
ACCESSION CF311813
VERSION CF311813.1 GI:33683574
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
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Db 14 AAAAAAAAAAAAAA 1

RESULT 770
CF318323/c
LOCUS
DEFINITION HD--08-G13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--08-G13, mRNA sequence.
ACCESSION CF318323
VERSION CF318323.1 GI:33690084
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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FEATURES
source
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 770
CF318323/c
LOCUS
DEFINITION HD--08-G13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--08-G13, mRNA sequence.
ACCESSION CF318323
VERSION CF318323.1 GI:33690084
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
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FEATURES
source
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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FEATURES
Location/Qualifiers
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
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cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
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Db 14 AAAAAAAAAAAAAA 1

RESULT 770
CF318323/c
LOCUS
DEFINITION HD--08-G13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--08-G13, mRNA sequence.
ACCESSION CF318323
VERSION CF318323.1 GI:33690084
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
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cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 771
CF318450/c
LOCUS
DEFINITION 14 bp mRNA linear EST 15-AUG-2003
library (HD) Oryza sativa cDNA clone HD--08-J08, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..14
/organism="Oryza sativa"
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cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 772
CF319826/c
LOCUS
DEFINITION 14 bp mRNA linear EST 15-AUG-2003
library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.

library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.
CF319826
VERSION
KEYWORDS
SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 773

CF321246/c

LOCUS

DEFINITION

14 bp mRNA linear EST 15-AUG-2003
library (HD) Oryza sativa cDNA clone HD--12-G24, mRNA sequence.

CF321246

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

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Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="callus"
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cDNA library (HD)"
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
14 AAAAAAAAAAAAAA 1
|||||

RESULT 774
CF327097/c
LOCUS
DEFINITION
NACL--01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa CDNA clone NACL--01-H01, mRNA sequence.
CF327097
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1. .14
/organism="Oryza sativa"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
14 AAAAAAAAAAAAAA 1
|||||

RESULT 776
CF327203/c
LOCUS
DEFINITION
NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa CDNA clone NACL--01-J16, mRNA sequence.
CF327203
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1. .14
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
14 AAAAAAAAAAAAAA 1
|||||

RESULT 775
CF327119/c
LOCUS
DEFINITION
NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa CDNA clone NACL--01-H14, mRNA sequence.
CF327119
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
14 AAAAAAAAAAAAAA 1
|||||

RESULT 776
CF327203/c
LOCUS
DEFINITION
NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa CDNA clone NACL--01-J16, mRNA sequence.
CF327203
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
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RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
14 AAAAAAAAAAAAAA 1
|||||

RESULT 775
CF327119/c
LOCUS
DEFINITION
NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa CDNA clone NACL--01-H14, mRNA sequence.
CF327119
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
14 AAAAAAAAAAAAAA 1
|||||
```

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Fax: 82 31 321 6355
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FEATURES

source

Location/Qualifiers
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
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Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA 1748

Db 14 CAAAAA 1

FEATURES

source

Location/Qualifiers
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QY 1735 CAAAAA 1748

Db 14 CAAAAA 1

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .14
/organism="Oryza sativa"
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Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA 1749

QY

Db 14 AAAAAA 1

FEATURES

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Location/Qualifiers
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

QY 1736 AAAAAA 1749

Db 14 AAAAAA 1

REFERENCE

AUTHORS

TITLE

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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .14
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Query Match

Best Local Similarity

Matches

14; Conservative

0; Mismatches

0; Indels

0; Gaps

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Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .14
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/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 780

CF328669/c

LOCUS

DEFINITION NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--03-K23, mRNA sequence.

ACCESSION

VERSION CF328669.1 GI:33805587

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

COMMENT Unpublished (2003)
Contact: Nahm B.H.

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Fax: 82 31 321 6355

Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .14
/organism="Oryza sativa"
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/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 781

CF328994/c

LOCUS

DEFINITION NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-C11, mRNA sequence.

ACCESSION

VERSION CF328994.1 GI:33806228

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

COMMENT

Unpublished (2003)
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FEATURES

source

Location/Qualifiers
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QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 782

CF329217/c

LOCUS

DEFINITION NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-H10, mRNA sequence.

ACCESSION

VERSION CF329217.1 GI:33806672

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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RESULT 783

CF329990
LOCUS
DEFINITION
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sativa cDNA clone NACL--05-I11, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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RESULT 784

CF330784/c
LOCUS
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sativa cDNA clone NACL--06-K10, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
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Db 14 AAAAAAAAAAAAAA 1

RESULT 785

CF331272/c
LOCUS
DEFINITION
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sativa cDNA clone NACL--07-F09, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL

[illegible]


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TITLE
JOURNAL
COMMENT
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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methyltransferase overexpression line."

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DEFINITION
JMT--02-E12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--02-E12, mRNA sequence.
CF333399
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 5.5e+02;
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RESULT 789
CF333399/c
LOCUS
DEFINITION
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library (JMT) Oryza sativa cDNA clone JMT--02-E12, mRNA sequence.
CF333399
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAAAAAAAAAAAA 14

RESULT 789
CF333399/c
LOCUS
DEFINITION
JMT--02-E12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--02-E12, mRNA sequence.
CF333399
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 1 AAAAAAAAAAAAAA 14

RESULT 790
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library (JMT) Oryza sativa cDNA clone JMT--03-G11, mRNA sequence.
CF334202
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 14 AAAAAAAAAAAAAA 1

RESULT 791
CF334281/c
LOCUS
DEFINITION
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library (JMT) Oryza sativa cDNA clone JMT--03-I05, mRNA sequence.
CF334281
ACCESSION
VERSION
KEYWORDS
CF334281.1 GI:33816894
EST.
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SOURCE
ORGANISM
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
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FEATURES
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Db 14 AAAAAAAAAAAAAA 1

RESULT 792
CF334290/c
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DEFINITION
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred.No. 5.5e+02;
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Db 14 AAAAAAAAAAAAAA 1

RESULT 793
CF335781/c
LOCUS
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library (JMT) Oryza sativa cDNA clone JMT--05-J13, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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methyltransferase overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 5.5e+02;
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Db 14 AAAAAAAAAAAAAA 1

RESULT 794

CF336094/c
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ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

CF336106
LOCUS
DEFINITION JMT--06-A17.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-A17, mRNA sequence.
ACCESSION CF336106
VERSION CF336106.1 GI:33820590
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--06-A17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 796
CF336287/c
LOCUS
DEFINITION JMT--06-E15.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.
ACCESSION CF336287
VERSION CF336287.1 GI:33820962
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--06-E15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 797
CF336906/c

LOCUS
DEFINITION JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-C05, mRNA sequence.

ACCESSION CF336906
VERSION CF336906.1 GI:33822182
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-C05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 798
CF295100/c

LOCUS
DEFINITION 30DGS--04-002.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--04-002, mRNA sequence.

ACCESSION CF295100
VERSION CF295100.1 GI:33664133
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--04-002"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 799
CF329379/c

LOCUS
DEFINITION CF329379 15 bp mRNA linear EST 18-AUG-2003
NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-K23, mRNA sequence.

ACCESSION CF329379
VERSION CF329379.1 GI:33806995
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-K23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 15 AAAAAAAAAAAAAA 2

RESULT 800
CF291803
LOCUS
DEFINITION 14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION CF291803
VERSION CF291803.1 GI:33660836
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 16)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-G05"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 3 AAAAAAAAAAAAAA 16

RESULT 801
AW250784/c
LOCUS
DEFINITION 2822335.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822335 3', mRNA sequence.
ACCESSION AW250784
VERSION AW250784.1 GI:6593777
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT
Unpublished (1999)
Other ESTs: 2822335.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence.
Plate: LLCM9 row: C column: 8.
Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822335"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAA 1

RESULT 802
AW249856/c
LOCUS
DEFINITION 2821566.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821566 3', mRNA sequence.
ACCESSION AW249856
VERSION AW249856.1 GI:6592849
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821566.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 18 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: C column: 7
High quality sequence stop: 9.

FEATURES
source

1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821566"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 6.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA1749
|||||
Db 15 CAAAAA1

RESULT 803
CF329020/c

LOCUS
DEFINITION
NACL--04-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-D03, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 18)

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers

1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-D03"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA1749
|||||
Db 14 AAAAAA1

RESULT 804
AW246446/c

LOCUS

DEFINITION
AW246446
2821601.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821601 3',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17)

NTH-MGC http://mgi.nh.gov/.

AUTHORS
TITLE
JOURNAL
COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Other ESTs: 2821601.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 17 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM7 row: D column: 18
High quality sequence stop: 9.

FEATURES
source

Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821601"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1747
| | | | |
Db 17 TTAACACAAAAA 1

RESULT 805
AW247949/c
LOCUS
DEFINITION AW247949 17 bp mRNA linear EST 07-JAN-2000
2820605.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820605 3',
mRNA sequence.
ACCESSION AW247949
VERSION AW247949.1 GI:6591037
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Other_ESTs: 2820605.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 17 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LNCM4 row: K column: 6.

FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820605"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAA 1752
| | | | |
Db 17 AAAAGTAAAAA 1

RESULT 806
BG673623

LOCUS
DEFINITION BG673623 17 bp mRNA linear EST 30-APR-2001
DRNAAQC09 Rat DRG Library Rattus norvegicus cDNA clone DRNAAQC09
5', mRNA sequence.
ACCESSION BG673623
VERSION BG673623.1 GI:13895722
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 17)
Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
22056133
12060780
Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA=No.

FEATURES
source
Location/Qualifiers
1. .17
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRNAAQC09"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1747
| | | | |
Db 1 TTTTAAAAA 17

RESULT 807
CF299675

LOCUS
DEFINITION CF299675 17 bp mRNA linear EST 15-AUG-2003
7LEAF--03-M14.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-M14, mRNA sequence.
ACCESSION CF299675
VERSION CF299675.1 GI:33671436
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
source     1. .17
           /organism="Oryza sativa"
           /mol_type="mRNA"
           /cultivar="Nackdong"
           /db_xref="taxon:4530"
           /clone="7LEAF--03-M14"
           /tissue_type="leaf"
           /dev_stage="7 days after germination"
           /lab_host="E.coli DH10B"
           /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
           /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1729 AGTTTACAAAAA 1745
      1 AATTTAAAAA 17
      |||||
      |||||

RESULT 808
CF314887/c
LOCUS
DEFINITION HD--03-J15.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa CDNA clone HD--03-J15, mRNA sequence.
ACCESSION CF314887.1 GI:33686648
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
source     1. .18
           /organism="Oryza sativa"
           /mol_type="mRNA"
           /cultivar="Nackdong"
           /db_xref="taxon:4530"
           /clone="HD--03-J15"
           /tissue_type="callus"
           /dev_stage="proliferated callus on 2N6 media for 2 weeks"
           /lab_host="E.coli DH10B"
           /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
           cDNA library (HD)"
           /note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
           treated with ABA(20um) for 1hr. Oligo-capped mRNA was
           reverse transcribed and then used for PCR. mRNA was

TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
source     1. .15
           /organism="Oryza sativa"
           /mol_type="mRNA"
           /cultivar="Nackdong"
           /db_xref="taxon:4530"
           /clone="14ROOT--01-A17"
           /tissue_type="root"
           /dev_stage="14 days after germination"
           /lab_host="E.coli DH10B"
           /clone_lib="Rice root plasmid cDNA library (14ROOT)"
           /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1736 AAAAAA 1750
      1 AAAAAA 15
      |||||
      |||||

RESULT 810
CF291030
LOCUS
DEFINITION 14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa CDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION CF291030
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
source     1. .15
           /organism="Oryza sativa"
           /mol_type="mRNA"
           /cultivar="Nackdong"
           /db_xref="taxon:4530"
           /clone="14ROOT--01-A17"
           /tissue_type="root"
           /dev_stage="14 days after germination"
           /lab_host="E.coli DH10B"
           /clone_lib="Rice root plasmid cDNA library (14ROOT)"
           /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1731 TTTACAAAAA 1747
      17 TTTAGTAAAAA 1
      |||||
      |||||

RESULT 809
CF290849
LOCUS
DEFINITION 14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa CDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION CF290849
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
source     1. .15
           /organism="Oryza sativa"
           /mol_type="mRNA"
           /cultivar="Nackdong"
           /db_xref="taxon:4530"
           /clone="14ROOT--01-A17"
           /tissue_type="root"
           /dev_stage="14 days after germination"
           /lab_host="E.coli DH10B"
           /clone_lib="Rice root plasmid cDNA library (14ROOT)"
           /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1736 AAAAAA 1750
      1 AAAAAA 15
      |||||
      |||||

RESULT 810
CF291030
LOCUS
DEFINITION 14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa CDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION CF291030
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
```

REFERENCE
AUTHORS Ehrhartoidae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-E19"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 811
CF301470/c
LOCUS 15 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-F15, mRNA sequence.
ACCESSION CF301470.1 GI:33673231
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-F15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 812
AI798250
LOCUS 16 bp mRNA linear EST 06-JUL-1999
DEFINITION tr32b08.x1 NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:2219991 3,
similar to TR:O79354 O79354 CYTOCHROME OXIDASE SUBUNIT III. ;, mRNA
sequence.
ACCESSION AI798250
VERSION AI798250.1 GI:5363722
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2219991"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ov23"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAA 1748
|||||
Db 2 AAAAAAAAAAAAAA 16

RESULT 813
AW250981/c
LOCUS 16 bp mRNA linear EST 07-JAN-2000

DEFINITION 2822267.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822267 3', mRNA sequence.

ACCESSION AW250981

VERSION AW250981.1 GI:6594070

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Other ESTs: 2822267.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 9 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM8 row: P column: 12

High quality sequence stop: 9.

Location/Qualifiers

1. .16

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2822267"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 13.4; DB 1; Length 16;

Best Local Similarity 93.3%; Pred. No. 6.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 ACAGGAAAAAAAAAAAA 45

Db 15 ACAGGAAAAAAAAAAAA 1

RESULT 814

AW251033/c

LOCUS AW251033

DEFINITION 2821399.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821399 3', mRNA sequence.

ACCESSION AW251033

VERSION AW251033.1 GI:6593979

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17)

NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Other ESTs: 2821399.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 17 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM6 row: L column: 8

High quality sequence stop: 17.

Location/Qualifiers

1. .17

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2821399"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 6.9e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAAAAAAAAA 1745

Db 15 TTTTCAAAAAAAAAAAAA 1

RESULT 815

BQ583549

LOCUS BQ583549

DEFINITION E011978-024-005-C14-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-005-C14 5-PRIME, mRNA sequence.

ACCESSION BQ583549

VERSION BQ583549.1 GI:26113126

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 13)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 5 row: C column: 14
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers

FEATURES

source
1. .13
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:183152"
/db_xref="taxon:161934"
/clone="024-005-C14"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
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Db 1 AAAAAAAAAAAAAA 13

RESULT 816
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LOCUS
DEFINITION
13 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-015-I22 3-PRIME, mRNA sequence.
ACCESSION
BQ589180
VERSION
BQ589180.1 GI:26118763
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
MEDLINE
PUBMED
22362189
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de

FEATURES

source
1. .13
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/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 817

BQ590337
LOCUS
DEFINITION
13 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-019-G12-SP6 MPiZ-ADIS-024-storage root Beta vulgaris
ACCESSION
BQ590337
VERSION
BQ590337.1 GI:26119920
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
MEDLINE
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
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Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers

FEATURES

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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
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QY 1736 AAAAAAAAAAAAAA 1748
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Db 1 AAAAAAAAAAAAAA 13

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RESULT 818
CF278426/c
LOCUS
DEFINITION
14ETL--04-F09.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--04-F09, mRNA sequence.
ACCESSION
CF278426
VERSION
CF278426.1 GI:33655812
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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FEATURES
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            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

```

```

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 1 AAAAAAAAAAAAAA 13

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RESULT 819
CF280420/c
LOCUS
DEFINITION
14ETL--07-B11.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-B11, mRNA sequence.
ACCESSION
CF280420
VERSION
CF280420.1 GI:33657806
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1736 AAAAAAAAAAAAAA 1748
    |||||
Db 13 AAAAAAAAAAAAAA 1

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RESULT 820
CF280707/c
LOCUS
DEFINITION
14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-H19, mRNA sequence.
ACCESSION
CF280707
VERSION
CF280707.1 GI:33658093
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

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FEATURES
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RESULT 820
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DEFINITION
14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-H19, mRNA sequence.
ACCESSION
CF280707
VERSION
CF280707.1 GI:33658093
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

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Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
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```

QY 1736 AAAAAAAAAAAAAA 1748
    |||||
Db 13 AAAAAAAAAAAAAA 1

```


Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .13
/organism="Oryza sativa"
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Qy 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 821

CF280757/c

LOCUS

DEFINITION 14ETL--07-I21.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-I21, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

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Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 822

CF282369/c

LOCUS

DEFINITION 14ETL--09-N16.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-N16, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

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Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 823

CF290970/c

LOCUS

DEFINITION 14ROOT--01-D13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-D13, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 824

CF290971

LOCUS 14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--01-D13, mRNA sequence.

ACCESSION CF290971

VERSION CF290971.1 GI:33660004

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. .13
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RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 13

RESULT 825

CF291011/c

LOCUS 14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--01-E10, mRNA sequence.

ACCESSION CF291011

VERSION CF291011.1 GI:33660044

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 826

CF291060/c

LOCUS 14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--01-F11, mRNA sequence.

ACCESSION CF291060

VERSION CF291060.1 GI:33660093

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 827

CF291061
LOCUS 14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--01-F11, mRNA sequence.

ACCESSION CF291061
VERSION CF291061.1 GI:33660094
KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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FEATURES

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1. .13
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 1 AAAAAAAAAAAAAA 13

RESULT 828

CF291167/c
LOCUS 14ROOT--01-H20.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--01-H20, mRNA sequence.

ACCESSION CF291167
VERSION CF291167.1 GI:33660200
KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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FEATURES

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 829

CF291214/c
LOCUS 14ROOT--01-I22.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--01-I22, mRNA sequence.

ACCESSION CF291214
VERSION CF291214.1 GI:33660247
KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

TITLE
JOURNAL
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 830

CF291427/c

LOCUS
DEFINITION
14ROOT--01-N14.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
CF291427.1 GI:33660460

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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FEATURES

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with oligoribonucleotides and then used as templates for
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 831

CF291469/c

LOCUS
DEFINITION
14ROOT--01-012.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-012, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
CF291469
CF291469.1 GI:33660502

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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FEATURES

source

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 832

CF291479/c

LOCUS
DEFINITION
14ROOT--01-017.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-017, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
CF291479
CF291479.1 GI:33660512

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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FEATURES

source

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RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 833

CF291514/c

LOCUS 14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--01-P13, mRNA sequence.

ACCESSION CF291514.1 GI:33660547

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

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FEATURES

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with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 834

CF291515

LOCUS 14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--01-P13, mRNA sequence.

ACCESSION CF291515

VERSION CF291515.1 GI:33660548

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

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FEATURES

source

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748

Db 1 AAAAAAAAAAAAAA 13

RESULT 835

CF291596/c

LOCUS 14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-B12, mRNA sequence.

ACCESSION CF291596

VERSION CF291596.1 GI:33660629

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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REFERENCE
AUTHORS      1 (bases 1 to 13)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
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Db      13 AAAAAAAAAAAAAA 1

RESULT 836
CF291597
LOCUS      14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-B12, mRNA sequence.
ACCESSION  CF291597
VERSION     CF291597.1 GI:33660630
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match      0.7%; Score 13; DB 1; Length 13;
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Db      13 AAAAAAAAAAAAAA 1

RESULT 836
CF291597
LOCUS      14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-B12, mRNA sequence.
ACCESSION  CF291597
VERSION     CF291597.1 GI:33660630
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
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              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db      13 AAAAAAAAAAAAAA 1

RESULT 838
CF291903
LOCUS      14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-I10, mRNA sequence.
ACCESSION  CF291903
VERSION     CF291903.1 GI:33660936
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
        |||||
Db      1 AAAAAAAAAAAAAA 13

RESULT 837
CF291726/c
LOCUS      14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-E10, mRNA sequence.
ACCESSION  CF291726
VERSION     CF291726.1 GI:33660759
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
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              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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  RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
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Db      13 AAAAAAAAAAAAAA 1

RESULT 838
CF291903
LOCUS      14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-I10, mRNA sequence.
ACCESSION  CF291903
VERSION     CF291903.1 GI:33660936
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
```


REFERENCE
AUTHORS Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

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1. .13
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/tissue_type="root"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
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Db 1 AAAAAAAAAAAAAA 13

RESULT 839
CF298590/c 13 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--02-A19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-A19, mRNA sequence.
ACCESSION CF298590
VERSION CF298590.1 GI:33670351
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

source
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 840
CF298592/c 13 bp mRNA linear EST 15-AUG-2003

LOCUS 7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-A21, mRNA sequence.
ACCESSION CF298592

VERSION CF298592.1 GI:33670353
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 841
CF298736/c 13 bp mRNA linear EST 15-AUG-2003

LOCUS 7LEAF--02-E22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-E22, mRNA sequence.
ACCESSION CF298736

VERSION CF298736.1 GI:33670497
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 842

CF298764/c

LOCUS CF298764 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-F20, mRNA sequence.

ACCESSION CF298764.1 GI:33670525

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .13

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone="7LEAF--02-F20"

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 843

CF298795/c

LOCUS CF298795 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--02-G14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-G14, mRNA sequence.

ACCESSION CF298795

VERSION CF298795.1 GI:33670556

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

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Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .13

/organism="Oryza sativa"

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with oligoribonucleotides and then used as templates for

RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 844

CF298908/c

LOCUS CF298908 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-K03, mRNA sequence.

ACCESSION CF298908

VERSION CF298908.1 GI:33670669

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1. .13

/organism="Oryza sativa"

/mol_type="mRNA"

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

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Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 845

CF299133/c

LOCUS 7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--03-A06, mRNA sequence.

CF299133

CF299133.1 GI:33670894

EST.

ORYZA SATIVA

ORYZA SATIVA

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 846

CF299359/c

LOCUS 7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--03-F15, mRNA sequence.

CF299359

CF299359.1 GI:33671120

EST.

ORYZA SATIVA

ORYZA SATIVA

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

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Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 847

CF299937/c

LOCUS 7LEAF--04-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--04-C12, mRNA sequence.

CF299937

CF299937.1 GI:33671698

EST.

ORYZA SATIVA

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ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
Db      13 AAAAAAAAAAAAAA 1

RESULT 848
CF300118/c
LOCUS      CF300118      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--04-G10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-G10, mRNA sequence.
ACCESSION      CF300118
VERSION      CF300118.1 GI:33671879
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
Db      13 AAAAAAAAAAAAAA 1

RESULT 848
CF300118/c
LOCUS      CF300118      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--04-G10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-G10, mRNA sequence.
ACCESSION      CF300118
VERSION      CF300118.1 GI:33671879
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..13
/organism="Oryza sativa"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
Db      13 AAAAAAAAAAAAAA 1

RESULT 849
CF300587/c
LOCUS      CF300587      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--05-C01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-C01, mRNA sequence.
ACCESSION      CF300587
VERSION      CF300587.1 GI:33672348
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..13
/organism="Oryza sativa"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
Db      13 AAAAAAAAAAAAAA 1

RESULT 850
CF300658/c
LOCUS      CF300658      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--05-D14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-D14, mRNA sequence.
ACCESSION      CF300658
VERSION      CF300658.1 GI:33672419
KEYWORDS      EST.
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SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-D14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 851
CF300929/c
LOCUS CF300929 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-J11, mRNA sequence.

ACCESSION CF300929.1 GI:33672690
VERSION
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 852
CF301247/c

LOCUS CF301247 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-A15, mRNA sequence.

ACCESSION CF301247
VERSION CF301247.1 GI:33673008
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-A15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 853
CF301286/c

LOCUS CF301286 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-B15, mRNA sequence.

ACCESSION CF301286
VERSION CF301286.1 GI:33673047

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 854
CF302158/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF302158
7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-G20, mRNA sequence.
CF302158
CF302158.1 GI:33673919
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 854
CF302158/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF302158
7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-G20, mRNA sequence.
CF302158
CF302158.1 GI:33673919
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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1. .13
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/cultivar="Nackdong"
/db_xref="taxon:4530"

/clone="7LEAF--07-G20"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 855
CF302830/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF302830
7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-L16, mRNA sequence.
CF302830
CF302830.1 GI:33674591
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 856
CF302898/c
LOCUS
DEFINITION
ACCESSION

CF302898
7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-N08, mRNA sequence.
CF302898

VERSION CF302898.1 GI:33674659
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 857
CF310516/c
LOCUS CF310516 13 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION CF310516
VERSION CF310516.1 GI:33682277
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
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/cultivar="Nackdong"

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/clone="ABF--05-D09"
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cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 858
CF310517
LOCUS CF310517 13 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION CF310517
VERSION CF310517.1 GI:33682278
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
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/cultivar="Nackdong"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 1 AAAAAAAAAAAAAA 13

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RESULT 859
CF312721/c
LOCUS      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-J13, mRNA sequence.
ACCESSION  CF312721
VERSION     CF312721.1 GI:33684482
KEYWORDS   EST.
SOURCE     Oryza sativa
           Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /tissue_type="leaf"
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                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
     Query Match      0.7%; Score 13; DB 1; Length 13;
     Best Local Similarity 100.0%; Pred. No. 6.8e+02;
     Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
        |||||
Db       13 AAAAAAAAAAAAAA 1

RESULT 860
CF313171/c
LOCUS      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION HD--01-D10.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.
ACCESSION  CF313171
VERSION     CF313171.1 GI:33684932
KEYWORDS   EST.
SOURCE     Oryza sativa
           Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..13
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
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     Best Local Similarity 100.0%; Pred. No. 6.8e+02;
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QY      1736 AAAAAAAAAAAAAA 1748
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Db       13 AAAAAAAAAAAAAA 1

RESULT 861
CF314239/c
LOCUS      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION HD--02-L01.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--02-L01, mRNA sequence.
ACCESSION  CF314239
VERSION     CF314239.1 GI:33686000
KEYWORDS   EST.
SOURCE     Oryza sativa
           Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, MyongJi University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:4530"
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                     /lab_host="E.coli DH10B"
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                     cDNA library (HD)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
     Query Match      0.7%; Score 13; DB 1; Length 13;
     Best Local Similarity 100.0%; Pred. No. 6.8e+02;
     Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 865
CF316440
LOCUS
DEFINITION HD--05-L17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--05-L17, mRNA sequence.
ACCESSION CF316440.1 GI:33688201
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 866
CF316440
LOCUS
DEFINITION HD--05-L17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--05-L17, mRNA sequence.
ACCESSION CF316440.1 GI:33688201
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
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RESULT 866
CF316637/c
LOCUS
DEFINITION HD--06-A04.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--06-A04, mRNA sequence.
ACCESSION CF316637
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
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RESULT 867
CF318290/c
LOCUS
DEFINITION HD--08-F19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.
ACCESSION CF318290
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
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/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
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RESULT 867
CF318290/c
LOCUS
DEFINITION HD--08-F19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.
ACCESSION CF318290
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
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/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
```

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 868

CF319066/c

LOCUS

DEFINITION CF319066 .13 bp mRNA linear EST 15-AUG-2003
HD--09-H02.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-H02, mRNA sequence.

ACCESSION

VERSION CF319066.1 GI:33690827

KEYWORDS

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS 1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
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/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 869

CF319531/c

LOCUS

DEFINITION CF319531 13 bp mRNA linear EST 15-AUG-2003
HD--10-B03.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.

ACCESSION

VERSION CF319531.1 GI:33691292

KEYWORDS

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS 1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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/lab_host="E.coli DH10B"

/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 870

CF319532

LOCUS

DEFINITION CF319532 13 bp mRNA linear EST 15-AUG-2003
HD--10-B03.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.

ACCESSION

VERSION CF319532.1 GI:33691293

KEYWORDS

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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1. .13
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cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 1 AAAAAAAAAAAAAA 13

RESULT 871

CF319919

LOCUS 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-J17.g1 OSHDAc1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-J17, mRNA sequence.

ACCESSION CF319919

VERSION CF319919.1 GI:33691680

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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1. .13
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/lab_host="E.coli DH10B"
/clone_lib="OSHDAc1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 1 AAAAAAAAAAAAAA 13

RESULT 872

CF320017/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-L20.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.

ACCESSION CF320017

VERSION CF320017.1 GI:33691778

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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1. .13
/organism="Oryza sativa"
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cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

Db 13 AAAAAAAAAAAAAA 1

RESULT 873

CF320018
LOCUS
DEFINITION HD--10-L20.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.
ACCESSION CF320018
VERSION CF320018.1 GI:33691779
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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line."

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Qy 1736 AAAAAAAAAAAAAA 1748
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Db 1 AAAAAAAAAAAAAA 13

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DEFINITION HD--10-O13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-O13, mRNA sequence.
ACCESSION CF320143
VERSION CF320143.1 GI:33691904
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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reverse transcribed and then used for PCR. mRNA was
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line."

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Db 13 AAAAAAAAAAAAAA 1

RESULT 875
CF320938/c
LOCUS
DEFINITION HD--12-A06.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--12-A06, mRNA sequence.
ACCESSION CF320938
VERSION CF320938.1 GI:33692699
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 13; DB 1; Length 13;
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Db 13 AAAAAAAAAAAAAA 1

RESULT 876
CF326844/c
LOCUS
DEFINITION NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-B12, mRNA sequence.
ACCESSION CF326844
VERSION CF326844.1 GI:33801943
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

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Db 13 AAAAAAAAAAAAAA 1

RESULT 877
CF327070/c
LOCUS
DEFINITION NACL--01-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-G09, mRNA sequence.
ACCESSION CF327070
VERSION CF327070.1 GI:33802396
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
| | | | | | | | | | | | | | |
Db 13 AAAAAAAAAAAAAA 1

RESULT 878
CF327339/c
LOCUS
DEFINITION NACL--01-M15.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-M15, mRNA sequence.
ACCESSION CF327339
VERSION CF327339.1 GI:33802936
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
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QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 879
CF327340
LOCUS NACL--01-M15.g1 Rice callus plasmid cDNA library (NACL) Oryza EST 18-AUG-2003
DEFINITION sativa cDNA clone NACL--01-M15, mRNA sequence.
ACCESSION CF327340
VERSION CF327340.1 GI:33802938
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 880
CF327576/c
LOCUS NACL--02-B22.b1 Rice callus plasmid cDNA library (NACL) Oryza EST 18-AUG-2003
DEFINITION sativa cDNA clone NACL--02-B22, mRNA sequence.
ACCESSION CF327576
VERSION CF327576.1 GI:33803404
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 881
CF327888/c
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DEFINITION sativa cDNA clone NACL--02-I22, mRNA sequence.
ACCESSION CF327888
VERSION CF327888.1 GI:33804024
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 13 AAAAAAAAAAAAAA 1

RESULT 882
CF327939/c
LOCUS      13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-K02.g1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION  CF327939
VERSION     CF327939.1 GI:33804127
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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REFERENCE  0.7%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 884
CF328228/c
LOCUS      13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-A13.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION  CF328228
VERSION     CF328228.1 GI:33804702
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 883
CF328153/c
LOCUS      13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-O19.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa CDNA clone NACL--02-O19, mRNA sequence.
ACCESSION  CF328153
VERSION     CF328153.1 GI:33804556
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAAAAAAAAAAAA 13

RESULT 888
CF329417/c

LOCUS 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-L19.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-L19, mRNA sequence.

ACCESSION CF329417
VERSION CF329417.1 GI:33807072
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .13
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/lab_host="E.coli DH10B"
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Query Match 0.7%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 889
CF329460/c

LOCUS 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-M18.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-M18, mRNA sequence.

ACCESSION CF329460
VERSION CF329460.1 GI:33807156
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-M18"
/tissue_type="callus"
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 890
CF329729

LOCUS 13 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-C14, mRNA sequence.

ACCESSION CF329729
VERSION CF329729.1 GI:33807674
KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers
1. .13
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 891
CF329800/c
LOCUS
DEFINITION NACL--05-E04.b1 13 bp mRNA linear EST 18-AUG-2003
sativa cDNA clone NACL--05-E04, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 892
CF329801
LOCUS
DEFINITION NACL--05-E04.g1 13 bp mRNA linear EST 18-AUG-2003
sativa cDNA clone NACL--05-E04, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 893
CF329869/c

LOCUS
DEFINITION NACL--05-F18.b1 13 bp mRNA linear EST 18-AUG-2003
sativa cDNA clone NACL--05-F18, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/lab_host="E.coli DH10B"
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with oligoribonucleotides and then used as templates for
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 894
CF329946/c
LOCUS      13 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-H12, mRNA sequence.
ACCESSION  CF329946
VERSION     CF329946.1 GI:33808114
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
1. .13
/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 895
CF329988/c
LOCUS      13 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-I10, mRNA sequence.
ACCESSION  CF329988
VERSION     CF329988.1 GI:33808198
KEYWORDS   EST.
SOURCE     Oryza sativa
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ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
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/lab_host="E.coli DH10B"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 896
CF330023/c
LOCUS      13 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--05-J05.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-J05, mRNA sequence.
ACCESSION  CF330023
VERSION     CF330023.1 GI:33808268
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
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/dev_stage="proliferated callus on 2N6 media for 30 days"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 897
CF330725 13 bp mRNA linear EST 18-AUG-2003
LOCUS
DEFINITION NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--06-J01, mRNA sequence.

ACCESSION CF330725 GI:33809672
VERSION
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
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Db 1 AAAAAAAAAAAAAA 13

RESULT 898
CF331041/c 13 bp mRNA linear EST 18-AUG-2003
LOCUS
DEFINITION NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-A04, mRNA sequence.

ACCESSION CF331041 GI:33810299
VERSION
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748

|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 899

CF331266/c

LOCUS

DEFINITION

NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--07-F06, mRNA sequence.

ACCESSION CF331266 GI:33810744

VERSION

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

1. .13
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 900
CF331273 13 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION CF331273
VERSION CF331273.1 GI:33810757
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .13
/organism="Oryza sativa"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 901
CF331903/c 13 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--08-D07, mRNA sequence.
ACCESSION CF331903
VERSION CF331903.1 GI:33812027

KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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ACCESSION CF332079
VERSION CF332079.1 GI:33812379
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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ACCESSION CF332695 13 bp mRNA linear EST 18-AUG-2003
VERSION JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
KEYWORDS library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.
SOURCE CF332695.1 GI:33813618
ORGANISM Oryza sativa
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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prepared from Arabidopsis Jasmonate Carboxyl
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library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.
ACCESSION CF332696 13 bp mRNA linear EST 18-AUG-2003
VERSION JMT--01-E21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
KEYWORDS library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.
SOURCE CF332696.1 GI:33815268
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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was reverse transcribed and then used for PCR. mRNA was
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Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
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DEFINITION JMT--01-E21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
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VERSION CF332696.1 GI:33813620
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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prepared from Arabidopsis Jasmonate Carboxyl
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VERSION JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
KEYWORDS library (JMT) Oryza sativa cDNA clone JMT--02-G11, mRNA sequence.
SOURCE CF333486.1 GI:33815268
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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ACCESSION
CF333972
VERSION
KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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ACCESSION
CF334347
VERSION
KEYWORDS
SOURCE
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
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CF333973
VERSION
KEYWORDS
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ORGANISM
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RESULT 908
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JMT--03-J19.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
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ACCESSION
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VERSION
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
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FEATURES

source

Location/Qualifiers
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CF337022/c

LOCUS

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ACCESSION

VERSION CF337022.1 GI:33822426

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 13)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.
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FEATURES

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Location/Qualifiers
1. .13
/organism="Oryza sativa"
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Db 13 AAAAAAAAAAAAAA 1

RESULT 910

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LOCUS

DEFINITION BQ591949 14 bp mRNA linear EST 06-DEC-2002
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cDNA clone 024-016-C15 5-PRIME, mRNA sequence.

ACCESSION

VERSION BQ591949.1 GI:26121532

KEYWORDS

SOURCE

ORGANISM

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Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

1 (bases 1 to 14)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de

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Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES

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Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.7%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 7e+02;

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Db 14 CAAAAAAAAAAAAA 2

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RESULT 911
CF543203      15 bp  mRNA  linear  EST 22-SEP-2003
LOCUS
DEFINITION    S014679-024-030-D05-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION     024-030-D05 5-PRIME, mRNA sequence.
VERSION       CF543203
KEYWORDS      CF543203.1 GI:34891643
SOURCE        EST.
ORGANISM      Beta vulgaris
               Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE     1 (bases 1 to 15)
AUTHORS       Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
               Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
               and Radelof,U.
TITLE         Construction of a 'unigene' cDNA clone set by oligonucleotide
               fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL       Plant J. 32 (5), 845-857 (2002)
MEDLINE       22362189
PUBMED        12472698
COMMENT       Contact: Weisshaar B
               ADIS DNA core facility at MPIZ
               Max-Planck-Institute for Plant Breeding Research
               Carl-von-Linne Weg 10, 50829 Koeln, Germany
               Fax: 00492215062851
               Email: weissaha@mpiz-koeln.mpg.de
               Insert Length: 15 Std Error: 0.00
               Plate: 30 row: D column: 05
               Seq primer: SP6.
               Location/Qualifiers
FEATURES      1..15
               /organism="Beta vulgaris"
               /mol_type="mRNA"
               /cultivar="KWS2320 (double haploid, monogerm breeding
               line)"
               /db_xref="GABI:936579"
               /db_xref="taxon:161934"
               /clone="024-030-D05"
               /tissue_type="leaf"
               /lab_host="EMDH10B"
               /clone_lib="MP1Z-ADIS-024-leaf"
               /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
               cDNA library from sugar beet, library provided by KWS
               Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
               b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
               orientation:
               SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
               Sequencing granted in the context of the GABI-Beet
               project, local PI: Dr. Katharina Schneider, coordinator:
               Prof. Christian Jung; Sequence submission managed by
               RZPD/GABI-Primary database:http://gabi.rzpd.de"
               Query Match      0.7%; Score 13; DB 1; Length 15;
               Best Local Similarity 100.0%; Pred. No. 7.2e+02;
               Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1747
   |||||
Db 3 CAAAAAATAAAAAA 15

RESULT 912
AA937877/c
LOCUS
DEFINITION    AA937877 16 bp  mRNA  linear  EST 30-APR-1998
               nw90e06.s1 NCI CGAP Pr12 Homo sapiens cDNA clone IMAGE:1253890
               similar to TR:Q35989 Q35989 CYTOCHROME C OXIDASE SUBUNIT 1 ;, mRNA
               sequence.
ACCESSION     AA937877
VERSION       AA937877.1 GI:3095988
KEYWORDS      EST.
SOURCE        Homo sapiens (human)

ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 16)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL       Unpublished (1997)
COMMENT       Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
               Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
               cDNA Library Preparation: David B. Krizman, Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
               Location/Qualifiers
FEATURES      1..16
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:1253890"
               /sex="male"
               /tissue_type="metastatic prostate bone lesion"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP Pr12"
               /note="Vector: pAMP10; mRNA made from metastatic prostate
               lesion of the bone, cDNA made by oligo-dT priming.
               Non-directionally cloned. Size-selected on agarose gel,
               average insert size 600 bp. Library made by D. Krizman,
               NIH."
               Query Match      0.7%; Score 12.8; DB 1; Length 16;
               Best Local Similarity 87.5%; Pred. No. 7.8e+02;
               Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAATAAAAAA 1751
   |||||
Db 16 AAAAAAATAAAAAA 1

RESULT 913
AW248540/c
LOCUS
DEFINITION    AW248540 16 bp  mRNA  linear  EST 07-JAN-2000
               2820844.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820844 3',
               mRNA sequence.
ACCESSION     AW248540
VERSION       AW248540.1 GI:6591533
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 16)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Other_ESTs: 2820844.5prime
               Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
               Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
               Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
               project Clone distribution: MGC clone distribution information can
               be found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
               Scores: PHRED from University of Washington Genome Center. Vector
```

Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LCM5 row: E column: 5
High quality sequence stop: 15.

FEATURES

source

1.16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820844"
/tissue type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.7%; Score 12.8; DB 1; Length 16;

Best Local Similarity 87.5%; Pred. No. 7.8e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1730 GTTTACAAAAA 1745

Db 16 GTTTTAAAAA 1

RESULT 914

AW246528/c

LOCUS

DEFINITION AW246528 17 bp mRNA linear EST 07-JAN-2000
2821879.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821879 3',
mRNA sequence.

ACCESSION AW246528

VERSION AW246528.1 GI:6589521

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2821879.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

<http://www.genome.washington.edu> Low Quality Sequence: 13

contiguous PHRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 17 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.

Plate: LCM7 row: P column: 8

High quality sequence stop: 13.

FEATURES

source

1.17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821879"
/tissue type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.7%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 7.9e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1730 GTTTACAAAAA 1745

Db 16 GTTTTAAAAA 1

RESULT 915

AU102457/c

LOCUS

DEFINITION

AU102457 50 bp mRNA linear EST 30-AUG-2001
AU102457 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
REC01020, mRNA sequence.

ACCESSION AU102457

VERSION AU102457.1 GI:13551977

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

FEATURES

source

1.50
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="REC01020"

/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 0.7%; Score 12.8; DB 1; Length 50;

Best Local Similarity 57.5%; Pred. No. 7.2e+02;

Matches 23; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 536 CGCCACCTCTGCTACCGCACGGGCTCCCTGAAGCCAAA 575
| | | | | | | | | | | | | | | | | | | | | |
Db 49 CACCCCTCTTCGTCGCCGACACTCGTTTGGGACTCCAGA 10
| | | | | | | | | | | | | | | | | | | | | |

RESULT 916
CF334023
LOCUS
DEFINITION JMT--03-C14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-C14, mRNA sequence.
ACCESSION CF334023.1 GI:33816351
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .29
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="JMT--03-C14"
/tissue type="leaf"
/dev stage="14 days after germination"
/lab host="E.coli DH10B"
/clone lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.7%; Score 12.6; DB 1; Length 29;
Best Local Similarity 66.7%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1690 TGTCTTCTCTTCTCCAATCAAGAAAT 1716
| | | | | | | | | | | | | | | | | | | | | |
Db 3 TTTTITTTTTTTTTTTCAGTAAACAAT 29
| | | | | | | | | | | | | | | | | | | | | |

RESULT 917
CF301021
LOCUS
DEFINITION 7LEAF--05-L10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
ACCESSION CF301021.1 GI:33672782
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:4530"
/clone="7LEAF--05-L10"
/tissue type="leaf"
/dev stage="7 days after germination"
/lab host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAATAAAAAAA 14
| | | | | | | | | | | | | | | | | | | | | |

RESULT 918
AW246551/c
LOCUS
DEFINITION AW246551.1 Homo sapiens cDNA clone IMAGE:2822090 3', mRNA sequence.
ACCESSION AW246551.1 GI:6589544
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 15)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2822090.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu/Low Quality Sequence: 14
contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM8 row: I column: 3
High quality sequence stop: 14.
Location/Qualifiers

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source      1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822090"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 8.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1730 GTTTACAAAAAAA 1743
||||| |||||||

Db 14 GTTTAAAAAAA 1

RESULT 919
CF332179
LOCUS
DEFINITION NACL--08-J10.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-J10, mRNA sequence.

ACCESSION CF332179.1 GI:33812582
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-J10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 8.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAAAA 1744
||||| |||||||

```

Db 2 TTTATAAAAAAAA 15

RESULT 920  

AW245338/c  

LOCUS  

DEFINITION AW245338.1 Homo sapiens cDNA clone IMAGE:2822905 3',  

mRNA sequence.  

ACCESSION AW245338  

VERSION AW245338.1 GI:6588331  

KEYWORDS EST.  

SOURCE Homo sapiens (human)  

ORGANISM Homo sapiens  

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  

REFERENCE 1 (bases 1 to 16)  

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  

JOURNAL Unpublished (1999)  

COMMENT Other_ESTs: 2822905.5prime  

Contact: Robert Strausberg, Ph.D.  

Email: cgapbs-remail.nih.gov  

Tissue Procurement: DCTD/Drp cDNA Library Preparation: Ling  

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  

project Clone distribution: MGC clone distribution information can  

be found through the I.M.A.G.E. Consortium/LLNL at:  

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  

Scores: PHRED from University of Washington Genome Center. Vector  

Trimming: cross match from University of Washington Genome Center  

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  

Drosophila Genome Project. University of Washington Genome Center:  

http://www.genome.washington.edu Low Quality Sequence: 15  

contiguous PHRED high quality bases following vector sequence. Very  

Low Quality Sequence: Trace file contained 16 contiguous distinct  

peaks following vector sequence. Polyadenylation: Based upon the  

presence of a XhoI site followed by a run of 14 or more T residues  

polyadenylated.  

Plate: L1CM10 row: K column: 2  

High quality sequence stop: 15.  

Location/Qualifiers  

1. .16  

/organism="Homo sapiens"  

/mol_type="mRNA"  

/db_xref="taxon:9606"  

/clone="IMAGE:2822905"  

/tissue_type="small cell carcinoma"  

/cell_line="MGC3"  

/lab_host="DH10B (phage-resistant)"  

/clone_lib="NIH_MGC_7"  

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site_2:  

EcoRI; cDNA made by oligo-dT priming. Directionally  

cloned into EcoRI/XhoI sites using the following 5'  

adaptor: GGCACGAG(G). Size-selected >500bp for average  

insert size 1.8kb. Library constructed by Ling Hong in  

the laboratory of Gerald M. Rubin (University of  

California, Berkeley) using ZAP-cDNA synthesis kit  

(Stratagene) and Superscript II RT (Life Technologies)."


Query Match 0.7%; Score 12.4; DB 1; Length 16;  

Best Local Similarity 92.9%; Pred. No. 8.5e+02;  

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



Qy 1734 ACACAAAAAAA 1747  

||||| |||||||



Db 14 ACACAAAAAAA 1



RESULT 921  

AZ764496/c  

LOCUS  

DEFINITION AZ764496 Mouse 10kb plasmid UUGC1M library Mus musculus genomic


```


clone UUGC1M0560H02 R, genomic survey sequence.

ACCESSION AZ764496
VERSION AZ764496.1 GI:12879519
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: H column: 02
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560H02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
source
1. .24
/organism="Mus musculus"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 12.2; DB 1; Length 24;
Best Local Similarity 82.4%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 AAAAAGTTTCTTTCT 67
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Db 24 AAAAATTTTCTTTT 8

RESULT 922
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LOCUS AZ764513 24 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0560D11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560D11 R, genomic survey sequence.

ACCESSION AZ764513
VERSION AZ764513.1 GI:12879553
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: D column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 12.2; DB 1; Length 24;
Best Local Similarity 82.4%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 AAAAAGTTTCTTTCT 67
|||||
Db 24 AAAAATTTTCTTTT 8

RESULT 923
AZ764519/c
LOCUS AZ764519 24 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0560P11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560P11 R, genomic survey sequence.


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VERSION      AZ764519.1  GI:12879566
KEYWORDS
SOURCE       Mus musculus (house mouse)
ORGANISM
REFERENCE    1 (bases 1 to 24)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0560 row: P column: 11
              Seq primer: CACACAGGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 24.
              Location/Qualifiers
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0560P11"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: FWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male); was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."

Query Match      0.7%; Score 12.2; DB 1; Length 24;
Best Local Similarity 82.4%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 AAAAAAGTTTCTTTTCT 67
    ||||| ||||| |||||
Db 24 AAAAAATTTTCTTTT 8

RESULT 924
TA321G11P/c
LOCUS      TA321G11P      26 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 321g11, forward sequence,
            genomic survey sequence.
ACCESSION  AL492371
VERSION     AL492371.1  GI:11867375
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KEYWORDS      GSS.
SOURCE         Trypanosoma brucei
ORGANISM       Trypanosoma brucei
              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
              Trypanosoma.
REFERENCE      1 (bases 1 to 26)
AUTHORS        Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
              Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
              Melville,S.E., Rajandream,M.A. and Barrell,B.G.
              Direct Submission
              Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh@sanger.ac.uk
              Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + i method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.
              Location/Qualifiers
                1..26
                /organism="Trypanosoma brucei"
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Query Match      0.7%; Score 12.2; DB 1; Length 26;
Best Local Similarity 82.4%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 AAAAAAGTTTCTTTTCT 67
    ||||| ||||| |||||
Db 26 AAAAAATTTTCTTTT 10

RESULT 925
AU102454/c
LOCUS      AU102454      50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION AU102454 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC01208, mRNA sequence.
ACCESSION  AU102454
VERSION     AU102454.1  GI:13551974
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 50)
              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isoqai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              EMBO Rep. 2 (5), 388-393 (2001)
              21270072
              11375929
              Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: ysuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).
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KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL 22362189
MEDLINE PUBMED
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 14 row: P column: 24
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1. .12
/organism="Beta vulgaris"
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line)"
/db_xref="GABI:187286"
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/clone="024-014-P24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
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Db 12 AAAAAAAAAAAAA 1

RESULT 929
BQ594698/c
LOCUS BQ594698 12 bp mRNA linear EST 06-DEC-2002
DEFINITION E012404-024-024-E05-T7 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-024-E05 3-PRIME, mRNA sequence.
ACCESSION BQ594698
VERSION BQ594698.1 GI:26124281
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL 22362189
MEDLINE PUBMED
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 24 row: E column: 05
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
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/organism="Beta vulgaris"
/mol_type="mRNA"
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line)"
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/db_xref="taxon:161934"
/clone="024-024-E05"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
| | | | |
Db 12 AAAAAAAAAAAAA 1

RESULT 930
CF279278/c
LOCUS CF279278 12 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--05-I10.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-I10, mRNA sequence.
ACCESSION CF279278
VERSION CF279278.1 GI:33656664
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .12

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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1747
Db 12 AAAAAAAAAA 1

RESULT 931
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DEFINITION      14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION      CF291428
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1747
Db 1 AAAAAAAAAA 12

RESULT 932
CF291428
LOCUS      12 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION      14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-N14, mRNA sequence.
ACCESSION      CF291428
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Source
1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ROOT--01-N14"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1747
Db 1 AAAAAAAAAA 12

RESULT 932
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CF291800/c
LOCUS      12 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION      14ROOT--02-G04.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-G04, mRNA sequence.
ACCESSION      CF291800
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1747
Db 12 AAAAAAAAAA 1

RESULT 933
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DEFINITION      14ROOT--02-G04.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-G04, mRNA sequence.
ACCESSION      CF291801
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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QY 1736 AAAAAAAAAA 1747
Db 1 AAAAAAAAAA 12

RESULT 934
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DEFINITION
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  sativa cDNA clone 14ROOT--02-I01, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
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  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 12)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 1 AAAAAAAAAA 12

RESULT 935
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DEFINITION
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  sativa cDNA clone 14ROOT--02-I01, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
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  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 1 AAAAAAAAAA 12

RESULT 936
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DEFINITION
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  sativa cDNA clone 14ROOT--02-M21, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 12)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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QY 1736 AAAAAAAAAA 1747
Db 12 AAAAAAAAAA 1
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Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

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Db 12 AAAAAAAAAAAAA 1

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RESULT 937
CF295593/c
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DEFINITION
30DGS--05-J18.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--05-J18, mRNA sequence.
ACCESSION
CF295593
VERSION
CF295593.1 GI:33664626
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
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Db 12 AAAAAAAAAAAAA 1

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RESULT 938
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sativa cDNA clone 7LEAF--02-D15, mRNA sequence.
ACCESSION
CF298686
VERSION
CF298686.1 GI:33670447
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
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FEATURES
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Db 12 AAAAAAAAAAAAA 1

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RESULT 939
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DEFINITION
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sativa cDNA clone 7LEAF--02-I17, mRNA sequence.
ACCESSION
CF298872
VERSION
CF298872.1 GI:33670633
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
```

```
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
```


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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Db 12 AAAAAAAAAAAAA 1

RESULT 940

CF299343
LOCUS
DEFINITION
7LEAF--03-F06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-F06, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
CF299343.1 GI:33671104

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Unpublished (2003)

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Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Db 1 AAAAAAAAAAAAA 12

RESULT 941

CF299514/c
LOCUS
DEFINITION
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sativa cDNA clone 7LEAF--03-J03, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
CF299514.1 GI:33671275

ORGANISM

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Db 12 AAAAAAAAAAAAA 1

RESULT 942

CF300272/c
LOCUS
DEFINITION
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sativa cDNA clone 7LEAF--04-J19, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
CF300272.1 GI:33672033

ORGANISM

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES

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Location/Qualifiers
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Db 12 AAAAAAAAAAAA 1

FEATURES

source

CF301006 12 bp mRNA linear EST 15-AUG-2003
7LEAF--05-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-L02, mRNA sequence.

ACCESSION CF301006

VERSION CF301006.1 GI:33672767

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Unpublished (2003)

TITLE

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COMMENT

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Fax: 82 31 321 6355

Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES

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Location/Qualifiers
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Db 12 AAAAAAAAAAAA 1
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FEATURES

source

CF301075 12 bp mRNA linear EST 15-AUG-2003
7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M15, mRNA sequence.

ACCESSION CF301075

VERSION CF301075.1 GI:33672836

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

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FEATURES

source

Location/Qualifiers
1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-M15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAA 1747

Db 12 AAAAAAAAAAAA 1

FEATURES

source

CF301489 12 bp mRNA linear EST 15-AUG-2003
7LEAF--06-G01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-G01, mRNA sequence.

ACCESSION CF301489

VERSION CF301489.1 GI:33673250

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

JOURNAL

COMMENT

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FEATURES

source

Location/Qualifiers
1. .12
/organism="Oryza sativa"
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/clone="7LEAF--06-G01"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1747

Db 12 AAAAAAAAAA 1

FEATURES

source

CF301940/c
LOCUS
DEFINITION
7LEAF--07-A01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-A01, mRNA sequence.

ACCESSION CF301940.1 GI:33673701

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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FEATURES

source

Location/Qualifiers
1. .12
/organism="Oryza sativa"
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Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1747

Db 12 AAAAAAAAAA 1

FEATURES

source

CF302029/c
LOCUS
DEFINITION
7LEAF--07-C18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-C18, mRNA sequence.

ACCESSION CF302029.1 GI:33673790

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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FEATURES

source

Location/Qualifiers
1. .12
/organism="Oryza sativa"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1747

Db 12 AAAAAAAAAA 1

FEATURES

source

CF302122/c
LOCUS
DEFINITION
7LEAF--07-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-F15, mRNA sequence.

ACCESSION CF302122.1 GI:33673883

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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FEATURES

source

1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747

Db 12 AAAAAAAAAAAAA 1

RESULT 952

CF302289/c

LOCUS

DEFINITION 7LEAF--07-K10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-K10, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Unpublished (2003)

COMMENT

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FEATURES

source

1. .12
/organism="Oryza sativa"
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RT-PCR."

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747

Db 12 AAAAAAAAAAAAA 1

RESULT 953

CF302486/c

LOCUS

DEFINITION 7LEAF--08-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-B02, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Unpublished (2003)

COMMENT

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FEATURES

source

1. .12
/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

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Best Local Similarity 100.0%; Pred. No. 8.3e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747

Db 12 AAAAAAAAAAAAA 1

RESULT 954

CF308112/c

LOCUS

DEFINITION ABF--01-M19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-M19, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

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FEATURES
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1. .12
/organism="Oryza sativa"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1747
Db 12 AAAAAAAAAAAAAA 1

RESULT 955
CF311835/c
LOCUS
DEFINITION ABF--07-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311835.1 GI:33683596
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .12
/organism="Oryza sativa"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1747
Db 12 AAAAAAAAAAAAAA 1

RESULT 956
CF311836
LOCUS
DEFINITION ABF--07-E11.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311836
VERSION CF311836.1 GI:33683597
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .12
/organism="Oryza sativa"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1747
Db 1 AAAAAAAAAAAAAA 12

RESULT 957
CF313356/c
LOCUS
DEFINITION HD--01-H09.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-H09, mRNA sequence.
ACCESSION CF313356
VERSION CF313356.1 GI:33685117
KEYWORDS

SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..12
/organism="Oryza sativa"
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CDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
|||||
Db 12 AAAAAAAAAAAAA 1

RESULT 958
CF315565/c
LOCUS
DEFINITION
HD--04-I14.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa CDNA clone HD--04-I14, mRNA sequence.
ACCESSION
CF315565
VERSION
CF315565.1 GI:33687326
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..12
/organism="Oryza sativa"
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/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
|||||
Db 12 AAAAAAAAAAAAA 1

RESULT 958
CF315565/c
LOCUS
DEFINITION
HD--04-I14.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa CDNA clone HD--04-I14, mRNA sequence.
ACCESSION
CF315565
VERSION
CF315565.1 GI:33687326
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
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FEATURES
source
1..12
/organism="Oryza sativa"
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/cultivar="Nackdong"
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CDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
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Db 12 AAAAAAAAAAAAA 1

RESULT 959
CF317551/c
LOCUS
DEFINITION
HD--07-E16.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa CDNA clone HD--07-E16, mRNA sequence.
ACCESSION
CF317551
VERSION
CF317551.1 GI:33689312
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/lab_host="E.coli DH10B"
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CDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
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Db 12 AAAAAAAAAAAAA 1

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RESULT 960
CF317798/c
LOCUS
DEFINITION
  HD--07-J24.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--07-J24, mRNA sequence.
ACCESSION
VERSION
  CF317798.1 GI:33689559
KEYWORDS
SOURCE
  EST.
ORGANISM
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 12)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.
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Db      12 AAAAAAAAAAAAAA 1

RESULT 961
CF320426/c
LOCUS
DEFINITION
  HD--11-F02.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--11-F02, mRNA sequence.
ACCESSION
VERSION
  CF320426.1 GI:33692187
KEYWORDS
SOURCE
  EST.
ORGANISM
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 12)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.
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      line."
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  Best Local Similarity 100.0%; Pred. No. 8.3e+02;
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Db      12 AAAAAAAAAAAAAA 1

RESULT 962
CF324793/c
LOCUS
DEFINITION
  JMT1--01-H22.g1 AtJMT-overexpressing transgenic rice lambda phage
  cDNA library (JMT1) Oryza sativa cDNA clone JMT1--01-H22, mRNA
  sequence.
ACCESSION
VERSION
  CF324793.1 GI:33797867
KEYWORDS
SOURCE
  EST.
ORGANISM
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 12)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
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  of Bioscience and Bioinformatics, MyongJi University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
Db 12 AAAAAAAAAAAAA 1

RESULT 963

CF326913/c

LOCUS CF326913 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-D01, mRNA sequence.

ACCESSION CF326913
VERSION CF326913.1 GI:33802082
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 12)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 AAAAAAAAAAAAA 1

RESULT 964

CF327376/c

LOCUS CF327376 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-N10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-N10, mRNA sequence.

ACCESSION CF327376
VERSION CF327376.1 GI:33803011
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 12)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
Db 12 AAAAAAAAAAAAA 1

RESULT 965

CF327962/c

LOCUS CF327962 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-K14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-K14, mRNA sequence.

ACCESSION CF327962
VERSION CF327962.1 GI:33804174
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747
Db 12 AAAAAAAAAAAAA 1

RESULT 966
CF328229

LOCUS CF328229 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-A13.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-A13, mRNA sequence.
ACCESSION CF328229
VERSION CF328229.1 GI:33804704
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747
Db 1 AAAAAAAAAAAAA 12

RESULT 967
CF329141/c

LOCUS CF329141 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-F18, mRNA sequence.
ACCESSION CF329141
VERSION CF329141.1 GI:33806519
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747
Db 12 AAAAAAAAAAAAA 1

RESULT 968
CF329142

LOCUS CF329142 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-F18.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-F18, mRNA sequence.
ACCESSION CF329142
VERSION CF329142.1 GI:33806520
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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Db 1 AAAAAAAAAAAAA 12

RESULT 969
CF329346/c
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DEFINITION NACL--04-K07.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF329346
VERSION CF329346.1 GI:33806928
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 AAAAAAAAAAAAA 1

RESULT 970
CF329872/c
LOCUS
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ACCESSION CF329872
VERSION CF329872.1 GI:33807965
KEYWORDS EST.
SOURCE Oryza sativa
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 AAAAAAAAAAAAA 1

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CF329929/c
LOCUS
DEFINITION NACL--05-H03.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF329929
VERSION CF329929.1 GI:33808079
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-H03"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
   |||||
Db 12 AAAAAAAAAAAAA 1

RESULT 972
CF329929/c
LOCUS
DEFINITION NACL--05-H03.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF329929
VERSION CF329929.1 GI:33808079
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-H03"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAA 1747
   |||||
Db 12 AAAAAAAAAAAAA 1

RESULT 970
CF329872/c
LOCUS
DEFINITION NACL--05-F19.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF329872
VERSION CF329872.1 GI:33807965
KEYWORDS EST.
SOURCE Oryza sativa
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.Coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747
|||||
Db 12 AAAAAAAAAAAAA 1

RESULT 972
CF331241/c
LOCUS
DEFINITION NACL--07-E15.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-E15, mRNA sequence.

ACCESSION
VERSION CF331241.1 GI:33810705
KEYWORDS
SOURCE EST.

ORGANISM
Oryza sativa

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

source

1. .12

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--07-E15"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.Coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747
|||||
Db 12 AAAAAAAAAAAAA 1

RESULT 973
CF331858
LOCUS
DEFINITION NACL--08-C08.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-C08, mRNA sequence.

ACCESSION

VERSION CF331858.1 GI:33811939

KEYWORDS EST.

SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

source

1. .12

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--08-C08"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.Coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747
|||||
Db 1 AAAAAAAAAAAAA 12

RESULT 974
CF331904

LOCUS

DEFINITION NACL--08-D07.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-D07, mRNA sequence.

ACCESSION

VERSION CF331904.1 GI:33812029

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

source

1. .12

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--08-D07"


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/tissue_type="callus"  
/dev_stage="proliferated callus on 2N6 media for 30 days"  
/lab_host="E.coli DH10B"  
/clone_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."
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Query Match      0.7%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAA 1747  
|||||  
Db 1 AAAAAAAAAAAAA 12
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RESULT 975  
CF331950/c  
LOCUS  
DEFINITION NACL--08-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--08-E07, mRNA sequence.  
ACCESSION CF331950  
VERSION CF331950.1 GI:33812121  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa
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REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.
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```
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)
```

```
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.
```

FEATURES

source

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1..12  
/organism="Oryza sativa"  
/mol_type="mRNA"  
/cultivar="Nackdong"  
/db_xref="taxon:4530"  
/clone="NACL--08-E07"  
/tissue_type="callus"  
/dev_stage="proliferated callus on 2N6 media for 30 days"  
/lab_host="E.coli DH10B"  
/clone_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."
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Query Match      0.7%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAA 1747  
|||||  
Db 12 AAAAAAAAAAAAA 1
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RESULT 976  
CF332993/c  
LOCUS  
DEFINITION JMT--01-L10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--01-L10, mRNA sequence.  
ACCESSION CF332993  
VERSION CF332993.1 GI:33814228
```

```
KEYWORDS  
SOURCE Oryza sativa  
ORGANISM Oryza sativa
```

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.
```

```
1 (bases 1 to 12)
```

```
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

```
TITLE Large-scale Sequencing Analysis of Rice ESTs
```

```
JOURNAL Unpublished (2003)
```

```
COMMENT Contact: Nahm B.H.
```

```
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355
```

```
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.
```

FEATURES

source

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1..12  
/organism="Oryza sativa"  
/mol_type="mRNA"  
/cultivar="Nackdong"  
/db_xref="taxon:4530"  
/clone="JMT--01-L10"  
/tissue_type="leaf"  
/dev_stage="14 days after germination"  
/lab_host="E.coli DH10B"  
/clone_lib="AtJMT-overexpressing transgenic rice plasmid  
cDNA library (JMT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
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prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."
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Query Match      0.7%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAA 1747  
|||||  
Db 12 AAAAAAAAAAAAA 1
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RESULT 977

CF333992/c

LOCUS

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DEFINITION CF333992 12 bp mRNA linear EST 18-AUG-2003  
JMT--03-B22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--03-B22, mRNA sequence.
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ACCESSION CF333992

VERSION CF333992.1 GI:33816288

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.
```

```
1 (bases 1 to 12)
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```
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

```
TITLE Large-scale Sequencing Analysis of Rice ESTs
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JOURNAL Unpublished (2003)
```

```
COMMENT Contact: Nahm B.H.
```

```
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355
```

```
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.
```

FEATURES

source

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1..12  
/organism="Oryza sativa"  
/mol_type="mRNA"
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/cultivar="Nackdong"
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 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.7%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747

Db 12 AAAAAAAAAAAAAA 1

RESULT 978

CF291593/c

LOCUS
 DEFINITION 14ROOT--02-B10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa cDNA clone 14ROOT--02-B10, mRNA sequence.

ACCESSION

VERSION

KEYWORDS CF291593.1 GI:33660626

SOURCE

ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .14

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ROOT--02-B10"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.7%; Score 12; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.8e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAA 1746

Db 12 CAAAAAAAAAAAA 1

RESULT 979

CF330198/c

LOCUS
 DEFINITION NACL--05-N04.g1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--05-N04, mRNA sequence.

ACCESSION

VERSION

KEYWORDS CF330198.1 GI:33808624

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .14

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--05-N04"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.7%; Score 12; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.8e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1747

Db 14 AAAAAAAAAAAAAA 3

RESULT 980

AW250872/c

LOCUS

DEFINITION 2821138.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821138 3',

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other_ESTs: 2821138.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu> Low Quality Sequence: 8 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 15 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM6 row: A column: 11
High quality sequence stop: 8.
Location/Qualifiers

FEATURES

source

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1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821138"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 0.7%; Score 12; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 9.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1747

Db 13 CAAAAAATAAAAAA 1

RESULT 981

AW248954/C

LOCUS

DEFINITION AW248954.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819408 3',
mRNA sequence.

ACCESSION AW248954

VERSION AW248954.1 GI:6591947

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 15)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other_ESTs: 2819408.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross_match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

<http://www.genome.washington.edu> Low Quality Sequence: 8 contiguous

PHRED high quality bases following vector sequence. Very Low

Quality Sequence: Trace file contained 15 contiguous distinct peaks

following vector sequence. Polyadenylation: Based upon the presence

of a XhoI site followed by a run of 14 or more T residues at the

beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM1 row: I column: 9

High quality sequence stop: 8.

FEATURES

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1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819408"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 0.7%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 9.5e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAAATAAAAA 1745

Db 15 TTCCCAAAAAAATAAAAA 1

RESULT 982

BM658732/C

LOCUS

DEFINITION BM658732 LZV602768445.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
sequence.

ACCESSION BM658732

VERSION BM658732.1 GI:18959003

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 15)

AUTHORS Adelson, D.L. and Gill, C.A.

TITLE Porcine ESTs

JOURNAL Unpublished (2002)

COMMENT Contact: David L. Adelson

Animal Breeding and Genetics

Texas A&M University

Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,

USA

Tel: 9798452616

Fax: 9798456970

Email: david.adelson@tamu.edu.

FEATURES

source

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1. .15
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone_lib="CSEQFXL37 pig adrenal"
/note="Organ: adrenal gland; Vector: pBluescript SK+;
Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNinsert)
GCGAATTGGAGTCCACCGGGTGGCGGCGGGCTCGAG. Sequence 3' of
the inserts (AAGAATCGATATCAAGTTATCGATACCGTCCGACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."
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Query Match

Best Local Similarity 0.7%; Score 11.8; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAATAAAAAA 1750

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Db          15 AAAAAAAAAAGAAAAA 1
|||||||
PUBMED
COMMENT
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
Location/Qualifiers
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC10032"
/clone_lib="Sugano Homo sapiens cDNA library"
Query Match      0.7%; Score 11.8; DB 1; Length 50;
Best Local Similarity 86.7%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 49 AGAAAAAGTTTCTT 63
|||||
Db 16 AGAAACCTTTTCTT 2
|||||
RESULT 985
CF291168
LOCUS
DEFINITION
14ROOT--01-H20.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-H20, mRNA sequence.
ACCESSION
CF291168
VERSION
CF291168.1 GI:33660201
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
source
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-H16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match      0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 9.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAATTAATAAAAA 15
|||||
RESULT 984
AU102455/c
LOCUS
DEFINITION
AU102455 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC10032, mRNA sequence.
ACCESSION
AU102455
VERSION
AU102455.1 GI:13551975
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
Query Match      0.6%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 9.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
|||||
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Db 1 AAAAAATAAAAAA 13

RESULT 986
CF327120 13 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--01-H14.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--01-H14, mRNA sequence.
ACCESSION CF327120.1 GI:33802495
VERSION CF327120
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--01-H14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 9.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAATAAAAAA 1748
Db 1 AAAAAATAAAAAA 13

RESULT 987
CA794555 15 bp mRNA linear EST 05-DEC-2002
LOCUS Cac BL_1497 Cac BL (Bean and Leaf from Amelonardo type Cacao)
DEFINITION Theobroma cacao cDNA clone Cac_BL_1497 5', mRNA sequence.
ACCESSION CA794555
VERSION CA794555.1 GI:26051631
KEYWORDS EST.
SOURCE Theobroma cacao (cacao)
ORGANISM Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
REFERENCE 1 (bases 1 to 15)
AUTHORS Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
Retzel,E.R. and Jones,C.A.
TITLE Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
JOURNAL Planta 216 (2), 255-264 (2002)
MEDLINE 22337596

PUBMED 12447539
COMMENT Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.
FEATURES
Location/Qualifiers
source 1. .15
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 1497"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac BL (Bean and Leaf from Amelonardo type
Cacao)"
/note="Vector: PBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

Query Match 0.6%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 336 GGGACCGGAGGAT 348
Db 2 GGGACCGGAGGAT 14

RESULT 988
CF330490 20 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--06-D16.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--06-D16, mRNA sequence.
ACCESSION CF330490
VERSION CF330490.1 GI:33809214
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source 1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-D16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 11.2; DB 1; Length 20;

Best Local Similarity 81.2%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 57 TTTTCTTTTCTGGAGT 72
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Db 5 TTTTCTTTTCTGGAGT 20

RESULT 989
BQ589109

LOCUS
DEFINITION S013715-024-015-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-015-B24 3-PRIME, mRNA sequence.

ACCESSION BQ589109
VERSION BQ589109
KEYWORDS
SOURCE EST.
ORGANISM Beta vulgaris

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 15 row: B column: 24
Seq primer: T7; GTAATACGACTCACTATAGGGC.

FEATURES
source
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:187957"
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/clone="024-015-B24"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746
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Db 1 AAAAAAAAAA 11

RESULT 990
BQ590590/c

LOCUS
DEFINITION BQ590590 11 bp mRNA linear EST 06-DEC-2002
E012846-024-019-D02-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-019-D02 3-PRIME, mRNA sequence.

ACCESSION BQ590590
VERSION BQ590590.1 GI:26120173
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 19 row: D column: 02
Seq primer: T7; GTAATACGACTCACTATAGGGC.

FEATURES
source
1. .11
/organism="Beta vulgaris"
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/cultivar="KWS2320 (double haploid, monogerm breeding line)"
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/clone="024-019-D02"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746
|||||
Db 11 AAAAAAAAAA 1

RESULT 991
BQ595827/c

LOCUS
DEFINITION BQ595827 11 bp mRNA linear EST 06-DEC-2002
S013315-024-021-P01-T7 MPIZ-ADIS-024-developing root Beta vulgaris
CDNA clone 024-021-P01 3-PRIME, mRNA sequence.

ACCESSION BQ595827
VERSION BQ595827.1 GI:26125410
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 21 row: p column: 01
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1..11
/organism="Beta vulgaris"
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line)"
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/clone="024-021-P01"
/tissue type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746
Db 11 AAAAAAAAAA 1

RESULT 992
BQ595834/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BQ595834
S013315-024-021-B01-T7 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-021-B01 3-PRIME, mRNA sequence.
BQ595834
BQ595834.1 GI:26125417
EST.
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 21 row: B column: 01
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1..11
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:191022"
/db_xref="taxon:161934"
/clone="024-021-B01"
/tissue type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746
Db 11 AAAAAAAAAA 1

RESULT 993
CF281971/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CF281971
14ETL--09-E07.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-E07, mRNA sequence.
CF281971 GI:33659358
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-E07"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA 1746
Db 11 AAAAAAAAAA 1

RESULT 994
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LOCUS
DEFINITION 14ROOT--01-C22.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-C22, mRNA sequence.
ACCESSION CF290941
VERSION CF290941.1 GI:33659974
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA 1746
Db 11 AAAAAAAAAA 1

RESULT 995
CF290942/c
LOCUS
DEFINITION 14ROOT--01-C22.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-C22, mRNA sequence.
ACCESSION CF290942
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CF290942.1 GI:33659975
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Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..11
/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
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Qy 1736 AAAAAAAAAA 1746
Db 1 AAAAAAAAAA 11

RESULT 996
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DEFINITION 14ROOT--01-004.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-004, mRNA sequence.
ACCESSION CF291453
VERSION CF291453.1 GI:33660486
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAAAAAAAA 11

RESULT 997
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LOCUS
DEFINITION 14ROOT--01-004.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-004, mRNA sequence.
ACCESSION CF291453
VERSION CF291453.1 GI:33660486
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
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Qy 1736 AAAAAAAAAA 1746
Db 1 AAAAAAAAAA 11

RESULT 998
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LOCUS
DEFINITION 14ROOT--01-004.b1 Rice root plasmid cDNA library (14ROOT) Oryza
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ACCESSION CF291453
VERSION CF291453.1 GI:33660486
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Qy 1736 AAAAAAAAAA 1746
Db 1 AAAAAAAAAA 11

RESULT 999
CF291453/c
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DEFINITION 14ROOT--01-C22.g1 Rice root plasmid cDNA library (14ROOT) Oryza
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ACCESSION CF290942
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA 1746
Db 1 AAAAAAAAAA 11

RESULT 1000
CF292236
LOCUS      11 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 14ROOT--02-P21.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-P21, mRNA sequence.
ACCESSION  CF292236
VERSION     CF292236.1 GI:33661269
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 11)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 AAAAAAAAAA 11

RESULT 1001
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LOCUS      11 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--01-C03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-C03, mRNA sequence.
ACCESSION  CF297948
VERSION     CF297948.1 GI:33669709
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 11)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Qy 1736 AAAAAAAAAA 1746
Db 1 AAAAAAAAAA 11

RESULT 1001
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ACCESSION  CF297318
VERSION     CF297318.1 GI:33666351
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 11)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY 1736 AAAAAAAAAA 1746
Db 11 AAAAAAAAAA 1

RESULT 1003
CF299806/c
LOCUS
DEFINITION
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sativa cDNA clone 7LEAF--02-G21, mRNA sequence.
ACCESSION
CF299806
VERSION
CF299806.1 GI:33670567
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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QY 1736 AAAAAAAAAA 1746
Db 11 AAAAAAAAAA 1

RESULT 1004
CF299648/c
LOCUS
DEFINITION
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sativa cDNA clone 7LEAF--04-A13, mRNA sequence.
ACCESSION
CF299648
VERSION
CF299648.1 GI:33671610
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
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QY 1736 AAAAAAAAAA 1746
Db 11 AAAAAAAAAA 1

RESULT 1004
CF299648/c
LOCUS
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sativa cDNA clone 7LEAF--03-M01, mRNA sequence.
ACCESSION
CF299648
VERSION
CF299648.1 GI:33671409
KEYWORDS
EST.
SOURCE
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ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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QY 1736 AAAAAAAAAA 1746
Db 11 AAAAAAAAAA 1

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DEFINITION
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sativa cDNA clone 7LEAF--04-A13, mRNA sequence.
ACCESSION
CF299849
VERSION
CF299849.1 GI:33671610
KEYWORDS
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SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Db 11 AAAAAAAAAA 1

RESULT 1006
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sativa cDNA clone 7LEAF--04-H16, mRNA sequence.
ACCESSION CF300174
VERSION CF300174.1 GI:33671935
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Db 11 AAAAAAAAAA 1

RESULT 1007
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sativa cDNA clone 7LEAF--06-B16, mRNA sequence.
ACCESSION CF301288
VERSION CF301288.1 GI:33673049
KEYWORDS EST.
SOURCE Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Db 11 AAAAAAAAAA 1

RESULT 1008
CF301713/c
LOCUS
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sativa cDNA clone 7LEAF--06-K21, mRNA sequence.
ACCESSION CF301713
VERSION CF301713.1 GI:33673474
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA 1746
Db 1 AAAAAAAAAA 11

RESULT 1009
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LOCUS
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sativa cDNA clone 7LEAF--06-L14, mRNA sequence.
ACCESSION
CF301744
VERSION
CF301744.1 GI:33673505
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA 1746
Db 1 AAAAAAAAAA 11

RESULT 1010
CF301744/c
LOCUS
DEFINITION
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sativa cDNA clone 7LEAF--06-L14, mRNA sequence.
ACCESSION
CF301744
VERSION
CF301744.1 GI:33673505
KEYWORDS
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SOURCE
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ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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ACCESSION
CF302896
VERSION
CF302896.1 GI:33674657
KEYWORDS
EST.
SOURCE
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ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 1 AAAAAAAAAA 11

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library (ABF) Oryza sativa cDNA clone ABF--01-G20, mRNA sequence.
ACCESSION
CF307845
VERSION
CF307845.1 GI:33679606
KEYWORDS
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SOURCE
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ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
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1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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```


Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

TITLE
JOURNAL
COMMENT

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Db 1 AAAAAAAAAA 11

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library (HD) Oryza sativa cDNA clone HD--03-B13, mRNA sequence.
ACCESSION CF314533
VERSION CF314533.1 GI:33686294
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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TITLE
JOURNAL
COMMENT

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line."

Query Match 0.6%; Score 11; DB 1; Length 11;
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Db 11 AAAAAAAAAA 1

RESULT 1016
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LOCUS
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library (HD) Oryza sativa cDNA clone HD--08-P20, mRNA sequence.
ACCESSION CF318741
VERSION CF318741.1 GI:33690502
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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TITLE
JOURNAL
COMMENT

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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA 1746
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Db 11 AAAAAAAAAA 1

RESULT 1017
CF326997/c
LOCUS
DEFINITION NACL--01-E20.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-E20, mRNA sequence.

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ACCESSION      CF326997
VERSION        CF326997.1  GI:33802249
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, MyongJi University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       11 AAAAAAAAAA 1

RESULT 1018
CF326998
LOCUS        CF326998
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ACCESSION    CF326998
VERSION      CF326998.1  GI:33802251
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, MyongJi University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
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                /mol_type="mRNA"

ACCESSION      CF326997
VERSION        CF326997.1  GI:33802249
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
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                Fax: 82 31 321 6355
                Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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                /clone_lib="Rice callus plasmid cDNA library (NACL)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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                RT-PCR."

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAA 1746
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Db       11 AAAAAAAAAA 1

RESULT 1018
CF326998
LOCUS        CF326998
DEFINITION  NACL--01-E20.g1 Rice callus plasmid cDNA library (NACL) Oryza
                sativa CDNA clone NACL--01-E20, mRNA sequence.
ACCESSION    CF326998
VERSION      CF326998.1  GI:33802251
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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                Fax: 82 31 321 6355
                Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
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                /organism="Oryza sativa"
                /mol_type="mRNA"
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                /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAA 1746
        |||||
Db       11 AAAAAAAAAA 1

RESULT 1020
CF328618/c
LOCUS        CF328618
DEFINITION  NACL--03-J20.b1 Rice callus plasmid cDNA library (NACL) Oryza
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                /lab_host="E.coli DH10B"
                /clone_lib="Rice callus plasmid cDNA library (NACL)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAA 1746
        |||||
Db       11 AAAAAAAAAA 1

RESULT 1019
CF327885
LOCUS        CF327885
DEFINITION  NACL--02-I20.g1 Rice callus plasmid cDNA library (NACL) Oryza
                sativa CDNA clone NACL--02-I20, mRNA sequence.
ACCESSION    CF327885
VERSION      CF327885.1  GI:33804018
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
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                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
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                /dev_stage="proliferated callus on 2N6 media for 30 days"
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                /clone_lib="Rice callus plasmid cDNA library (NACL)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAA 1746
        |||||
Db       11 AAAAAAAAAA 1

RESULT 1020
CF328618/c
LOCUS        CF328618
DEFINITION  NACL--03-J20.b1 Rice callus plasmid cDNA library (NACL) Oryza
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sativa cDNA clone NACL--03-J20, mRNA sequence.

ACCESSION CF328618
VERSION CF328618.1 GI:33805485
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..11

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

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/tissue_type="callus"

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/lab_host="E.coli DH10B"

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

Best Local Similarity 0.6%; Score 11; DB 1; Length 11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746

Db 11 AAAAAAAAAA 1

RESULT 1021

CF328619

LOCUS

DEFINITION NACL--03-J20.g1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--03-J20, mRNA sequence.

ACCESSION CF328619

VERSION CF328619.1 GI:33805487

KEYWORDS EST.

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa"

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Query Match

Best Local Similarity 0.6%; Score 11; DB 1; Length 11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746

Db 1 AAAAAAAAAA 11

RESULT 1022

CF329242/c

LOCUS

DEFINITION NACL--04-H23.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--04-H23, mRNA sequence.

ACCESSION CF329242

VERSION CF329242.1 GI:33806721

KEYWORDS EST.

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..11

/organism="Oryza sativa"

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Best Local Similarity 0.6%; Score 11; DB 1; Length 11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746

Db 11 AAAAAAAAAA 1

RESULT 1023

CF329344/c

LOCUS

DEFINITION NACL--04-H23.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--04-H23, mRNA sequence.

ACCESSION CF329344

VERSION CF329344.1 GI:33806721

KEYWORDS EST.

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

DEFINITION NACL--04-K06.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-K06, mRNA sequence.
ACCESSION CF329344
VERSION CF329344.1 GI:33806925
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 11)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746
|||||
Db 11 AAAAAAAAAA 1

RESULT 1024
CF329345
LOCUS CF329345 11 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-K06.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-K06, mRNA sequence.
ACCESSION CF329345
VERSION CF329345.1 GI:33806926
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 11)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746
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Db 1 AAAAAAAAAA 11

RESULT 1025
CF331049/c
LOCUS CF331049 11 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--07-A08.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-A08, mRNA sequence.
ACCESSION CF331049
VERSION CF331049.1 GI:33810315
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 11)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746
|||||
Db 11 AAAAAAAAAA 1

RESULT 1026
CF331066/c

LOCUS CF331066 11 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--07-A17.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-A17, mRNA sequence.

ACCESSION CF331066
VERSION CF331066.1 GI:33810350
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 11)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

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Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

source 1..11

/organism="Oryza sativa"

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/cultivar="Nackdong"

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/clone="NACL--07-A17"

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/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.6%; Score 11; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746

|||||

11 AAAAAAAAAA 1

Db

RESULT 1027

CF331814/c

LOCUS CF331814 11 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--08-B09.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--08-B09, mRNA sequence.

ACCESSION CF331814

VERSION CF331814.1 GI:33811850

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 11)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

source 1..11

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone="NACL--08-B09"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

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RT-PCR."

Query Match 0.6%; Score 11; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746

|||||

11 AAAAAAAAAA 1

Db

RESULT 1028

CF331815

LOCUS CF331815 11 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--08-B09.g1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--08-B09, mRNA sequence.

ACCESSION CF331815

VERSION CF331815.1 GI:33811852

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 11)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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FEATURES Location/Qualifiers

source 1..11

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--08-B09"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.6%; Score 11; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1746

|||||

11 AAAAAAAAAA 1

Db

Search completed: August 16, 2004, 16:46:28

Job time : 24 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 15:30:11 ; Search time 21 Seconds
(without alignments)
3.625 Million cell updates/sec

Title: us-10-008-789-3
Perfect score: 1755
Sequence: 1 cgccggcaggtcccaaa.....aaaaaaaaaaaaaaaa 1755

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1219 seqs, 21686 residues

Total number of hits satisfying chosen parameters: 2438

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1223 summaries

Database : rnpbdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	22.4	1.3	24	1	US-10-002-536A-4
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C 7	21.4	1.2	24	1	US-09-853-526-10
C 8	21.4	1.2	26	1	US-09-923-480-7
C 9	21.4	1.2	26	1	US-09-923-236-7
C 10	21.4	1.2	26	1	US-09-923-469-38
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c 131	20	1.1	20	1	US-09-916-369A-1	Sequence 1, Appli	c 204	20	1.1	20	1	US-10-008-789-60	Sequence 60, Appl
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c 133	20	1.1	20	1	US-10-181-200-10	Sequence 10, Appl	c 206	20	1.1	20	1	US-10-008-789-62	Sequence 62, Appl
c 134	20	1.1	20	1	US-10-181-200-15	Sequence 15, Appl	c 207	20	1.1	20	1	US-10-008-789-63	Sequence 63, Appl
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c 159	20	1.1	20	1	US-10-008-789-15	Sequence 15, Appl	c 232	20	1.1	20	1	US-10-716-829-55	Sequence 55, Appl
c 160	20	1.1	20	1	US-10-008-789-16	Sequence 16, Appl	c 233	20	1.1	20	1	US-10-671-395-178	Sequence 178, App
c 161	20	1.1	20	1	US-10-008-789-17	Sequence 17, Appl	c 234	20	1.1	20	1	US-10-671-395-179	Sequence 179, App
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c 163	20	1.1	20	1	US-10-008-789-19	Sequence 19, Appl	c 236	20	1.1	20	1	US-10-671-395-181	Sequence 181, App
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c 165	20	1.1	20	1	US-10-008-789-21	Sequence 21, Appl	c 238	20	1.1	20	1	US-10-671-395-183	Sequence 183, App
c 166	20	1.1	20	1	US-10-008-789-22	Sequence 22, Appl	c 239	20	1.1	20	1	US-10-671-395-184	Sequence 184, App
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c 168	20	1.1	20	1	US-10-008-789-24	Sequence 24, Appl	c 241	20	1.1	20	1	US-10-671-395-186	Sequence 186, App
c 169	20	1.1	20	1	US-10-008-789-25	Sequence 25, Appl	c 242	20	1.1	20	1	US-10-671-395-187	Sequence 187, App
c 170	20	1.1	20	1	US-10-008-789-26	Sequence 26, Appl	c 243	20	1.1	20	1	US-10-671-395-188	Sequence 188, App
c 171	20	1.1	20	1	US-10-008-789-27	Sequence 27, Appl	c 244	20	1.1	20	1	US-10-671-395-189	Sequence 189, App
c 172	20	1.1	20	1	US-10-008-789-28	Sequence 28, Appl	c 245	20	1.1	20	1	US-10-671-395-190	Sequence 190, App
c 173	20	1.1	20	1	US-10-008-789-29	Sequence 29, Appl	c 246	20	1.1	20	1	US-10-671-395-191	Sequence 191, App
c 174	20	1.1	20	1	US-10-008-789-30	Sequence 30, Appl	c 247	20	1.1	20	1	US-10-671-395-192	Sequence 192, App
c 175	20	1.1	20	1	US-10-008-789-31	Sequence 31, Appl	c 248	20	1.1	20	1	US-10-671-395-193	Sequence 193, App
c 176	20	1.1	20	1	US-10-008-789-32	Sequence 32, Appl	c 249	20	1.1	20	1	US-10-671-395-194	Sequence 194, App
c 177	20	1.1	20	1	US-10-008-789-33	Sequence 33, Appl	c 250	20	1.1	20	1	US-10-671-395-195	Sequence 195, App
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c 179	20	1.1	20	1	US-10-008-789-35	Sequence 35, Appl	c 252	20	1.1	20	1	US-10-671-395-197	Sequence 197, App

C 253	20	1.1	20	1	US-10-671-395-198	Sequence 198, App	Sequence 198, App	19	1.1	19	1	US-10-098-816-15	Sequence 15, Appl
C 254	20	1.1	20	1	US-10-671-395-199	Sequence 199, App	Sequence 199, App	19	1.1	19	1	US-10-098-816-16	Sequence 16, Appl
C 255	20	1.1	20	1	US-10-671-395-200	Sequence 200, App	Sequence 200, App	19	1.1	19	1	US-10-098-816-17	Sequence 17, Appl
C 256	20	1.1	20	1	US-10-671-395-201	Sequence 201, App	Sequence 201, App	19	1.1	19	1	US-10-098-816-18	Sequence 18, Appl
C 257	20	1.1	20	1	US-10-671-395-202	Sequence 202, App	Sequence 202, App	19	1.1	19	1	US-10-098-816-26	Sequence 26, Appl
C 258	20	1.1	20	1	US-10-671-395-203	Sequence 203, App	Sequence 203, App	19	1.1	19	1	US-10-322-242-1	Sequence 1, Appli
C 259	20	1.1	20	1	US-10-671-395-204	Sequence 204, App	Sequence 204, App	19	1.1	19	1	US-10-371-600-14	Sequence 14, Appl
C 260	20	1.1	20	1	US-10-671-395-205	Sequence 205, App	Sequence 205, App	19	1.1	19	1	US-10-170-172-16	Sequence 16, Appl
C 261	20	1.1	20	1	US-10-671-395-206	Sequence 206, App	Sequence 206, App	19	1.1	19	1	US-10-205-309-325	Sequence 325, App
C 262	20	1.1	20	1	US-10-671-395-207	Sequence 207, App	Sequence 207, App	19	1.1	19	1	US-10-205-309-650	Sequence 650, App
C 263	20	1.1	20	1	US-10-671-395-208	Sequence 208, App	Sequence 208, App	19	1.1	19	1	US-10-331-109-33	Sequence 33, Appl
C 264	20	1.1	20	1	US-10-671-395-262	Sequence 262, App	Sequence 262, App	19	1.1	19	1	US-10-359-328-5	Sequence 5, Appli
C 265	20	1.1	20	1	US-10-671-395-274	Sequence 274, App	Sequence 274, App	19	1.1	19	1	US-10-359-328-26	Sequence 26, Appl
C 266	20	1.1	20	1	US-10-671-395-275	Sequence 275, App	Sequence 275, App	19	1.1	19	1	US-10-387-346B-154	Sequence 154, App
C 267	20	1.1	20	1	US-10-671-395-276	Sequence 276, App	Sequence 276, App	19	1.1	20	1	US-09-005-243-32	Sequence 32, Appl
C 268	20	1.1	20	1	US-10-671-395-277	Sequence 277, App	Sequence 277, App	19	1.1	20	1	US-09-224-683-32	Sequence 32, Appl
C 269	20	1.1	20	1	US-10-671-395-311	Sequence 311, App	Sequence 311, App	19	1.1	20	1	US-09-916-369A-3	Sequence 3, Appli
C 270	20	1.1	20	1	US-10-671-395-338	Sequence 338, App	Sequence 338, App	19	1.1	20	1	US-10-671-395-654	Sequence 654, App
C 271	20	1.1	20	1	US-10-671-395-376	Sequence 376, App	Sequence 376, App	19	1.1	24	1	US-10-182-434-1	Sequence 1, Appli
C 272	20	1.1	20	1	US-10-671-395-403	Sequence 403, App	Sequence 403, App	19	1.1	25	1	US-09-754-853A-686	Sequence 686, App
C 273	20	1.1	20	1	US-10-671-395-427	Sequence 427, App	Sequence 427, App	19	1.1	25	1	US-10-396-551-15	Sequence 15, Appl
C 274	20	1.1	20	1	US-10-671-395-433	Sequence 433, App	Sequence 433, App	18.8	1.1	24	1	US-10-309-775A-20	Sequence 20, Appl
C 275	20	1.1	20	1	US-10-671-395-444	Sequence 444, App	Sequence 444, App	18.8	1.1	24	1	US-10-309-775A-27	Sequence 27, Appl
C 276	20	1.1	20	1	US-10-671-395-487	Sequence 487, App	Sequence 487, App	18.8	1.1	24	1	US-10-309-775A-28	Sequence 28, Appl
C 277	20	1.1	20	1	US-10-671-395-575	Sequence 575, App	Sequence 575, App	18.4	1.0	20	1	US-09-005-243-33	Sequence 33, Appl
C 278	20	1.1	21	1	US-09-888-326-840	Sequence 840, App	Sequence 840, App	18.4	1.0	20	1	US-09-005-243-34	Sequence 34, Appl
C 279	20	1.1	21	1	US-09-912-014-2	Sequence 2, Appli	Sequence 2, Appli	18.4	1.0	20	1	US-09-224-683-33	Sequence 33, Appl
C 280	20	1.1	21	1	US-09-997-672-41	Sequence 41, Appl	Sequence 41, Appl	18.4	1.0	20	1	US-09-224-683-34	Sequence 34, Appl
C 281	20	1.1	21	1	US-09-776-479-912	Sequence 912, App	Sequence 912, App	18.4	1.0	20	1	US-10-728-399-87	Sequence 87, Appl
C 282	20	1.1	21	1	US-09-776-479-912	Sequence 912, App	Sequence 912, App	18.4	1.0	21	1	US-10-418-182-106	Sequence 106, App
C 283	20	1.1	21	1	US-10-144-179A-41	Sequence 41, Appl	Sequence 41, Appl	18.4	1.0	22	1	US-09-995-898A-27	Sequence 27, Appl
C 284	20	1.1	21	1	US-10-314-578-912	Sequence 912, App	Sequence 912, App	18.4	1.0	22	1	US-10-420-034A-27	Sequence 27, Appl
C 285	20	1.1	21	1	US-10-096-221-4	Sequence 4, Appli	Sequence 4, Appli	18.4	1.0	24	1	US-10-309-775A-21	Sequence 21, Appl
C 286	20	1.1	21	1	US-10-112-653-881	Sequence 881, App	Sequence 881, App	18.2	1.0	19	1	US-09-371-307-85	Sequence 85, Appl
C 287	20	1.1	21	1	US-10-017-995-912	Sequence 912, App	Sequence 912, App	18.2	1.0	19	1	US-10-176-884-44	Sequence 44, Appl
C 288	20	1.1	21	1	US-10-100-321-23	Sequence 23, Appl	Sequence 23, Appl	18.2	1.0	19	1	US-10-177-478-1	Sequence 1, Appli
C 289	20	1.1	21	1	US-10-371-066-2	Sequence 2, Appli	Sequence 2, Appli	18.2	1.0	19	1	US-10-182-230-196	Sequence 196, App
C 290	20	1.1	21	1	US-10-170-172-2	Sequence 2, Appli	Sequence 2, Appli	18.2	1.0	19	1	US-10-401-321-85	Sequence 85, Appl
C 291	20	1.1	21	1	US-10-410-031-188	Sequence 188, App	Sequence 188, App	18	1.0	18	1	US-09-809-545A-84	Sequence 84, Appl
C 292	20	1.1	21	1	US-10-410-031-189	Sequence 189, App	Sequence 189, App	18	1.0	18	1	US-09-888-326-837	Sequence 837, App
C 293	20	1.1	21	1	US-10-435-489-41	Sequence 41, Appl	Sequence 41, Appl	18	1.0	18	1	US-09-994-311-6	Sequence 6, Appli
C 294	20	1.1	21	1	US-10-278-760-2	Sequence 2, Appli	Sequence 2, Appli	18	1.0	18	1	US-09-776-479-913	Sequence 913, App
C 295	19.4	1.1	24	1	US-10-401-520-118	Sequence 118, App	Sequence 118, App	18	1.0	18	1	US-09-776-479-913	Sequence 913, App
C 296	19.2	1.1	24	1	US-10-038-335-4	Sequence 4, Appli	Sequence 4, Appli	18	1.0	18	1	US-09-776-479-939	Sequence 939, App
C 297	19.2	1.1	24	1	US-10-232-927A-29	Sequence 29, Appl	Sequence 29, Appl	18	1.0	18	1	US-09-776-479-939	Sequence 939, App
C 298	19.2	1.1	24	1	US-10-232-927A-32	Sequence 32, Appl	Sequence 32, Appl	18	1.0	18	1	US-09-370-541-14	Sequence 14, Appl
C 299	19.2	1.1	24	1	US-10-232-927A-34	Sequence 34, Appl	Sequence 34, Appl	18	1.0	18	1	US-09-979-275A-7	Sequence 7, Appli
C 300	19.2	1.1	24	1	US-10-118-854-29	Sequence 29, Appl	Sequence 29, Appl	18	1.0	18	1	US-10-389-417-97	Sequence 97, Appl
C 301	19.2	1.1	24	1	US-10-607-455-29	Sequence 29, Appl	Sequence 29, Appl	18	1.0	18	1	US-10-292-088-144	Sequence 144, App
C 302	19	1.1	19	1	US-09-917-138-1	Sequence 1, Appli	Sequence 1, Appli	18	1.0	18	1	US-10-314-578-913	Sequence 913, App
C 303	19	1.1	19	1	US-09-901-484A-515	Sequence 515, App	Sequence 515, App	18	1.0	18	1	US-10-125-295-9	Sequence 9, Appli
C 304	19	1.1	19	1	US-09-853-526-515	Sequence 515, App	Sequence 515, App	18	1.0	18	1	US-10-208-357-24	Sequence 24, Appl
C 305	19	1.1	19	1	US-09-970-971A-15	Sequence 15, Appl	Sequence 15, Appl	18	1.0	18	1	US-10-112-653-882	Sequence 882, App
C 306	19	1.1	19	1	US-09-970-971A-16	Sequence 16, Appl	Sequence 16, Appl	18	1.0	18	1	US-10-017-995-913	Sequence 913, App
C 307	19	1.1	19	1	US-09-970-971A-26	Sequence 26, Appl	Sequence 26, Appl	18	1.0	18	1	US-10-017-995-939	Sequence 939, App
C 308	19	1.1	19	1	US-10-208-357-25	Sequence 25, Appl	Sequence 25, Appl	18	1.0	18	1	US-10-206-613-4	Sequence 4, Appli
C 309	19	1.1	19	1	US-10-123-597-1	Sequence 1, Appli	Sequence 1, Appli	18	1.0	18	1	US-10-056-479A-15	Sequence 15, Appl
C 310	19	1.1	19	1	US-10-123-597-2	Sequence 2, Appli	Sequence 2, Appli	18	1.0	18	1	US-10-352-704-12	Sequence 12, Appl
C 311	19	1.1	19	1	US-10-123-597-3	Sequence 3, Appli	Sequence 3, Appli	18	1.0	18	1	US-10-352-704-18	Sequence 18, Appl
C 312	19	1.1	19	1	US-10-123-597-4	Sequence 4, Appli	Sequence 4, Appli	18	1.0	18	1	US-10-075-335-9	Sequence 9, Appli
C 313	19	1.1	19	1	US-10-123-597-5	Sequence 5, Appli	Sequence 5, Appli	18	1.0	18	1	US-10-389-155-97	Sequence 97, Appl
C 314	19	1.1	19	1	US-10-123-597-6	Sequence 6, Appli	Sequence 6, Appli	18	1.0	18	1	US-10-271-602B-84	Sequence 84, Appl
C 315	19	1.1	19	1	US-10-123-597-7	Sequence 7, Appli	Sequence 7, Appli	18	1.0	18	1	US-10-334-143-204	Sequence 204, App
C 316	19	1.1	19	1	US-10-123-597-8	Sequence 8, Appli	Sequence 8, Appli	18	1.0	18	1	US-10-653-416-26	Sequence 26, Appl
C 317	19	1.1	19	1	US-10-123-597-12	Sequence 12, Appl	Sequence 12, Appl	18	1.0	18	1	US-10-785-744-15	Sequence 15, Appl
C 318	19	1.1	19	1	US-10-123-597-14	Sequence 14, Appl	Sequence 14, Appl	18	1.0	18	1	US-09-917-138-2	Sequence 2, Appli
C 319	19	1.1	19	1	US-10-123-597-15	Sequence 15, Appl	Sequence 15, Appl	18	1.0	19	1	US-09-996-292A-54	Sequence 54, Appl
C 320	19	1.1	19	1	US-10-123-597-25	Sequence 25, Appl	Sequence 25, Appl	18	1.0	19	1	US-09-996-292A-55	Sequence 55, Appl
C 321	19	1.1	19	1	US-10-100-321-24	Sequence 24, Appl	Sequence 24, Appl	18	1.0	19	1	US-10-096-221-3	Sequence 3, Appli
C 322	19	1.1	19	1	US-10-232-881-1	Sequence 1, Appli	Sequence 1, Appli	18	1.0	19	1	US-10-100-321-22	Sequence 22, Appl
C 323	19	1.1	19	1	US-10-247-893-3	Sequence 3, Appli	Sequence 3, Appli	18	1.0	19	1	US-10-013-295-54	Sequence 54, Appl
C 324	19	1.1	19	1	US-10-247-893-7	Sequence 7, Appli	Sequence 7, Appli	18	1.0	19	1	US-10-013-295-55	Sequence 55, Appl
C 325	19	1.1	19	1	US-10-247-893-13	Sequence 13, Appl	Sequence 13, Appl	18	1.0	19	1		

C 399	18	1.0	20	1	US-10-671-395-558	Sequence 558, Appl	C 472	16	0.9	17	1	US-10-380-255-8	Sequence 8, Appli
400	17.4	1.0	20	1	US-09-955-410-4	Sequence 4, Appli	C 473	16	0.9	17	1	US-10-138-674-1074	Sequence 1074, Ap
401	17.4	1.0	20	1	US-10-154-890-4	Sequence 4, Appli	C 474	16	0.9	17	1	US-10-138-674-1075	Sequence 1075, Ap
C 402	17.4	1.0	20	1	US-10-728-399-141	Sequence 141, App	C 475	16	0.9	17	1	US-10-287-949A-1074	Sequence 1074, Ap
C 403	17.2	1.0	22	1	US-09-776-479-61	Sequence 61, Appl	C 476	16	0.9	17	1	US-10-287-949A-1075	Sequence 1075, Ap
C 404	17.2	1.0	22	1	US-09-776-479-61	Sequence 61, Appl	C 477	16	0.9	18	1	US-09-994-311-7	Sequence 7, Appli
C 405	17.2	1.0	22	1	US-10-314-578-61	Sequence 61, Appl	C 478	16	0.9	20	1	US-10-275-080A-5	Sequence 5, Appli
C 406	17.2	1.0	22	1	US-10-112-653-55	Sequence 55, Appl	C 479	16	0.9	20	1	US-10-363-198-47	Sequence 47, Appl
C 407	17.2	1.0	22	1	US-10-017-995-61	Sequence 61, Appl	C 480	16	0.9	20	1	US-10-671-395-990	Sequence 990, App
C 408	17	1.0	17	1	US-09-843-676-132	Sequence 132, App	C 481	15.8	0.9	20	1	US-09-982-262B-57	Sequence 57, Appl
C 409	17	1.0	17	1	US-09-766-253-132	Sequence 132, App	C 482	15.8	0.9	20	1	US-09-899-440-1	Sequence 1, Appli
C 410	17	1.0	17	1	US-09-438-486-132	Sequence 132, App	C 483	15.8	0.9	20	1	US-09-915-814-96	Sequence 96, Appl
C 411	17	1.0	17	1	US-10-208-357-23	Sequence 23, Appl	C 484	15.8	0.9	20	1	US-10-454-663-57	Sequence 57, Appl
C 412	17	1.0	17	1	US-10-053-758-132	Sequence 132, App	C 485	15.8	0.9	20	1	US-10-006-430-26	Sequence 26, Appl
C 413	17	1.0	17	1	US-10-054-295-132	Sequence 132, App	C 486	15.8	0.9	20	1	US-10-688-706-13	Sequence 13, Appl
C 414	17	1.0	17	1	US-10-117-267-5	Sequence 5, Appli	C 487	15.8	0.9	20	1	US-10-688-706-49	Sequence 49, Appl
C 415	17	1.0	17	1	US-10-054-611-132	Sequence 132, App	C 488	15.8	0.9	20	1	US-10-316-755-105	Sequence 105, App
C 416	17	1.0	17	1	US-10-324-409B-16	Sequence 16, Appl	C 489	15.8	0.9	20	1	US-10-728-399-292	Sequence 292, App
C 417	17	1.0	18	1	US-09-994-311-5	Sequence 5, Appli	C 490	15.8	0.9	21	1	US-09-964-261-73	Sequence 73, Appl
C 418	17	1.0	20	1	US-10-671-395-616	Sequence 616, App	C 491	15.8	0.9	21	1	US-10-349-143-10471	Sequence 10471, A
C 419	16.8	1.0	20	1	US-09-263-959-849	Sequence 849, App	C 492	15.6	0.9	17	1	US-10-301-764-17	Sequence 17, Appl
C 420	16.8	1.0	20	1	US-10-181-846-68	Sequence 68, Appl	C 493	15.6	0.9	17	1	US-10-146-474-17	Sequence 17, Appl
C 421	16.8	1.0	20	1	US-10-728-399-199	Sequence 199, App	C 494	15.4	0.9	17	1	US-09-780-533A-2364	Sequence 2364, Ap
C 422	16.8	1.0	20	1	US-10-728-399-273	Sequence 273, App	C 495	15.4	0.9	17	1	US-10-156-306-521	Sequence 521, App
C 423	16.8	1.0	20	1	US-10-728-399-400	Sequence 400, App	C 496	15.4	0.9	17	1	US-10-156-306-524	Sequence 524, App
C 424	16.4	0.9	18	1	US-09-775-479-9	Sequence 9, Appli	C 497	15.4	0.9	18	1	US-09-808-602-46	Sequence 46, Appl
C 425	16.4	0.9	18	1	US-10-333-461-18	Sequence 18, Appl	C 498	15.4	0.9	18	1	US-09-808-602-47	Sequence 47, Appl
C 426	16.4	0.9	18	1	US-10-352-253A-18	Sequence 18, Appl	C 499	15.4	0.9	18	1	US-09-994-177-7	Sequence 7, Appli
C 427	16.4	0.9	18	1	US-10-352-255A-18	Sequence 18, Appl	C 500	15.4	0.9	20	1	US-10-275-080A-7	Sequence 7, Appli
C 428	16.4	0.9	19	1	US-10-665-951-991	Sequence 991, App	C 501	15.4	0.9	20	1	US-10-216-484-94	Sequence 94, Appl
C 429	16.4	0.9	19	1	US-10-665-951-1315	Sequence 1315, App	C 502	15.4	0.9	20	1	US-10-216-484-98	Sequence 98, Appl
C 430	16.4	0.9	20	1	US-10-275-080A-6	Sequence 6, Appli	C 503	15.4	0.9	20	1	US-10-188-404-49	Sequence 49, Appl
C 431	16.4	0.9	20	1	US-10-289-762-2140	Sequence 2140, App	C 504	15.4	0.9	20	1	US-10-026-106E-3	Sequence 3, Appli
C 432	16.4	0.9	21	1	US-09-775-479-17	Sequence 17, Appl	C 505	15.4	0.9	20	1	US-10-384-933-94	Sequence 94, Appl
C 433	16.4	0.9	21	1	US-10-252-155-511	Sequence 511, App	C 506	15.4	0.9	20	1	US-10-384-933-98	Sequence 98, Appl
C 434	16.4	0.9	21	1	US-10-252-155-512	Sequence 512, App	C 507	15.2	0.9	17	1	US-10-380-596A-5	Sequence 5, Appli
C 435	16.4	0.9	21	1	US-10-418-182-128	Sequence 128, App	C 508	15.2	0.9	17	1	US-10-015-593-2	Sequence 2, Appli
C 436	16.2	0.9	18	1	US-09-981-397A-1	Sequence 1, Appli	C 509	15.2	0.9	20	1	US-09-790-264-26	Sequence 26, Appl
C 437	16.2	0.9	19	1	US-10-103-614A-4	Sequence 4, Appli	C 510	15.2	0.9	20	1	US-09-823-634A-18	Sequence 18, Appl
C 438	16	0.9	16	1	US-09-739-928-2	Sequence 2, Appli	C 511	15.2	0.9	20	1	US-09-823-647B-18	Sequence 18, Appl
C 439	16	0.9	16	1	US-09-152-059-70	Sequence 70, Appl	C 512	15.2	0.9	20	1	US-09-263-959-894	Sequence 894, App
C 440	16	0.9	16	1	US-09-805-296D-9	Sequence 9, Appli	C 513	15.2	0.9	20	1	US-09-964-261-36	Sequence 36, Appl
C 441	16	0.9	16	1	US-09-843-676-131	Sequence 131, App	C 514	15.2	0.9	20	1	US-09-916-369A-9	Sequence 9, Appli
C 442	16	0.9	16	1	US-09-766-253-131	Sequence 131, App	C 515	15.2	0.9	20	1	US-10-113-824-6	Sequence 6, Appli
C 443	16	0.9	16	1	US-09-438-486-131	Sequence 131, App	C 516	15.2	0.9	20	1	US-10-269-353-26	Sequence 26, Appl
C 444	16	0.9	16	1	US-09-895-585-9	Sequence 9, Appli	C 517	15.2	0.9	20	1	US-10-001-863-7	Sequence 7, Appli
C 445	16	0.9	16	1	US-10-208-357-22	Sequence 22, Appl	C 518	15.2	0.9	20	1	US-10-367-470-18	Sequence 18, Appl
C 446	16	0.9	16	1	US-10-053-758-131	Sequence 131, App	C 519	15.2	0.9	20	1	US-10-114-544-12	Sequence 12, Appl
C 447	16	0.9	16	1	US-10-054-295-131	Sequence 131, App	C 520	15.2	0.9	20	1	US-10-159-834-26	Sequence 26, Appl
C 448	16	0.9	16	1	US-10-054-611-131	Sequence 131, App	C 521	15.2	0.9	20	1	US-10-388-329-9	Sequence 9, Appli
C 449	16	0.9	16	1	US-10-072-975-9	Sequence 9, Appli	C 522	15.2	0.9	20	1	US-10-349-143-6563	Sequence 6563, Ap
C 450	16	0.9	16	1	US-10-227-001-21	Sequence 21, Appl	C 523	15.2	0.9	20	1	US-10-349-143-10187	Sequence 10187, A
C 451	16	0.9	16	1	US-10-008-029-70	Sequence 70, Appl	C 524	15.2	0.9	20	1	US-10-188-470-21	Sequence 21, Appl
C 452	16	0.9	16	1	US-10-051-436-9	Sequence 9, Appli	C 525	15.2	0.9	20	1	US-10-309-775A-72	Sequence 72, Appl
C 453	16	0.9	16	1	US-10-208-650-70	Sequence 70, Appl	C 526	15.2	0.9	20	1	US-10-240-403-7	Sequence 7, Appli
C 454	16	0.9	16	1	US-10-203-780-9	Sequence 9, Appli	C 527	15.2	0.9	20	1	US-10-671-395-924	Sequence 924, App
C 455	16	0.9	16	1	US-10-360-275-9	Sequence 9, Appli	C 528	15.2	0.9	20	1	US-10-671-395-938	Sequence 938, App
C 456	16	0.9	16	1	US-10-611-629-4	Sequence 4, Appli	C 529	15	0.9	15	1	US-09-504-231A-22	Sequence 22, Appl
C 457	16	0.9	16	1	US-10-776-099-9	Sequence 3, Appli	C 530	15	0.9	15	1	US-09-930-218-5	Sequence 5, Appli
C 458	16	0.9	17	1	US-09-788-362-3	Sequence 106, App	C 531	15	0.9	15	1	US-09-274-553D-22	Sequence 22, Appl
C 459	16	0.9	17	1	US-09-090-672B-106	Sequence 3, Appli	C 532	15	0.9	15	1	US-09-976-874A-5	Sequence 5, Appli
C 460	16	0.9	17	1	US-09-788-338-3	Sequence 906, App	C 533	15	0.9	15	1	US-09-955-410-17	Sequence 17, Appl
C 461	16	0.9	17	1	US-09-848-754A-906	Sequence 907, App	C 534	15	0.9	15	1	US-09-955-410-18	Sequence 18, Appl
C 462	16	0.9	17	1	US-09-848-754A-907	Sequence 108, App	C 535	15	0.9	15	1	US-09-805-296D-10	Sequence 10, Appl
C 463	16	0.9	17	1	US-09-730-559B-108	Sequence 5, Appli	C 536	15	0.9	15	1	US-09-983-210-19	Sequence 19, Appl
C 464	16	0.9	17	1	US-10-380-254-5	Sequence 4, Appli	C 537	15	0.9	15	1	US-09-983-210-20	Sequence 20, Appl
C 465	16	0.9	17	1	US-10-398-885A-4	Sequence 20, Appl	C 538	15	0.9	15	1	US-09-850-982B-4	Sequence 4, Appli
C 466	16	0.9	17	1	US-10-398-877-20	Sequence 64, Appl	C 539	15	0.9	15	1	US-09-988-113-5	Sequence 5, Appli
C 467	16	0.9	17	1	US-10-291-808-64	Sequence 24, Appl	C 540	15	0.9	15	1	US-09-793-146-54	Sequence 54, Appl
C 468	16	0.9	17	1	US-10-333-461-24	Sequence 24, Appl	C 541	15	0.9	15	1	US-09-793-146-55	Sequence 55, Appl
C 469	16	0.9	17	1	US-10-352-253A-24	Sequence 24, Appl	C 542	15	0.9	15	1	US-10-433-005-4	Sequence 4, Appli
C 470	16	0.9	17	1	US-10-220-373-9	Sequence 9, Appli	C 543	15	0.9	15	1	US-10-637-935-9	Sequence 9, Appli
C 471	16	0.9	17	1	US-10-352-255A-24	Sequence 24, Appl	C 544	15	0.9	15	1	US-10-239-655A-4	Sequence 4, Appli

C 545	15	0.9	15	1	US-10-291-808-68	Sequence 68, Appl	C 618	14.8	0.8	18	1	US-10-388-578-28	Sequence 28, Appl
546	15	0.9	15	1	US-10-208-357-21	Sequence 21, Appl	C 619	14.8	0.8	18	1	US-10-188-404-32	Sequence 32, Appl
547	15	0.9	15	1	US-10-176-055-9	Sequence 9, Appl	C 620	14.8	0.8	18	1	US-10-188-404-33	Sequence 33, Appl
C 548	15	0.9	15	1	US-10-202-189-9	Sequence 9, Appl	C 621	14.8	0.8	18	1	US-10-314-405-44	Sequence 44, Appl
C 549	15	0.9	15	1	US-10-072-975-10	Sequence 10, Appl	C 622	14.8	0.8	18	1	US-10-359-935-35	Sequence 35, Appl
C 550	15	0.9	15	1	US-10-227-001-23	Sequence 23, Appl	C 623	14.8	0.8	18	1	US-10-359-935-36	Sequence 36, Appl
C 551	15	0.9	15	1	US-10-051-436-10	Sequence 10, Appl	C 624	14.8	0.8	18	1	US-10-178-325-169	Sequence 169, App
C 552	15	0.9	15	1	US-10-341-582-5	Sequence 5, Appl	C 625	14.8	0.8	18	1	US-10-089-887-25	Sequence 25, Appl
C 553	15	0.9	15	1	US-10-106-749-1	Sequence 1, Appl	C 626	14.8	0.8	18	1	US-10-455-229-28	Sequence 28, Appl
C 554	15	0.9	15	1	US-10-106-749-5	Sequence 5, Appl	C 627	14.8	0.8	18	1	US-10-138-674-1471	Sequence 1471, Ap
C 555	15	0.9	15	1	US-10-384-451-5	Sequence 5, Appl	C 628	14.8	0.8	18	1	US-10-432-962-3	Sequence 3, Appli
C 556	15	0.9	15	1	US-10-269-031A-54	Sequence 54, Appl	C 629	14.8	0.8	18	1	US-10-287-949A-1471	Sequence 1471, Ap
C 557	15	0.9	15	1	US-10-352-704-10	Sequence 10, Appl	C 630	14.8	0.8	19	1	US-10-251-117-247	Sequence 247, App
558	15	0.9	15	1	US-10-352-704-16	Sequence 16, Appl	C 631	14.8	0.8	19	1	US-10-251-117-496	Sequence 496, App
C 559	15	0.9	15	1	US-10-154-890-17	Sequence 17, Appl	C 632	14.8	0.8	19	1	US-10-636-065-2	Sequence 2, Appli
560	15	0.9	15	1	US-10-154-890-18	Sequence 18, Appl	C 633	14.8	0.8	19	1	US-10-665-951-1534	Sequence 1534, Ap
C 561	15	0.9	15	1	US-10-431-438-5	Sequence 5, Appl	C 634	14.8	0.8	19	1	US-10-665-951-1781	Sequence 1781, Ap
C 562	15	0.9	15	1	US-10-091-231-2	Sequence 2, Appl	C 635	14.8	0.8	16	1	US-10-287-919-1636	Sequence 1636, Ap
C 563	15	0.9	15	1	US-10-384-450-5	Sequence 5, Appl	C 636	14.4	0.8	16	1	US-10-712-672-1775	Sequence 1775, Ap
C 564	15	0.9	15	1	US-10-371-218A-5	Sequence 5, Appl	C 637	14.4	0.8	17	1	US-09-866-108-7877	Sequence 7877, Ap
C 565	15	0.9	15	1	US-10-045-674-622	Sequence 622, App	C 638	14.4	0.8	17	1	US-09-866-108-7878	Sequence 7878, Ap
C 566	15	0.9	15	1	US-10-456-573-5	Sequence 5, Appl	C 639	14.4	0.8	17	1	US-09-814-777A-85	Sequence 85, Appl
C 567	15	0.9	15	1	US-10-360-275-10	Sequence 10, Appl	C 640	14.4	0.8	17	1	US-09-814-777A-87	Sequence 87, Appl
C 568	15	0.9	15	1	US-10-344-092-2	Sequence 2, Appl	C 641	14.4	0.8	17	1	US-09-864-785-288	Sequence 288, App
C 569	15	0.9	15	1	US-10-785-116-5	Sequence 5, Appl	C 642	14.4	0.8	17	1	US-09-864-785-397	Sequence 397, App
C 570	15	0.9	16	1	US-09-739-928-3	Sequence 3, Appl	C 643	14.4	0.8	17	1	US-09-864-785-398	Sequence 398, App
C 571	15	0.9	16	1	US-09-739-928-4	Sequence 4, Appl	C 644	14.4	0.8	17	1	US-09-780-533A-2363	Sequence 2363, Ap
C 572	15	0.9	16	1	US-09-739-928-5	Sequence 5, Appl	C 645	14.4	0.8	17	1	US-09-930-423-856	Sequence 856, App
C 573	15	0.9	16	1	US-09-739-928-6	Sequence 6, Appl	C 646	14.4	0.8	17	1	US-09-780-164-800	Sequence 800, App
C 574	15	0.9	16	1	US-09-739-928-7	Sequence 7, Appl	C 647	14.4	0.8	17	1	US-09-827-395A-272	Sequence 272, App
C 575	15	0.9	16	1	US-09-739-928-8	Sequence 8, Appl	C 648	14.4	0.8	17	1	US-09-827-395A-273	Sequence 273, App
C 576	15	0.9	16	1	US-10-227-001-20	Sequence 20, Appl	C 649	14.4	0.8	17	1	US-09-745-237A-856	Sequence 856, App
577	15	0.9	16	1	US-10-164-915-2	Sequence 2, Appl	C 650	14.4	0.8	17	1	US-10-430-882-272	Sequence 272, App
C 578	15	0.9	17	1	US-09-090-672B-105	Sequence 105, App	C 651	14.4	0.8	17	1	US-10-430-882-273	Sequence 273, App
C 579	15	0.9	17	1	US-09-090-672B-107	Sequence 107, App	C 652	14.4	0.8	17	1	US-10-163-552-593	Sequence 593, App
580	15	0.9	17	1	US-09-848-754A-35	Sequence 35, Appl	C 653	14.4	0.8	17	1	US-10-156-306-520	Sequence 520, App
581	15	0.9	17	1	US-09-848-754A-3119	Sequence 3119, Ap	C 654	14.4	0.8	17	1	US-10-156-306-522	Sequence 522, App
C 582	15	0.9	17	1	US-09-730-559B-107	Sequence 107, App	C 655	14.4	0.8	17	1	US-10-156-306-523	Sequence 523, App
C 583	15	0.9	17	1	US-09-730-559B-109	Sequence 3, Appl	C 656	14.4	0.8	17	1	US-10-156-306-525	Sequence 525, App
C 584	15	0.9	17	1	US-10-380-254-3	Sequence 4, Appl	C 657	14.4	0.8	17	1	US-10-156-306-5854	Sequence 5854, Ap
C 585	15	0.9	17	1	US-10-380-254-4	Sequence 2, Appl	C 658	14.4	0.8	17	1	US-10-238-700-1031	Sequence 1031, Ap
C 586	15	0.9	17	1	US-10-398-885A-2	Sequence 3, Appl	C 659	14.4	0.8	17	1	US-10-238-700-3484	Sequence 3484, Ap
C 587	15	0.9	17	1	US-10-398-885A-3	Sequence 18, Appl	C 660	14.4	0.8	17	1	US-10-138-674-8797	Sequence 8797, Ap
C 588	15	0.9	17	1	US-10-398-877-18	Sequence 19, Appl	C 661	14.4	0.8	17	1	US-10-287-949A-8797	Sequence 8797, Ap
C 589	15	0.9	17	1	US-10-398-877-19	Sequence 63, Appl	C 662	14.4	0.8	17	1	Sequence 1234, Ap	
C 590	15	0.9	17	1	US-10-291-808-63	Sequence 5, Appl	C 663	14.4	0.8	17	1	Sequence 2021, Ap	
C 591	15	0.9	17	1	US-10-408-025-5	Sequence 1503, Ap	C 664	14.4	0.8	17	1	Sequence 7877, Ap	
C 592	15	0.9	17	1	US-10-061-201-1503	Sequence 1504, Ap	C 665	14.4	0.8	17	1	Sequence 7878, Ap	
C 593	15	0.9	17	1	US-10-061-201-1504	Sequence 1505, Ap	C 666	14.4	0.8	17	1	Sequence 4070, Ap	
C 594	15	0.9	17	1	US-10-061-201-1505	Sequence 3, Appl	C 667	14.4	0.8	18	1	Sequence 2609, Ap	
C 595	15	0.9	17	1	US-10-309-152A-3	Sequence 7, Appl	C 668	14.4	0.8	18	1	Sequence 148, App	
C 596	15	0.9	17	1	US-10-220-373-7	Sequence 8, Appl	C 669	14.4	0.8	19	1	Sequence 1577, Ap	
C 597	15	0.9	17	1	US-10-220-373-8	Sequence 6, Appl	C 670	14.4	0.8	19	1	Sequence 1860, Ap	
C 598	15	0.9	17	1	US-10-380-255-6	Sequence 7, Appl	C 671	14.4	0.8	19	1	Sequence 42, Appl	
C 599	15	0.9	17	1	US-10-380-255-7	Sequence 1073, Ap	C 672	14.4	0.8	19	1	Sequence 148, App	
C 600	15	0.9	17	1	US-10-138-674-1073	Sequence 1076, Ap	C 673	14.4	0.8	19	1	Sequence 31, Appl	
C 601	15	0.9	17	1	US-10-138-674-1076	Sequence 1073, Ap	C 674	14.4	0.8	20	1	Sequence 7, Appli	
C 602	15	0.9	17	1	US-10-287-949A-1073	Sequence 1076, Ap	C 675	14.2	0.8	15	1	Sequence 65, Appl	
C 603	15	0.9	17	1	US-10-287-949A-1076	Sequence 1, Appl	C 676	14	0.8	14	1	Sequence 55, Appl	
C 604	15	0.9	18	1	US-09-904-744-1	Sequence 2, Appl	C 677	14	0.8	14	1	Sequence 66, Appl	
C 605	15	0.9	18	1	US-09-904-744-2	Sequence 8, Appl	C 678	14	0.8	14	1	Sequence 67, Appl	
C 606	15	0.9	18	1	US-09-775-479-8	Sequence 3, Appl	C 679	14	0.8	14	1	Sequence 68, Appl	
C 607	15	0.9	20	1	US-10-618-540-3	Sequence 1, Appl	C 680	14	0.8	14	1	Sequence 80, Appl	
C 608	15	0.9	20	1	US-10-164-915-1	Sequence 11, Appl	C 681	14	0.8	14	1	Sequence 81, Appl	
C 609	15	0.9	20	1	US-10-167-241-11	Sequence 51, Appl	C 682	14	0.8	14	1	Sequence 82, Appl	
C 610	15	0.9	20	1	US-10-407-078-51	Sequence 116, App	C 683	14	0.8	14	1	Sequence 83, Appl	
C 611	15	0.9	20	1	US-10-380-931-116	Sequence 2, Appl	C 684	14	0.8	14	1	Sequence 84, Appl	
C 612	15	0.9	20	1	US-10-374-686-2	Sequence 65, Appl	C 685	14	0.8	14	1	Sequence 85, Appl	
C 613	15	0.9	20	1	US-10-212-993-65	Sequence 35, Appl	C 686	14	0.8	14	1	Sequence 86, Appl	
C 614	14.8	0.8	18	1	US-09-057-351-35	Sequence 36, Appl	C 687	14	0.8	14	1	Sequence 87, Appl	
C 615	14.8	0.8	18	1	US-09-057-351-36	Sequence 9, Appl	C 688	14	0.8	14	1	Sequence 88, Appl	
C 616	14.8	0.8	18	1	US-09-947-659-9	Sequence 716, App	C 689	14	0.8	14	1	Sequence 89, Appl	
C 617	14.8	0.8	18	1	US-09-263-959-716		C 690	14	0.8	14	1	Sequence 90, Appl	

691	14	0.8	14	1	US-09-152-059-91	Sequence 91, Appl	c 764	14	0.8	14	1	US-10-008-029-92	Sequence 92, Appl
c 692	14	0.8	14	1	US-09-152-059-92	Sequence 92, Appl	765	14	0.8	14	1	US-10-008-029-93	Sequence 93, Appl
693	14	0.8	14	1	US-09-152-059-93	Sequence 93, Appl	766	14	0.8	14	1	US-10-008-029-94	Sequence 94, Appl
694	14	0.8	14	1	US-09-152-059-94	Sequence 94, Appl	767	14	0.8	14	1	US-10-008-029-96	Sequence 96, Appl
695	14	0.8	14	1	US-09-152-059-96	Sequence 96, Appl	768	14	0.8	14	1	US-10-008-029-97	Sequence 97, Appl
696	14	0.8	14	1	US-09-152-059-97	Sequence 97, Appl	c 769	14	0.8	14	1	US-10-008-029-98	Sequence 98, Appl
c 697	14	0.8	14	1	US-09-152-059-98	Sequence 98, Appl	770	14	0.8	14	1	US-10-008-029-99	Sequence 99, Appl
698	14	0.8	14	1	US-09-152-059-99	Sequence 99, Appl	771	14	0.8	14	1	US-10-008-029-100	Sequence 100, App
699	14	0.8	14	1	US-09-152-059-100	Sequence 100, App	c 772	14	0.8	14	1	US-10-008-029-101	Sequence 101, App
c 700	14	0.8	14	1	US-09-152-059-101	Sequence 101, App	773	14	0.8	14	1	US-10-008-029-102	Sequence 102, App
701	14	0.8	14	1	US-09-152-059-102	Sequence 102, App	774	14	0.8	14	1	US-10-008-029-103	Sequence 103, App
702	14	0.8	14	1	US-09-152-059-103	Sequence 103, App	c 775	14	0.8	14	1	US-10-008-029-104	Sequence 104, App
c 703	14	0.8	14	1	US-09-152-059-104	Sequence 104, App	776	14	0.8	14	1	US-10-008-029-105	Sequence 105, App
704	14	0.8	14	1	US-09-152-059-105	Sequence 105, App	777	14	0.8	14	1	US-10-008-029-106	Sequence 106, App
705	14	0.8	14	1	US-09-152-059-106	Sequence 106, App	c 778	14	0.8	14	1	US-10-008-029-107	Sequence 107, App
c 706	14	0.8	14	1	US-09-152-059-107	Sequence 107, App	779	14	0.8	14	1	US-10-008-029-108	Sequence 108, App
707	14	0.8	14	1	US-09-152-059-108	Sequence 108, App	780	14	0.8	14	1	US-10-008-029-109	Sequence 109, App
708	14	0.8	14	1	US-09-152-059-109	Sequence 109, App	c 781	14	0.8	14	1	US-10-008-029-110	Sequence 110, App
c 709	14	0.8	14	1	US-09-152-059-110	Sequence 110, App	782	14	0.8	14	1	US-10-008-029-111	Sequence 111, App
710	14	0.8	14	1	US-09-152-059-111	Sequence 111, App	783	14	0.8	14	1	US-10-008-029-112	Sequence 112, App
711	14	0.8	14	1	US-09-152-059-112	Sequence 112, App	c 784	14	0.8	14	1	US-10-008-029-113	Sequence 113, App
712	14	0.8	14	1	US-09-152-059-113	Sequence 113, App	785	14	0.8	14	1	US-10-008-029-114	Sequence 114, App
713	14	0.8	14	1	US-09-152-059-114	Sequence 114, App	786	14	0.8	14	1	US-10-008-029-115	Sequence 115, App
714	14	0.8	14	1	US-09-152-059-115	Sequence 115, App	c 787	14	0.8	14	1	US-10-008-029-117	Sequence 117, App
c 715	14	0.8	14	1	US-09-152-059-117	Sequence 117, App	788	14	0.8	14	1	US-10-008-029-118	Sequence 118, App
716	14	0.8	14	1	US-09-152-059-118	Sequence 118, App	789	14	0.8	14	1	US-10-008-029-119	Sequence 119, App
717	14	0.8	14	1	US-09-152-059-119	Sequence 119, App	c 790	14	0.8	14	1	US-10-008-029-120	Sequence 120, App
c 718	14	0.8	14	1	US-09-152-059-120	Sequence 120, App	791	14	0.8	14	1	US-10-008-029-121	Sequence 121, App
719	14	0.8	14	1	US-09-152-059-121	Sequence 121, App	792	14	0.8	14	1	US-10-008-029-122	Sequence 122, App
720	14	0.8	14	1	US-09-152-059-122	Sequence 122, App	c 793	14	0.8	14	1	US-10-008-029-123	Sequence 123, App
c 721	14	0.8	14	1	US-09-152-059-123	Sequence 123, App	794	14	0.8	14	1	US-10-008-029-124	Sequence 124, App
722	14	0.8	14	1	US-09-152-059-124	Sequence 124, App	795	14	0.8	14	1	US-10-008-029-125	Sequence 125, App
723	14	0.8	14	1	US-09-152-059-125	Sequence 125, App	c 796	14	0.8	14	1	US-10-008-029-126	Sequence 126, App
c 724	14	0.8	14	1	US-09-152-059-126	Sequence 126, App	797	14	0.8	14	1	US-10-008-029-127	Sequence 127, App
725	14	0.8	14	1	US-09-152-059-127	Sequence 127, App	c 798	14	0.8	14	1	US-10-008-029-128	Sequence 128, App
726	14	0.8	14	1	US-09-152-059-128	Sequence 128, App	c 799	14	0.8	14	1	US-10-008-029-129	Sequence 129, App
c 727	14	0.8	14	1	US-09-152-059-129	Sequence 129, App	800	14	0.8	14	1	US-10-008-029-130	Sequence 130, App
728	14	0.8	14	1	US-09-152-059-130	Sequence 130, App	801	14	0.8	14	1	US-10-008-029-131	Sequence 131, App
c 729	14	0.8	14	1	US-09-152-059-131	Sequence 131, App	c 802	14	0.8	14	1	US-10-008-029-132	Sequence 132, App
730	14	0.8	14	1	US-09-152-059-132	Sequence 132, App	803	14	0.8	14	1	US-10-008-029-133	Sequence 133, App
c 731	14	0.8	14	1	US-09-152-059-133	Sequence 133, App	804	14	0.8	14	1	US-10-008-029-134	Sequence 134, App
732	14	0.8	14	1	US-09-152-059-134	Sequence 134, App	c 805	14	0.8	14	1	US-10-008-029-135	Sequence 135, App
c 733	14	0.8	14	1	US-09-152-059-135	Sequence 135, App	806	14	0.8	14	1	US-10-008-029-136	Sequence 136, App
734	14	0.8	14	1	US-09-152-059-136	Sequence 136, App	807	14	0.8	14	1	US-10-008-029-137	Sequence 137, App
735	14	0.8	14	1	US-09-152-059-137	Sequence 137, App	c 808	14	0.8	14	1	US-10-008-029-138	Sequence 138, App
c 736	14	0.8	14	1	US-09-152-059-138	Sequence 138, App	809	14	0.8	14	1	US-10-008-029-139	Sequence 139, App
737	14	0.8	14	1	US-09-152-059-139	Sequence 139, App	810	14	0.8	14	1	US-10-008-029-140	Sequence 140, App
c 738	14	0.8	14	1	US-09-152-059-140	Sequence 140, App	811	14	0.8	14	1	US-10-008-029-141	Sequence 141, App
739	14	0.8	14	1	US-09-152-059-141	Sequence 141, App	812	14	0.8	14	1	US-10-008-029-142	Sequence 142, App
740	14	0.8	14	1	US-09-152-059-142	Sequence 142, App	813	14	0.8	14	1	US-10-008-029-143	Sequence 143, App
741	14	0.8	14	1	US-09-152-059-143	Sequence 143, App	c 814	14	0.8	14	1	US-10-008-029-144	Sequence 144, App
c 742	14	0.8	14	1	US-09-152-059-144	Sequence 144, App	815	14	0.8	14	1	US-10-008-029-145	Sequence 145, App
743	14	0.8	14	1	US-09-152-059-145	Sequence 145, App	816	14	0.8	14	1	US-10-008-029-146	Sequence 146, App
744	14	0.8	14	1	US-09-152-059-146	Sequence 146, App	c 817	14	0.8	14	1	US-10-208-650-65	Sequence 65, Appl
745	14	0.8	14	1	US-10-096-075-11	Sequence 11, Appl	c 818	14	0.8	14	1	US-10-208-650-66	Sequence 66, Appl
746	14	0.8	14	1	US-10-208-357-20	Sequence 20, Appl	c 819	14	0.8	14	1	US-10-208-650-67	Sequence 67, Appl
747	14	0.8	14	1	US-10-301-844-20	Sequence 20, Appl	c 820	14	0.8	14	1	US-10-208-650-68	Sequence 68, Appl
c 748	14	0.8	14	1	US-10-008-029-65	Sequence 65, Appl	c 821	14	0.8	14	1	US-10-208-650-80	Sequence 80, Appl
c 749	14	0.8	14	1	US-10-008-029-66	Sequence 66, Appl	822	14	0.8	14	1	US-10-208-650-81	Sequence 81, Appl
c 750	14	0.8	14	1	US-10-008-029-67	Sequence 67, Appl	823	14	0.8	14	1	US-10-208-650-82	Sequence 82, Appl
c 751	14	0.8	14	1	US-10-008-029-68	Sequence 68, Appl	c 824	14	0.8	14	1	US-10-208-650-83	Sequence 83, Appl
c 752	14	0.8	14	1	US-10-008-029-80	Sequence 80, Appl	825	14	0.8	14	1	US-10-208-650-84	Sequence 84, Appl
753	14	0.8	14	1	US-10-008-029-81	Sequence 81, Appl	826	14	0.8	14	1	US-10-208-650-85	Sequence 85, Appl
754	14	0.8	14	1	US-10-008-029-82	Sequence 82, Appl	c 827	14	0.8	14	1	US-10-208-650-86	Sequence 86, Appl
c 755	14	0.8	14	1	US-10-008-029-83	Sequence 83, Appl	828	14	0.8	14	1	US-10-208-650-87	Sequence 87, Appl
756	14	0.8	14	1	US-10-008-029-84	Sequence 84, Appl	829	14	0.8	14	1	US-10-208-650-88	Sequence 88, Appl
757	14	0.8	14	1	US-10-008-029-85	Sequence 85, Appl	c 830	14	0.8	14	1	US-10-208-650-89	Sequence 89, Appl
c 758	14	0.8	14	1	US-10-008-029-86	Sequence 86, Appl	831	14	0.8	14	1	US-10-208-650-90	Sequence 90, Appl
759	14	0.8	14	1	US-10-008-029-87	Sequence 87, Appl	832	14	0.8	14	1	US-10-208-650-91	Sequence 91, Appl
760	14	0.8	14	1	US-10-008-029-88	Sequence 88, Appl	c 833	14	0.8	14	1	US-10-208-650-92	Sequence 92, Appl
c 761	14	0.8	14	1	US-10-008-029-89	Sequence 89, Appl	834	14	0.8	14	1	US-10-208-650-93	Sequence 93, Appl
762	14	0.8	14	1	US-10-008-029-90	Sequence 90, Appl	835	14	0.8	14	1	US-10-208-650-94	Sequence 94, Appl
763	14	0.8	14	1	US-10-008-029-91	Sequence 91, Appl	836	14	0.8	14	1	US-10-208-650-96	Sequence 96, Appl

837	14	0.8	14	1	US-10-208-650-97	Sequence 97, Appl	Sequence 97, Appl
C 838	14	0.8	14	1	US-10-208-650-98	Sequence 98, Appl	Sequence 98, Appl
839	14	0.8	14	1	US-10-208-650-99	Sequence 99, Appl	Sequence 99, Appl
840	14	0.8	14	1	US-10-208-650-100	Sequence 100, App	Sequence 100, App
C 841	14	0.8	14	1	US-10-208-650-101	Sequence 101, App	Sequence 101, App
842	14	0.8	14	1	US-10-208-650-102	Sequence 102, App	Sequence 102, App
843	14	0.8	14	1	US-10-208-650-103	Sequence 103, App	Sequence 103, App
C 844	14	0.8	14	1	US-10-208-650-104	Sequence 104, App	Sequence 104, App
845	14	0.8	14	1	US-10-208-650-105	Sequence 105, App	Sequence 105, App
846	14	0.8	14	1	US-10-208-650-106	Sequence 106, App	Sequence 106, App
C 847	14	0.8	14	1	US-10-208-650-107	Sequence 107, App	Sequence 107, App
848	14	0.8	14	1	US-10-208-650-108	Sequence 108, App	Sequence 108, App
849	14	0.8	14	1	US-10-208-650-109	Sequence 109, App	Sequence 109, App
C 850	14	0.8	14	1	US-10-208-650-110	Sequence 110, App	Sequence 110, App
851	14	0.8	14	1	US-10-208-650-111	Sequence 111, App	Sequence 111, App
852	14	0.8	14	1	US-10-208-650-112	Sequence 112, App	Sequence 112, App
C 853	14	0.8	14	1	US-10-208-650-113	Sequence 113, App	Sequence 113, App
854	14	0.8	14	1	US-10-208-650-114	Sequence 114, App	Sequence 114, App
855	14	0.8	14	1	US-10-208-650-115	Sequence 115, App	Sequence 115, App
C 856	14	0.8	14	1	US-10-208-650-117	Sequence 117, App	Sequence 117, App
857	14	0.8	14	1	US-10-208-650-118	Sequence 118, App	Sequence 118, App
858	14	0.8	14	1	US-10-208-650-119	Sequence 119, App	Sequence 119, App
C 859	14	0.8	14	1	US-10-208-650-120	Sequence 120, App	Sequence 120, App
860	14	0.8	14	1	US-10-208-650-121	Sequence 121, App	Sequence 121, App
861	14	0.8	14	1	US-10-208-650-122	Sequence 122, App	Sequence 122, App
C 862	14	0.8	14	1	US-10-208-650-123	Sequence 123, App	Sequence 123, App
863	14	0.8	14	1	US-10-208-650-124	Sequence 124, App	Sequence 124, App
864	14	0.8	14	1	US-10-208-650-125	Sequence 125, App	Sequence 125, App
C 865	14	0.8	14	1	US-10-208-650-126	Sequence 126, App	Sequence 126, App
866	14	0.8	14	1	US-10-208-650-127	Sequence 127, App	Sequence 127, App
867	14	0.8	14	1	US-10-208-650-128	Sequence 128, App	Sequence 128, App
C 868	14	0.8	14	1	US-10-208-650-129	Sequence 129, App	Sequence 129, App
869	14	0.8	14	1	US-10-208-650-130	Sequence 130, App	Sequence 130, App
870	14	0.8	14	1	US-10-208-650-131	Sequence 131, App	Sequence 131, App
C 871	14	0.8	14	1	US-10-208-650-132	Sequence 132, App	Sequence 132, App
872	14	0.8	14	1	US-10-208-650-133	Sequence 133, App	Sequence 133, App
873	14	0.8	14	1	US-10-208-650-134	Sequence 134, App	Sequence 134, App
C 874	14	0.8	14	1	US-10-208-650-135	Sequence 135, App	Sequence 135, App
875	14	0.8	14	1	US-10-208-650-136	Sequence 136, App	Sequence 136, App
876	14	0.8	14	1	US-10-208-650-137	Sequence 137, App	Sequence 137, App
C 877	14	0.8	14	1	US-10-208-650-138	Sequence 138, App	Sequence 138, App
878	14	0.8	14	1	US-10-208-650-139	Sequence 139, App	Sequence 139, App
C 880	14	0.8	14	1	US-10-208-650-141	Sequence 141, App	Sequence 141, App
881	14	0.8	14	1	US-10-208-650-142	Sequence 142, App	Sequence 142, App
882	14	0.8	14	1	US-10-208-650-143	Sequence 143, App	Sequence 143, App
C 883	14	0.8	14	1	US-10-208-650-144	Sequence 144, App	Sequence 144, App
884	14	0.8	14	1	US-10-208-650-145	Sequence 145, App	Sequence 145, App
885	14	0.8	14	1	US-10-208-650-146	Sequence 146, App	Sequence 146, App
886	14	0.8	14	1	US-10-106-749-4	Sequence 4, Appl	Sequence 4, Appl
887	14	0.8	14	1	US-10-151-061-16	Sequence 16, Appl	Sequence 16, Appl
C 888	14	0.8	14	1	US-10-324-409B-17	Sequence 17, Appl	Sequence 17, Appl
889	14	0.8	14	1	US-10-468-753-42	Sequence 42, Appl	Sequence 42, Appl
C 890	14	0.8	14	1	US-10-468-753-47	Sequence 47, Appl	Sequence 47, Appl
891	14	0.8	14	1	US-10-468-753-50	Sequence 50, Appl	Sequence 50, Appl
C 892	14	0.8	14	1	US-10-468-753-51	Sequence 51, Appl	Sequence 51, Appl
893	14	0.8	14	1	US-10-056-414-16	Sequence 16, Appl	Sequence 16, Appl
C 894	14	0.8	14	1	US-10-001-24	Sequence 24, Appl	Sequence 24, Appl
895	14	0.8	14	1	US-09-894-159-64	Sequence 64, Appl	Sequence 64, Appl
C 896	14	0.8	14	1	US-09-880-727-8	Sequence 8, Appl	Sequence 8, Appl
C 897	14	0.8	14	1	US-10-324-409B-33	Sequence 33, Appl	Sequence 33, Appl
898	14	0.8	14	1	US-09-848-754A-905	Sequence 905, App	Sequence 905, App
C 899	14	0.8	14	1	US-10-061-201-1502	Sequence 1502, Ap	Sequence 1502, Ap
C 900	14	0.8	14	1	US-10-061-201-1506	Sequence 1506, Ap	Sequence 1506, Ap
901	14	0.8	14	1	US-10-338-777-196	Sequence 196, App	Sequence 196, App
C 902	14	0.8	14	1	US-10-138-674-1072	Sequence 1072, Ap	Sequence 1072, Ap
C 903	14	0.8	14	1	US-10-138-674-1077	Sequence 1077, Ap	Sequence 1077, Ap
C 904	14	0.8	14	1	US-10-287-949A-1072	Sequence 1072, Ap	Sequence 1072, Ap
C 905	14	0.8	14	1	US-10-287-949A-1077	Sequence 1077, Ap	Sequence 1077, Ap
C 906	14	0.8	14	1	US-10-712-672-2015	Sequence 2015, Ap	Sequence 2015, Ap
C 907	14	0.8	14	1	US-09-823-887C-7	Sequence 7, Appl	Sequence 7, Appl
C 908	14	0.8	14	1	US-10-328-578-142	Sequence 142, App	Sequence 142, App
909	14	0.8	14	1	US-10-407-089-22	Sequence 22, Appl	Sequence 22, Appl
1	18	0.8	18	1	US-10-106-799-3	Sequence 3, Appl	Sequence 3, Appl
1	18	0.8	18	1	US-10-056-908-11	Sequence 11, Appl	Sequence 11, Appl
1	18	0.8	18	1	US-10-109-363-18	Sequence 18, Appl	Sequence 18, Appl
1	18	0.8	18	1	US-10-623-371-142	Sequence 142, App	Sequence 142, App
1	17	0.8	13.8	1	US-09-866-108-896	Sequence 896, App	Sequence 896, App
1	17	0.8	13.8	1	US-09-866-108-879	Sequence 879, Ap	Sequence 879, Ap
1	17	0.8	13.8	1	US-09-866-108-10022	Sequence 10022, A	Sequence 10022, A
1	17	0.8	13.8	1	US-09-866-108-10502	Sequence 10502, A	Sequence 10502, A
1	17	0.8	13.8	1	US-09-866-108-10504	Sequence 10504, A	Sequence 10504, A
1	17	0.8	13.8	1	US-09-866-108-10505	Sequence 10505, A	Sequence 10505, A
1	17	0.8	13.8	1	US-09-866-108-10506	Sequence 10506, A	Sequence 10506, A
1	17	0.8	13.8	1	US-09-827-998-484	Sequence 484, App	Sequence 484, App
1	17	0.8	13.8	1	US-09-263-959-744	Sequence 744, App	Sequence 744, App
1	17	0.8	13.8	1	US-09-864-785-2145	Sequence 2145, Ap	Sequence 2145, Ap
1	17	0.8	13.8	1	US-09-825-805-466	Sequence 466, App	Sequence 466, App
1	17	0.8	13.8	1	US-09-825-805-563	Sequence 563, App	Sequence 563, App
1	17	0.8	13.8	1	US-09-961-077-881	Sequence 881, App	Sequence 881, App
1	17	0.8	13.8	1	US-09-780-533A-1375	Sequence 1375, Ap	Sequence 1375, Ap
1	17	0.8	13.8	1	US-09-780-533A-2357	Sequence 2357, Ap	Sequence 2357, Ap
1	17	0.8	13.8	1	US-09-780-533A-2358	Sequence 2358, Ap	Sequence 2358, Ap
1	17	0.8	13.8	1	US-09-780-533A-2367	Sequence 2367, Ap	Sequence 2367, Ap
1	17	0.8	13.8	1	US-09-848-754A-2551	Sequence 2551, Ap	Sequence 2551, Ap
1	17	0.8	13.8	1	US-09-930-423-1448	Sequence 3385, Ap	Sequence 3385, Ap
1	17	0.8	13.8	1	US-09-780-164-1043	Sequence 1448, Ap	Sequence 1448, Ap
1	17	0.8	13.8	1	US-09-827-395A-646	Sequence 1043, Ap	Sequence 1043, Ap
1	17	0.8	13.8	1	US-09-740-332-106	Sequence 646, App	Sequence 646, App
1	17	0.8	13.8	1	US-09-740-332-2617	Sequence 106, App	Sequence 106, App
1	17	0.8	13.8	1	US-09-740-332-3100	Sequence 2617, Ap	Sequence 2617, Ap
1	17	0.8	13.8	1	US-09-792-818-92	Sequence 3100, Ap	Sequence 3100, Ap
1	17	0.8	13.8	1	US-09-792-818-275	Sequence 92, Appl	Sequence 92, Appl
1	17	0.8	13.8	1	US-09-792-818-276	Sequence 275, App	Sequence 275, App
1	17	0.8	13.8	1	US-09-792-818-373	Sequence 276, App	Sequence 276, App
1	17	0.8	13.8	1	US-09-792-818-521	Sequence 373, App	Sequence 373, App
1	17	0.8	13.8	1	US-09-745-237A-1448	Sequence 521, App	Sequence 521, App
1	17	0.8	13.8	1	US-09-817-879-106	Sequence 1448, Ap	Sequence 1448, Ap
1	17	0.8	13.8	1	US-09-817-879-2617	Sequence 106, App	Sequence 106, App
1	17	0.8	13.8	1	US-09-817-879-3100	Sequence 2617, Ap	Sequence 2617, Ap
1	17	0.8	13.8	1	US-10-675-685-484	Sequence 3100, Ap	Sequence 3100, Ap
1	17	0.8	13.8	1	US-09-915-152-31	Sequence 484, App	Sequence 484, App
1	17	0.8	13.8	1	US-10-430-882-646	Sequence 31, Appl	Sequence 31, Appl
1	17	0.8	13.8	1	US-10-060-756A-384	Sequence 646, App	Sequence 646, App
1	17	0.8	13.8	1	US-10-060-756A-647	Sequence 384, App	Sequence 384, App
1	17	0.8	13.8	1	US-10-060-895A-228	Sequence 647, App	Sequence 647, App
1	17	0.8	13.8	1	US-10-060-895A-229	Sequence 228, App	Sequence 228, App
1	17	0.8	13.8	1	US-10-060-895A-230	Sequence 229, App	Sequence 229, App
1	17	0.8	13.8	1	US-10-060-895A-257	Sequence 230, App	Sequence 230, App
1	17	0.8	13.8	1	US-10-163-552-6	Sequence 257, App	Sequence 257, App
1	17	0.8	13.8	1	US-10-163-552-826	Sequence 6, Appl	Sequence 6, Appl
1	17	0.8	13.8	1	US-10-081-646-23	Sequence 826, App	Sequence 826, App
1	17	0.8	13.8	1	US-10-156-306-517	Sequence 23, Appl	Sequence 23, Appl
1	17	0.8	13.8	1	US-10-156-306-518	Sequence 517, App	Sequence 517, App
1	17	0.8	13.8	1	US-10-156-306-519	Sequence 518, App	Sequence 518, App
1	17	0.8	13.8	1	US-10-189-956-62	Sequence 519, App	Sequence 519, App
1	17	0.8	13.8	1	US-10-238-700-2807	Sequence 62, Appl	Sequence 62, Appl
1	17	0.8	13.8	1	US-10-238-700-2872	Sequence 2807, Ap	Sequence 2807, Ap
1	17	0.8	13.8	1	US-10-339-782-67	Sequence 2872, Ap	Sequence 2872, Ap
1	17	0.8	13.8	1	US-10-061-201-1507	Sequence 67, Appl	Sequence 67, Appl
1	17	0.8	13.8	1	US-10-230-006-523	Sequence 1507, Ap	Sequence 1507, Ap
1	17	0.8	13.8	1	US-10-230-006-1288	Sequence 523, App	Sequence 523, App
1	17	0.8	13.8	1	US-10-230-006-2124	Sequence 1288, Ap	Sequence 1288, Ap
1	17	0.8	13.8	1	US-10-138-674-675	Sequence 2124, Ap	Sequence 2124, Ap
1	17	0.8	13.8	1	US-10-138-674-1078	Sequence 675, App	Sequence 675, App
1	17	0.8	13.8	1	US-10-138-674-1079	Sequence 1078, Ap	Sequence 1078, Ap
1	17	0.8	13.8	1	US-10-138-674-3602	Sequence 1079, Ap	Sequence 1079, Ap
1	17	0.8	13.8	1	US-10-138-674-3603	Sequence 3602, Ap	Sequence 3602, Ap
1	17	0.8	13.8	1	US-10-138-674-3604	Sequence 3603, Ap	Sequence 3603, Ap
1	17	0.8	13.8	1	US-10-138-674-3605	Sequence 3604, Ap	Sequence 3604, Ap
1	17	0.8	13.8	1	US-10-138-674-3607	Sequence 3605, Ap	Sequence 3605, Ap
1	17	0.8	13.8	1	US-10-138-674-5015	Sequence 3607, Ap	Sequence 3607, Ap
1	17	0.8	13.8	1	US-10-138-674-7840	Sequence 5015, Ap	Sequence 5015, Ap
1	17	0.8	13.8	1	US-10-676-154-407	Sequence 7840, Ap	Sequence 7

c 983	13.8	0.8	17	1	US-10-287-949A-675	Sequence 675, App	c1056	13.4	0.8	17	1	US-09-866-108-10281	Sequence 10281, A
c 984	13.8	0.8	17	1	US-10-287-949A-1078	Sequence 1078, Ap	c1057	13.4	0.8	17	1	US-09-866-108-10282	Sequence 10282, A
c 985	13.8	0.8	17	1	US-10-287-949A-1079	Sequence 1079, Ap	c1058	13.4	0.8	17	1	US-09-866-108-10283	Sequence 10283, A
c 986	13.8	0.8	17	1	US-10-287-949A-3602	Sequence 3602, Ap	1059	13.4	0.8	17	1	US-09-866-108-10500	Sequence 10500, A
c 987	13.8	0.8	17	1	US-10-287-949A-3603	Sequence 3603, Ap	1060	13.4	0.8	17	1	US-09-866-108-10501	Sequence 10501, A
c 988	13.8	0.8	17	1	US-10-287-949A-3604	Sequence 3604, Ap	1061	13.4	0.8	17	1	US-09-866-108-10503	Sequence 10503, A
c 989	13.8	0.8	17	1	US-10-287-949A-3605	Sequence 3605, Ap	1062	13.4	0.8	17	1	US-09-417-386-8	Sequence 8, Appli
c 990	13.8	0.8	17	1	US-10-287-949A-3607	Sequence 3607, Ap	c1063	13.4	0.8	17	1	US-09-864-785-289	Sequence 289, App
c 991	13.8	0.8	17	1	US-10-287-949A-5015	Sequence 5015, Ap	1064	13.4	0.8	17	1	US-09-864-785-396	Sequence 396, App
c 992	13.8	0.8	17	1	US-10-287-949A-7840	Sequence 7840, Ap	c1065	13.4	0.8	17	1	US-09-864-785-694	Sequence 694, App
c 993	13.8	0.8	17	1	US-10-287-949A-637	Sequence 637, App	1066	13.4	0.8	17	1	US-09-864-785-1439	Sequence 1439, Ap
994	13.8	0.8	17	1	US-10-712-672-902	Sequence 902, App	1067	13.4	0.8	17	1	US-09-864-785-1440	Sequence 1440, Ap
995	13.8	0.8	17	1	US-10-712-672-1370	Sequence 1370, Ap	c1068	13.4	0.8	17	1	US-09-864-785-1552	Sequence 1552, Ap
996	13.8	0.8	17	1	US-10-712-672-2044	Sequence 2044, Ap	1069	13.4	0.8	17	1	US-09-864-785-2828	Sequence 2828, Ap
997	13.8	0.8	17	1	US-10-712-672-2080	Sequence 2080, Ap	c1070	13.4	0.8	17	1	US-09-818-875-3406	Sequence 3406, Ap
998	13.8	0.8	17	1	US-10-669-841-2699	Sequence 2699, Ap	1071	13.4	0.8	17	1	US-09-818-875-3407	Sequence 3407, Ap
999	13.8	0.8	17	1	US-10-669-841-5210	Sequence 5210, Ap	1072	13.4	0.8	17	1	US-09-780-533A-2365	Sequence 2365, Ap
c1000	13.8	0.8	17	1	US-10-669-841-5693	Sequence 5693, Ap	c1073	13.4	0.8	17	1	US-09-848-754A-931	Sequence 931, App
1001	13.8	0.8	17	1	US-10-723-361-896	Sequence 896, App	1074	13.4	0.8	17	1	US-09-848-754A-999	Sequence 999, App
1002	13.8	0.8	17	1	US-10-723-361-7879	Sequence 7879, Ap	c1075	13.4	0.8	17	1	US-09-848-754A-1327	Sequence 1327, Ap
1003	13.8	0.8	17	1	US-10-723-361-10022	Sequence 10022, A	1076	13.4	0.8	17	1	US-09-848-754A-2220	Sequence 2220, Ap
1004	13.8	0.8	17	1	US-10-723-361-10502	Sequence 10502, A	1077	13.4	0.8	17	1	US-09-930-423-27	Sequence 27, Appl
1005	13.8	0.8	17	1	US-10-723-361-10504	Sequence 10504, A	1078	13.4	0.8	17	1	US-09-930-423-497	Sequence 497, App
1006	13.8	0.8	17	1	US-10-723-361-10505	Sequence 10505, A	1079	13.4	0.8	17	1	US-09-930-423-1320	Sequence 1320, Ap
1007	13.8	0.8	17	1	US-10-723-361-10506	Sequence 10506, A	1080	13.4	0.8	17	1	US-09-780-164-1035	Sequence 1035, Ap
c1008	13.8	0.8	17	1	US-10-766-118-31	Sequence 31, Appl	c1081	13.4	0.8	17	1	US-09-827-395A-37	Sequence 37, Appl
1009	13.8	0.8	18	1	US-09-942-588A-22	Sequence 22, Appl	c1082	13.4	0.8	17	1	US-09-827-395A-559	Sequence 559, App
1010	13.8	0.8	18	1	US-09-764-420A-23	Sequence 23, Appl	c1083	13.4	0.8	17	1	US-09-827-395A-856	Sequence 856, App
1011	13.8	0.8	18	1	US-09-764-420A-23	Sequence 23, Appl	c1084	13.4	0.8	17	1	US-09-740-332-4449	Sequence 4449, Ap
c1012	13.8	0.8	18	1	US-09-969-373-2606	Sequence 2606, Ap	1085	13.4	0.8	17	1	US-09-745-237A-27	Sequence 27, Appl
1013	13.8	0.8	18	1	US-09-969-373-3605	Sequence 3605, Ap	1086	13.4	0.8	17	1	US-09-745-237A-497	Sequence 497, App
1014	13.8	0.8	18	1	US-09-728-574-2	Sequence 2, Appli	1087	13.4	0.8	17	1	US-09-745-237A-1320	Sequence 1320, Ap
1015	13.8	0.8	18	1	US-09-942-596A-22	Sequence 22, Appl	c1088	13.4	0.8	17	1	US-09-817-879-4449	Sequence 4449, Ap
1016	13.8	0.8	18	1	US-09-988-873A-22	Sequence 22, Appl	1089	13.4	0.8	17	1	US-10-426-179-8	Sequence 8, Appli
1017	13.8	0.8	18	1	US-09-925-388-30	Sequence 30, Appl	c1090	13.4	0.8	17	1	US-09-927-046-403	Sequence 403, App
1018	13.8	0.8	18	1	US-09-942-662A-22	Sequence 22, Appl	c1091	13.4	0.8	17	1	US-09-927-046-2136	Sequence 2136, Ap
c1019	13.8	0.8	18	1	US-10-463-549-23	Sequence 23, Appl	c1092	13.4	0.8	17	1	US-09-927-046-2137	Sequence 2137, Ap
1020	13.8	0.8	18	1	US-10-231-302-22	Sequence 22, Appl	c1093	13.4	0.8	17	1	US-10-430-882-37	Sequence 37, Appl
c1021	13.8	0.8	18	1	US-10-153-401-52	Sequence 52, Appl	c1094	13.4	0.8	17	1	US-10-430-882-559	Sequence 559, App
1022	13.8	0.8	18	1	US-10-082-502-15	Sequence 15, Appl	c1095	13.4	0.8	17	1	US-10-430-882-856	Sequence 856, App
c1023	13.8	0.8	18	1	US-10-306-878-18	Sequence 18, Appl	c1096	13.4	0.8	17	1	US-10-060-756A-648	Sequence 648, App
1024	13.8	0.8	18	1	US-10-025-145A-60	Sequence 60, Appl	c1097	13.4	0.8	17	1	US-10-060-756A-649	Sequence 649, App
1025	13.8	0.8	18	1	US-10-431-846-30	Sequence 30, Appl	c1098	13.4	0.8	17	1	US-10-156-306-526	Sequence 526, App
1026	13.8	0.8	18	1	US-10-608-804-22	Sequence 22, Appl	c1099	13.4	0.8	17	1	US-10-156-306-5855	Sequence 5855, Ap
1027	13.8	0.8	18	1	US-10-634-510-22	Sequence 22, Appl	c1100	13.4	0.8	17	1	US-10-156-306-5868	Sequence 5868, Ap
c1028	13.8	0.8	18	1	US-10-138-674-4028	Sequence 4028, Ap	c1101	13.4	0.8	17	1	US-10-156-306-6933	Sequence 6933, Ap
c1029	13.8	0.8	18	1	US-10-287-949A-4028	Sequence 4028, Ap	c1102	13.4	0.8	17	1	US-10-156-306-6937	Sequence 6937, Ap
1030	13.8	0.8	18	1	US-10-716-824-15	Sequence 15, Appl	c1103	13.4	0.8	17	1	US-10-156-306-6938	Sequence 6938, Ap
1031	13.8	0.8	18	1	US-10-481-044-8	Sequence 8, Appli	c1104	13.4	0.8	17	1	US-10-238-700-18	Sequence 18, Appl
c1032	13.4	0.8	15	1	US-09-805-296D-12	Sequence 12, Appl	c1105	13.4	0.8	17	1	US-10-238-700-2977	Sequence 2977, Ap
1033	13.4	0.8	15	1	US-09-880-313A-143	Sequence 143, App	1106	13.4	0.8	17	1	US-10-238-700-3413	Sequence 3413, Ap
c1034	13.4	0.8	15	1	US-09-848-754A-9214	Sequence 9214, Ap	c1108	13.4	0.8	17	1	US-10-314-321A-51	Sequence 51, Appl
1035	13.4	0.8	15	1	US-09-848-754A-9265	Sequence 9265, Ap	1109	13.4	0.8	17	1	US-10-230-006-2122	Sequence 2122, Ap
c1036	13.4	0.8	15	1	US-10-339-674-267	Sequence 267, App	1110	13.4	0.8	17	1	US-10-230-006-2123	Sequence 2123, Ap
c1037	13.4	0.8	15	1	US-10-339-674-3455	Sequence 3455, Ap	c1111	13.4	0.8	17	1	US-10-209-787-3406	Sequence 3406, Ap
c1038	13.4	0.8	15	1	US-10-072-975-12	Sequence 12, Appl	1112	13.4	0.8	17	1	US-10-209-787-3407	Sequence 3407, Ap
c1039	13.4	0.8	15	1	US-10-051-436-12	Sequence 12, Appl	c1113	13.4	0.8	17	1	US-10-261-185-3406	Sequence 3406, Ap
c1040	13.4	0.8	15	1	US-10-360-275-12	Sequence 12, Appl	1114	13.4	0.8	17	1	US-10-261-185-3407	Sequence 3407, Ap
1041	13.4	0.8	16	1	US-10-287-919-2610	Sequence 2610, Ap	c1115	13.4	0.8	17	1	US-10-138-674-1300	Sequence 1300, Ap
1042	13.4	0.8	16	1	US-10-164-915-3	Sequence 3, Appli	c1116	13.4	0.8	17	1	US-10-138-674-1301	Sequence 1301, Ap
c1043	13.4	0.8	16	1	US-10-191-997-38	Sequence 38, Appl	c1117	13.4	0.8	17	1	US-10-138-674-1302	Sequence 1302, Ap
1044	13.4	0.8	16	1	US-10-321-039-561	Sequence 561, App	1118	13.4	0.8	17	1	US-10-138-674-5090	Sequence 5090, Ap
1045	13.4	0.8	16	1	US-10-712-672-1517	Sequence 1517, Ap	c1119	13.4	0.8	17	1	US-10-138-674-7735	Sequence 7735, Ap
1046	13.4	0.8	16	1	US-10-712-672-1655	Sequence 1655, Ap	1120	13.4	0.8	17	1	US-10-138-674-7887	Sequence 7887, Ap
1047	13.4	0.8	17	1	US-10-230-006-2124	Sequence 2124, Ap	1121	13.4	0.8	17	1	US-10-138-674-8938	Sequence 8938, Ap
1048	13.4	0.8	17	1	US-09-866-108-6390	Sequence 6390, Ap	c1122	13.4	0.8	17	1	US-10-287-949A-1300	Sequence 1300, Ap
1049	13.4	0.8	17	1	US-09-866-108-6391	Sequence 6391, Ap	c1123	13.4	0.8	17	1	US-10-287-949A-1301	Sequence 1301, Ap
1050	13.4	0.8	17	1	US-09-866-108-6392	Sequence 6392, Ap	c1124	13.4	0.8	17	1	US-10-287-949A-1302	Sequence 1302, Ap
1051	13.4	0.8	17	1	US-09-866-108-7876	Sequence 7876, Ap	1125	13.4	0.8	17	1	US-10-287-949A-5090	Sequence 5090, Ap
1052	13.4	0.8	17	1	US-09-866-108-7880	Sequence 7880, Ap	c1126	13.4	0.8	17	1	US-10-287-949A-7735	Sequence 7735, Ap
1053	13.4	0.8	17	1	US-09-866-108-7881	Sequence 7881, Ap	1127	13.4	0.8	17	1	US-10-287-949A-7887	Sequence 7887, Ap
1054	13.4	0.8	17	1	US-09-866-108-10020	Sequence 10020, A	1128	13.4	0.8	17	1	US-10-287-949A-8938	Sequence 8938, Ap
1055	13.4	0.8	17	1	US-09-866-108-10021	Sequence 10021, A							


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; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-008-789-6

Query Match      1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1046 TTGATCGCGTCTTTCACGTGGC 1068
Db 1 TTGATCGCGTCTTTCACGTGGC 23

RESULT 3
US-10-002-536A-3/c
; Sequence 3, Application US/10002536A
; Publication No. US20030108874A1
; GENERAL INFORMATION:
; APPLICANT: Kane, Michael D.
; APPLICANT: Nagel, Aaron C.
; APPLICANT: Dombkowski, Alan A.
; TITLE OF INVENTION: COMPOSITIONS AND SYSTEMS FOR IDENTIFYING AND COMPARING EXPRESSED
; FILE REFERENCE: 65446-87
; CURRENT APPLICATION NUMBER: US/10/002,536A
; CURRENT FILING DATE: 2003-02-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This is a synthesized sequence.
US-10-002-536A-3

Query Match      1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 46;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1730 GTTTACAAAAA 1753
Db 24 GTTTAAAAA 1

RESULT 4
US-10-002-536A-4
; Sequence 4, Application US/10002536A
; Publication No. US20030108874A1
; GENERAL INFORMATION:
; APPLICANT: Kane, Michael D.
; APPLICANT: Nagel, Aaron C.
; APPLICANT: Dombkowski, Alan A.
; TITLE OF INVENTION: COMPOSITIONS AND SYSTEMS FOR IDENTIFYING AND COMPARING EXPRESSED
; FILE REFERENCE: 65446-87
; CURRENT APPLICATION NUMBER: US/10/002,536A
; CURRENT FILING DATE: 2003-02-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This is a synthesized sequence.
US-10-002-536A-4

Query Match      1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 46;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1730 GTTTACAAAAA 1753
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Db 1 GTTTAAAAA 24

RESULT 5
US-10-331-780-6
; Sequence 6, Application US/10331780
; Publication No. US20030162210A1
; GENERAL INFORMATION:
; APPLICANT: Chetverin, Alexander B.
; APPLICANT: Kramer, Fred Russel
; TITLE OF INVENTION: NOVEL OLIGONUCLEOTIDE ARRAYS AND THEIR USE FOR SORTING,
; TITLE OF INVENTION: ISOLATING, SEQUENCING, AND MANIPULATING NUCLEIC ACIDS
; FILE REFERENCE: 07763-004002
; CURRENT APPLICATION NUMBER: US/10/331,780
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/08/473,010
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/247,530
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: US 07/833,607
; PRIOR FILING DATE: 1992-02-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically derived DNA
US-10-331-780-6

Query Match      1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 46;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1754
Db 1 TTTAAAAA 24

RESULT 6
US-09-901-484A-10/c
; Sequence 10, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T11XC3D2
; CURRENT APPLICATION NUMBER: US/09/901,484A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/853,526
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(24)
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; OTHER INFORMATION: primer oligonucleotide PGRT32
US-09-901-484A-10

Query Match      1.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 65;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1754
Db 23 TTTCAAAAAA 1

RESULT 7
US-09-853-526-10/c
; Sequence 10, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/218,207
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 10
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..24
; OTHER INFORMATION: primer oligonucleotide PGRT32
US-09-853-526-10

Query Match      1.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 65;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1754
Db 23 TTTCAAAAAA 1

RESULT 8
US-09-922-480-7/c
; Sequence 7, Application US/09922480
; Patent No. US20020081701A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,480
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-922-480-7

Query Match      1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 26 TAAAAAAA 4

RESULT 9
US-09-923-236-7/c
; Sequence 7, Application US/09923236
; Patent No. US20020090677A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/923,236
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-923-236-7

Query Match      1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 26 TAAAAAAA 4

RESULT 10
US-09-923-246-38/c
; Sequence 38, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
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; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-923-246-38

Query Match      1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 11
US-09-922-469-7/c
; Sequence 7, Application US/09922469
; Patent No. US20020173027A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,469
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-922-469-7

Query Match      1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 12
US-10-295-723-38/c
; Sequence 38, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
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; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-10-295-723-38

Query Match      1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 13
US-10-659-684-38/c
; Sequence 38, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-10-659-684-38

Query Match      1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 14
US-10-008-789-5/c
; Sequence 5, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
```

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; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-008-789-5

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1074 TGTATGTTCTACATGCCGGGC 1094
Db      21  TGTATGTTCTACATGCCGGGC 1

RESULT 15
US-10-410-031-190/c
; Sequence 190, Application US/10410031
; Publication No. US20040010817A1
; GENERAL INFORMATION:
; APPLICANT: Shockey, Jay M.
; APPLICANT: Schmurr, Judy
; APPLICANT: Browne, John A.
; TITLE OF INVENTION: Plant Acyl-CoA Synthetases
; FILE REFERENCE: DOW-07654
; CURRENT APPLICATION NUMBER: US/10/410,031
; CURRENT FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 190
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-410-031-190

Query Match          1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA..... 1755
Db      21  CAAAAA..... 1

RESULT 16
US-10-081-969-18
; Sequence 18, Application US/10081969
; Publication No. US20030104625A1
; GENERAL INFORMATION:
; APPLICANT: Cheng, Cheng
; APPLICANT: Clarke, Lori
; APPLICANT: Connelly, Sheila
; APPLICANT: Ennist, David
; APPLICANT: Forry-Schaudies, Suzanne
; APPLICANT: Gorziglia, Mario
; APPLICANT: Hallenbeck, Paul
; APPLICANT: Hay, Carl
; APPLICANT: Jakubczak, John
; APPLICANT: Kaleko, Michael
; APPLICANT: Phipps, Sandrina
; APPLICANT: Police, Seshidhar
; APPLICANT: Ryan, Patricia
; APPLICANT: Steward, David
```

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; APPLICANT: Xie, Yuefeng
; TITLE OF INVENTION: No. US20030104625A1el Oncolytic Adenoviral Vectors
; FILE REFERENCE: 4-31704A/GTI
; CURRENT APPLICATION NUMBER: US/10/081,969
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 60/270,922
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/295,037
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/348,670
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Viral vector sequence
; NAME/KEY: misc feature
; LOCATION: (1)..(24)
; OTHER INFORMATION: Fig. 1C. SV40 early Poly(A) site
US-10-081-969-18

Query Match          1.2%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA..... 1755
Db      2  CAAAAA..... 22

RESULT 17
US-09-853-646-4
; Sequence 4, Application US/09853646
; Patent No. US20020055106A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaidis, Nicholas
; APPLICANT: Sass, Philip
; APPLICANT: Grasso, Luigi
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: A METHOD FOR GENERATING HYPERMUTABLE
; TITLE OF INVENTION: ORGANISMS
; FILE REFERENCE: 01107.00138
; CURRENT APPLICATION NUMBER: US/09/853,646
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/204,769
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant DNA
US-09-853-646-4

Query Match          1.2%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA..... 1755
Db      5  CAAAAA..... 25
```



```
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-099-823-14

Query Match      1.2%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA
Db      26 CAAAAA

RESULT 22
US-09-853-646-3
; Sequence 3, Application US/09853646
; Patent No. US20020055106A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas
; APPLICANT: Sass, Philip
; APPLICANT: Grasso, Luigi
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: A METHOD FOR GENERATING HYPERMUTABLE
; TITLE OF INVENTION: ORGANISMS
; FILE REFERENCE: 01107.00138
; CURRENT APPLICATION NUMBER: US/09/853,646
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/204,769
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant DNA
US-09-853-646-3

Query Match      1.2%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA
Db      5 CAAAAA

RESULT 23
US-10-344-741-21/c
; Sequence 21, Application US/10344741
; Publication No. US20040038371A1
; GENERAL INFORMATION:
; APPLICANT: Basten, Danielle
; APPLICANT: Dekker, Petrus, Jacobus, Theodorus
; APPLICANT: Schuurhuizen, Paul, William
; APPLICANT: Schaap, petrus, Johannes
; APPLICANT: Visser, Jacob
; APPLICANT: DSM NV
; TITLE OF INVENTION: No. US20040038371A1el Aminopeptidase
; FILE REFERENCE: 24615-20187.00
; CURRENT APPLICATION NUMBER: US/10/344,741
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: EP/NL 00202995.7
; PRIOR FILING DATE: 2000-08-23
```

```
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Poly-T primer
US-10-344-741-21

Query Match      1.2%; Score 20.6; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 86;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1733 TACAAAAA
Db      24 BAAAAA

RESULT 24
US-09-922-480-6/c
; Sequence 6, Application US/09922480
; Patent No. US20020081701A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,480
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-922-480-6

Query Match      1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 92;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1733 TACAAAAA
Db      26 BAAAAA

RESULT 25
US-09-923-236-6/c
; Sequence 6, Application US/09923236
; Patent No. US20020090677A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/923,236
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-923-236-6
```

```
Query Match      1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 92;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 BAAAAA 4

RESULT 26
US-09-922-469-6/c
; Sequence 6, Application US/09922469
; Patent No. US20020173027A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,469
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-922-469-6

Query Match      1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 92;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 BAAAAA 4

RESULT 27
US-10-039-876A-10/c
; Sequence 10, Application US/10039876A
; Publication No. US20030032792A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Blumberg, Hal
; TITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, Z219A
; FILE REFERENCE: 97-63C1
; CURRENT APPLICATION NUMBER: US/10/039,876A
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/061,712
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: US 09/167,513
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-10-039-876A-10

Query Match      1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 92;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 BAAAAA 4
```

```
Db 26 BAAAAA 4

RESULT 28
US-10-196-703-43/c
; Sequence 43, Application US/10196703
; Publication No. US20030055019A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: Genes and Proteins Predictive and Therapeutic for
; TITLE OF INVENTION: Stroke, Hypertension, Diabetes, and Obesity
; FILE REFERENCE: 15966-527
; CURRENT APPLICATION NUMBER: US/10/196,703
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US/09/161,939
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligo(dT)<25>V
US-10-196-703-43

Query Match      1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 92;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 BAAAAA 4

RESULT 29
US-10-352-253A-36/c
; Sequence 36, Application US/10352253A
; Publication No. US20030175908A1
; GENERAL INFORMATION:
; APPLICANT: Limmarsson, Sten
; APPLICANT: Ernfors, Patrik
; APPLICANT: Bauren, Goran
; APPLICANT: Metsis, Ats
; APPLICANT: Pihlak, Arno
; APPLICANT: Montelius, Andreas
; TITLE OF INVENTION: Methods And Means For Manipulating Nucleic Acid
; FILE REFERENCE: 620-234
; CURRENT APPLICATION NUMBER: US/10/352,253A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,215
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)
; OTHER INFORMATION: v is a, c or g
US-10-352-253A-36

Query Match      1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 92;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 BAAAAA 4
```


Db 26 BAAAAAAAAAAAAAAAAAAAAA 4

RESULT 30
US-10-224-289-20/c
; Sequence 20, Application US/10224289
; Publication No. US20030207288A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, DAVID A.
; APPLICANT: STEWART, TIMOTHY A.
; TITLE OF INVENTION: GPCR-LIKE RETINOIC ACID-INDUCED GENE 1 PROTEIN AND
; TITLE OF INVENTION: NUCLEIC ACID
; FILE REFERENCE: 9800081-0085
; CURRENT APPLICATION NUMBER: US/10/224,289
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/313,940
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-224-289-20

Query Match 1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 92;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 BAAAAAAAAAAAAAAAAAAAAA 4

RESULT 31
US-10-071-214-42/c
; Sequence 42, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5'-RACE cDNA synthesis primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (27)..(27)
; OTHER INFORMATION: n is a o r g o r c o r t
US-10-071-214-42

Query Match 1.2%; Score 20.6; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 95;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 BAAAAAAAAAAAAAAAAAAAAA 4

RESULT 32
US-10-216-122-94
; Sequence 94, Application US/10216122
; Publication No. US20030121063A1
; GENERAL INFORMATION:
; APPLICANT: Kazazian, Haig H.
; APPLICANT: Ostertag, Eric
; APPLICANT: DeBerardinis, Ralph
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS
; FILE REFERENCE: 053893-5006-03
; CURRENT APPLICATION NUMBER: US/10/216,122
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 09/653,812
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 08/847,844
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: US 08/749,805
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/006,831
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-216-122-94

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 85;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 33
US-10-335-573-6/c
; Sequence 6, Application US/10335573
; Publication No. US20040126770A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Gyanendra
; APPLICANT: Abarzua, Patricia
; TITLE OF INVENTION: ROLLING CIRCLE AMPLIFICATION OF RNA
; FILE REFERENCE: 13172.0021U1
; CURRENT APPLICATION NUMBER: US/10/335,573
; CURRENT FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Note =
; OTHER INFORMATION: synthetic construct
US-10-335-573-6

Query Match 1.2%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 85;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 34
US-09-426-548-126
; Sequence 126, Application US/09426548

```
; Patent No. US20010044936A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, David
; APPLICANT: Lin-Goerke, Juili L.
; APPLICANT: Ling, Jessica
; TITLE OF INVENTION: No. US20010044936A1el Mutations in Human MLH1 and MSH2 Genes Usef
; FILE REFERENCE: DEX-0054
; CURRENT APPLICATION NUMBER: US/09/426,548
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-426-548-126

Query Match      1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 88;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1754
Db 2 TAAAAA 23

RESULT 35
US-09-920-342-12/c
; Sequence 12, Application US/09920342
; Patent No. US20020137709A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Lin, Shi-Lung
; APPLICANT: Chuong, Cheng-Ming
; APPLICANT: Widelitz, Randall B.
; TITLE OF INVENTION: GENE SILENCING USING MRNA-CDNA HYBRIDS
; FILE REFERENCE: 13761-7024
; CURRENT APPLICATION NUMBER: US/09/920,342
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 60/222,479
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Poly(dT)24 primer
US-09-920-342-12

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAA 1755
Db 24 AAAAAA 3

RESULT 36
US-09-920-313-148/c
; Sequence 148, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; TITLE OF INVENTION: Treatment of Gastric Ulcers
; FILE REFERENCE: C1037/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-01
```

```
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-920-313-148

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAA 1755
Db 24 AAAAAA 3

RESULT 37
US-09-949-305B-6/c
; Sequence 6, Application US/09949305B
; Publication No. US20030022318A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Shi-Lung
; APPLICANT: Ying, Shao-Yao
; TITLE OF INVENTION: Method for Thermocycling Amplification of Nucleic Acid Sequences
; TITLE OF INVENTION: Generation of Related Peptides Thereof
; FILE REFERENCE: 266/014
; CURRENT APPLICATION NUMBER: US/09/949,305B
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/494,212
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligo(dT) primer for RNA polymerase thermocycling procedure
US-09-949-305B-6

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAA 1755
Db 24 AAAAAA 3

RESULT 38
US-09-888-326-841/c
; Sequence 841, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 841
; LENGTH: 24
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-841

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 39
US-09-776-479-433/c
; Sequence 433, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 433
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-433

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 40
US-09-776-479-433/c
; Sequence 433, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 433
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-433

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 41
US-09-776-479-961/c
; Sequence 961, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 961
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-961

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 42
US-09-776-479-961/c
; Sequence 961, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 961
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-961

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Matches	21;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Qy	1734 AC	AAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAA	1755
Db	24 AA	AAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAA	3

```

RESULT 43
US-09-776-479-962
; Sequence 962, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fournon, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 962
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-962

```

```
Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1734 ACACAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 22

RESULT 44
US-09-776-479-962
; Sequence 962, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourn, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 962
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-962

```

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy	1734	ACAAAAAAAAAAAAAAAAAAAA	1755
Db	1	AAAAAAAAAAAAAAAAAAAA	22

```

RESULT 45
US-10-058-270A-140/c
; Sequence 140, Application US/10058270A
; Publication No. US20040029114A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-005210US
; CURRENT APPLICATION NUMBER: US/10/058,270A
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:T7-T24 oligo
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (8)..(24)
; OTHER INFORMATION: t at positions 8-24 may be present or absent
US-10-058-270A-140

```

Query Match	1.2%;	Score 20.4;	DB 1;	Length 24;
Best Local Similarity	95.5%;	Pred. No. 92;		
Matches 21;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1734	ACAAAAAAAAAAAAAAAAAAAA	1755	
Db	24	AAAAAAAAAAAAAAAAAAAAAAA	3	

```

RESULT 46
US-10-314-578-433/c
; Sequence 433, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 433
; LENGTH: 24

```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-433

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db      24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 47
US-10-314-578-961/c
; Sequence 961, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 961
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-961

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db      24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 48
US-10-314-578-962.
; Sequence 962, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 962
```

```
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-962

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db      1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 49
US-10-671-628-10/c
; Sequence 10, Application US/10671628
; Publication No. US20040068105A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Kikukatsu
; TITLE OF INVENTION: Plant Thermogenic Genes and Proteins
; FILE REFERENCE: 2003-1386A/WMC/00653
; CURRENT APPLICATION NUMBER: US/10/671,628
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: 10/009,962
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: PCT/JP00/03806
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: JP11-167439
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA Primer
US-10-671-628-10

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db      24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 50
US-10-043-415-4
; Sequence 4, Application US/10043415
; Publication No. US20020182620A1
; GENERAL INFORMATION:
; APPLICANT: Kurn, Nurith
; APPLICANT: Patel, Rajesh D.
; TITLE OF INVENTION: Quantitative Determination of Nucleic
; FILE REFERENCE: BEH-7408
; CURRENT APPLICATION NUMBER: US/10/043,415
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US/09/025,639
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_binding
```

```
; LOCATION: (1)...(24)
; OTHER INFORMATION: Synthetic DNA Probe
US-10-043-415-4

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 51
US-10-112-653-415/c
; Sequence 415, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 415
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-415

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 52
US-10-112-653-919/c
; Sequence 919, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 919
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-919

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 53
US-10-112-653-920
; Sequence 920, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-920

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 54
US-10-017-995-433/c
; Sequence 433, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 433
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-433

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 55
US-10-017-995-961/c
; Sequence 961, Application US/10017995
```



```

; PRIOR APPLICATION NUMBER: 60/355,374
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-360-511-14

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db      24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 64
US-10-062-188-106/c
; Sequence 106, Application US/10062188
; Publication No. US20040096826A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Methods For Creating Recombination
; TITLE OF INVENTION: Products Between Nucleotide Sequences
; FILE REFERENCE: P-EA 5008
; CURRENT APPLICATION NUMBER: US/10/062,188
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-062-188-106

Query Match      1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 92;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db      24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 65
US-09-282-734-23/c
; Sequence 23, Application US/09282734A
; Publication No. US20020182597A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis et al.
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
; FILE REFERENCE: 50036/009002
; CURRENT APPLICATION NUMBER: US/09/282,734A
; CURRENT FILING DATE: 1999-03-03
; EARLIER APPLICATION NUMBER: 60/080,686
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Capture probe sequence
US-09-282-734-23
```

```

Query Match      1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 95;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db      25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 66
US-10-239-655A-9/c
; Sequence 9, Application US/10239655A
; Publication No. US20040048816A1
; GENERAL INFORMATION:
; APPLICANT: ZOHLNHOFFER, DIETLIND
; APPLICANT: BAUERLE, PATRICK
; APPLICANT: KLEIN, CHRISTOPH
; APPLICANT: NEUMANN, FRANZ-JOSEF
; TITLE OF INVENTION: RESTENOSIS TREATMENT
; FILE REFERENCE: 029976/0103
; CURRENT APPLICATION NUMBER: US/10/239,655A
; CURRENT FILING DATE: 2003-02-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03312
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00106468.2
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-239-655A-9

Query Match      1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 95;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db      25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 67
US-10-348-627-23/c
; Sequence 23, Application US/10348627
; Publication No. US20030143616A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis et al.
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
; FILE REFERENCE: 50036/009002
; CURRENT APPLICATION NUMBER: US/10/348,627
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US/09/282,734A
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/080,686
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Capture probe sequence
US-10-348-627-23

Query Match      1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 95;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```


APPLICATION NUMBER: US/09/092,296
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 60/048,810
APPLICATION NUMBER: 05-JUN-1997
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6104.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:

```
Query Match      1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

RESULT 72

```

US-09-949-305B-4/c
; Sequence 4, Application US/09949305B
; Publication No. US20030022318A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Shi-Lung
; APPLICANT: Ying, Shao-Yao
; TITLE OF INVENTION: Method for Thermocycling
; TITLE OF INVENTION: Generation of Related
; FILE REFERENCE: 266/014
; CURRENT APPLICATION NUMBER: US/09/949,305B
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/494,212
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: poly(dT) primer
US-09-949-305B-4

```

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 73

```

RESULTS
US-10-053-883-53/c
; Sequence 53, Application US/10053883
; Publication No. US20030113737A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Morten Lorentz
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION
; FILE REFERENCE: PEDERSEN=1A
; CURRENT APPLICATION NUMBER: US/10/053.883

```

```

; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: PA 2001 001266
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/267,704
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; US-10-053--883-53

```

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 74

```

US-10-295-723-39/c
; Sequence 39, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764b
US-10-295-723-39

```

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 99;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 75

RESULT 75
US-10-659-684-39/c
; Sequence 39, Application US/10659684

Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 83

US-10-017-995-911/c
; Sequence 911, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 911
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-911

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 84

US-10-102-720-18/c
; Sequence 18, Application US/10102720
; Publication No. US20030152937A1
; GENERAL INFORMATION:
; APPLICANT: Weindel, Kurt
; APPLICANT: Brand, Joachim
; TITLE OF INVENTION: DNA DETECTION BY MEANS OF A STRAND REASSOCIATION COMPLEX
; FILE REFERENCE: 101614-00014
; CURRENT APPLICATION NUMBER: US/10/102,720
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/325,554
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent-In version 3.1
; SEQ ID NO 18
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: (27)-(27)
; OTHER INFORMATION: Y means incorporation of Aminolinker-phosphoramidite subsequently
; OTHER INFORMATION: esterified with 3-O carboxymethyl digoxigenin
US-10-102-720-18

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 85

US-10-133-937-99/c
; Sequence 99, Application US/10133937
; Publication No. US20030207278A1

; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-133-937-99

Query Match 1.2%; Score 20.2; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 87;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755

Db 21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 86

US-10-159-563-99/c
; Sequence 99, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-159-563-99

Query Match 1.2%; Score 20.2; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 87;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755

Db 21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 87

US-10-314-321A-56/c
; Sequence 56, Application US/10314321A
; Publication No. US20030190648A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi, Ltd.
; TITLE OF INVENTION: Gene Predicting Method
; FILE REFERENCE: 310101185US1

```

; CURRENT APPLICATION NUMBER: US/10/314,321A
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: JP 2002-103333
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)
; OTHER INFORMATION: partial sequence of AL365356, n is a, c, g or t
US-10-314-321A-56

Query Match      1.2%; Score 20.2; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 91;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1755
Db 21 BAAAAA..... 1

RESULT 88
US-10-002-536A-2/c
; Sequence 2, Application US/10002536A
; Publication No. US20030108874A1
; GENERAL INFORMATION:
; APPLICANT: Kane, Michael D.
; APPLICANT: Nagel, Aaron C.
; APPLICANT: Dombkowski, Alan A.
; TITLE OF INVENTION: COMPOSITIONS AND SYSTEMS FOR IDENTIFYING AND COMPARING EXPRESSED
; TITLE OF INVENTION: (mrnas) IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 65446-87
; CURRENT APPLICATION NUMBER: US/10/002,536A
; CURRENT FILING DATE: 2003-02-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This is a synthesized sequence.
; NAME/KEY: misc_feature
; LOCATION: (23)..(25)
; OTHER INFORMATION: n may be selected from a or c or g or t.
US-10-002-536A-2

Query Match      1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 1e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1755
Db 22 BAAAAA..... 2

RESULT 89
US-09-973-788A-55
; Sequence 55, Application US/09973788A
; Patent No. US20020127574A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
```

```

; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i10
; CURRENT APPLICATION NUMBER: US/09/973,788A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-973-788A-55

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAA..... 1755
Db 1 AAAAAA..... 20

RESULT 90
US-09-973-638A-55
; Sequence 55, Application US/09973638A
; Patent No. US20020137070A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i9
; CURRENT APPLICATION NUMBER: US/09/973,638A
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
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US-09-973-638A-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
Dd 1 AAAAAAAAAAAAAAAAAA 20

RESULT 91

US-09-974-007-55
; Sequence 55, Application US/09974007
; Patent No. US20020137071A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00-713-18

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 93

US-09-961-949A-55
; Sequence 55, Application US/09961949A
; Patent No. US20020146720A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i1
; CURRENT APPLICATION NUMBER: US/09/961,949A

```

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

	1736	AAAAAAAAAAAAAAAAAAAA	1755
Qy			
D _b	1	AAAAAAAAAAAAAAAAAAAA	20

RESULT 92

US-09-976-617A-55
; Sequence 55, Application US/09976617A
; Patent No. US20020137072A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-124

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1755
Db      1 AAAAAAAAAAAAAAAAAA 20

RESULT 94
US-09-760-500A-55
; Sequence 55, Application US/09760500A
; Patent No. US20020155442A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-715-A
; CURRENT APPLICATION NUMBER: US/09/760,500A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; US-09-760-500A-55

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1755
Db      1 AAAAAAAAAAAAAAAAAA 20

RESULT 95
US-09-967-409A-55
; Sequence 55, Application US/09967409A
; Patent No. US20020155458A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-i6
; CURRENT APPLICATION NUMBER: US/09/967,409A
; CURRENT FILING DATE: 2001-09-28
```

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1755
Db      1 AAAAAAAAAAAAAAAAAA 20

RESULT 96
US-09-975-062A-55
; Sequence 55, Application US/09975062A
; Patent No. US20020155459A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-ii1
; CURRENT APPLICATION NUMBER: US/09/975,062A
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; US-09-975-062A-55

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1755
Db      1 AAAAAAAAAAAAAAAAAA 20

RESULT 97
US-09-967-409A-55
; Sequence 55, Application US/09967409A
; Patent No. US20020155458A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-i6
; CURRENT APPLICATION NUMBER: US/09/967,409A
; CURRENT FILING DATE: 2001-09-28
```

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 97
US-09-976-378A-55
; Sequence 55, Application US/09976378A
; Patent No. US20020155461A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-125
; CURRENT APPLICATION NUMBER: US/09/976,378A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-976-378A-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 98
US-09-976-577-55
; Sequence 55, Application US/09976577
; Patent No. US20020155462A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-120
; CURRENT APPLICATION NUMBER: US/09/976,577
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
```

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; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-976-577-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 99
US-09-771-554-5/c
; Sequence 5, Application US/09771554
; Patent No. US20020155496A1
; GENERAL INFORMATION:
; APPLICANT: CHARLES, Marie Helene
; APPLICANT: FIGA, Nadia
; APPLICANT: BATTAIL-POIROT, Nicole
; APPLICANT: VERON, Laurent
; APPLICANT: DELAIR, Thierry
; APPLICANT: MANDRAND, Bernard
; TITLE OF INVENTION: SATURATED AND UNSATURATED ABIETANE DERIVATIVES, DERIVED CONJUGATES
; TITLE OF INVENTION: USES IN A DIAGNOSTIC COMPOSITION, A REAGENT AND A DEVICE
; FILE REFERENCE: 108473
; CURRENT APPLICATION NUMBER: US/09/771,554
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: PCT/FR99/01846
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: FR 98/10084
; PRIOR FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-771-554-5

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 100
US-09-966-312-55
; Sequence 55, Application US/09966312
; Patent No. US20020164605A1
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; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-i5
; CURRENT APPLICATION NUMBER: US/09/966,312
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-966-312-55

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
        |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 101
US-09-927-777A-55
; Sequence 55, Application US/09927777A
; Patent No. US20020172953A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; APPLICANT: Garimella, Viswanadham
; APPLICANT: Li, Zhi
; APPLICANT: Park, So-Jung
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-653-A
; CURRENT APPLICATION NUMBER: US/09/927,777A
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/820,279
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/760,500
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
```

```
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; APPLICANT: Garimella, Viswanadham
; APPLICANT: Li, Zhi
; APPLICANT: Park, So-Jung
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-653-A
; CURRENT APPLICATION NUMBER: US/09/927,777A
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/820,279
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/760,500
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/176,409
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/192,699
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/213,906
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/224,631
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/254,392
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/255,235
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-927-777A-55

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
        |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 102
US-09-927-777A-70
; Sequence 70, Application US/09927777A
; Patent No. US20020172953A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; APPLICANT: Garimella, Viswanadham
; APPLICANT: Li, Zhi
; APPLICANT: Park, So-Jung
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-653-A
; CURRENT APPLICATION NUMBER: US/09/927,777A
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/820,279
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/760,500
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/176,409
; PRIOR FILING DATE: 2000-01-13
```

```
; PRIOR APPLICATION NUMBER: 60/192,699
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/213,906
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/224,631
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/254,392
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/255,235
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-927-777A-70
```

```
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
```

```
RESULT 103
US-09-966-491A-55
; Sequence 55, Application US/09966491A
; Publication No. US20020182611A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-14
; CURRENT APPLICATION NUMBER: US/09/966,491A
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-966-491A-55
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```
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
```

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 104
US-09-976-971A-55
; Sequence 55, Application US/09976971A
; Publication No. US20020182613A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-118
; CURRENT APPLICATION NUMBER: US/09/976,971A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-976-971A-55
```

```
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
```

```
RESULT 105
US-09-880-505-83
; Sequence 83, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007C2
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
```

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-880-505-83

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 106

US-09-820-279B-55
; Sequence 55, Application US/09820279B
; Publication No. US20030022169A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR

; FILE REFERENCE: 00-1085-A
; CURRENT APPLICATION NUMBER: US/09/820,279B
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence

US-09-820-279B-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 107

US-09-888-326-2
; Sequence 2, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther

; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-2

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 108

US-09-888-326-838/c
; Sequence 838, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 838
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-838

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 109

US-09-888-326-839/c
; Sequence 839, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced

```
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 839
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-839

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
      |||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
      |||||

RESULT 110
US-09-981-344-55
; Sequence 55, Application US/09981344
; Publication No. US20030044805A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-122
; CURRENT APPLICATION NUMBER: US/09/981,344
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-981-344-55

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 111
US-09-957-318A-55
; Sequence 55, Application US/09957318A
; Publication No. US20030049630A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-12
; CURRENT APPLICATION NUMBER: US/09/957,318A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-957-318A-55

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
      |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 112
US-09-974-500A-55
; Sequence 55, Application US/09974500A
; Publication No. US20030049631A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-17
; CURRENT APPLICATION NUMBER: US/09/974,500A
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
```

;; PRIOR APPLICATION NUMBER: PCT/US97/12783
;; PRIOR FILING DATE: 1997-07-21
;; PRIOR APPLICATION NUMBER: 60/031,809
;; PRIOR FILING DATE: 1996-07-29
;; PRIOR APPLICATION NUMBER: 60/200,161
;; PRIOR FILING DATE: 2000-04-26
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: Microsoft Word 2000
;; SEQ ID NO 55
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:random
;; OTHER INFORMATION: synthetic sequence
US-09-974-500A-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 113
US-09-975-376A-55
; Sequence 55, Application US/09975376A
; Publication No. US20030054358A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-i12
; CURRENT APPLICATION NUMBER: US/09/975,376A
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/031,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-975-376A-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 114
US-09-957-313A-55
; Sequence 55, Application US/09957313A
; Publication No. US20030059777A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-i3
; CURRENT APPLICATION NUMBER: US/09/957,313A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/031,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-957-313A-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 115
US-09-912-014-16/c
; Sequence 16, Application US/09912014
; Publication No. US20030059929A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; MICROELECTRONIC SYSTEMS AND DEVICES FOR
; MOLECULAR BIOLOGICAL ANALYSIS AND
; DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/912,014
; FILING DATE: 24-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,504
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 203/218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-912-014-16

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 116

US-09-997-672-40/c
; Sequence 40, Application US/09997672
; Publication No. US20030061632A1
; GENERAL INFORMATION:
; APPLICANT: Weterings, Koen
; APPLICANT: Apuya, Nestor R.
; APPLICANT: Tatarinova, Tatiana
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; APPLICANT: Ceres, Inc.
; TITLE OF INVENTION: Polynucleotides Useful for Modulating Transcription
; FILE REFERENCE: 023070-115810US
; CURRENT APPLICATION NUMBER: US/09/997,672
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,672
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo(dT-20)
; OTHER INFORMATION: primer
US-09-997-672-40

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 117

US-09-976-863A-55
; Sequence 55, Application US/09976863A
; Publication No. US20030068622A1

; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-il9
; CURRENT APPLICATION NUMBER: US/09/976,863A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-976-863A-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 118

US-09-881-535-2/c
; Sequence 2, Application US/09881535
; Publication No. US20030069410A1
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga T.
; TITLE OF INVENTION: Methods For Preparing Oligonucleotides Having Chiral Phosphorothioic Acid Linkages
; FILE REFERENCE: ISIS4785
; CURRENT APPLICATION NUMBER: US/09/881,535
; CURRENT FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030069410A1e1 Sequence
US-09-881-535-2

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 119
US-09-776-479-226/c
; Sequence 226, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 226
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-226

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 120
US-09-776-479-226/c
; Sequence 226, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 226
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-226

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 121
US-09-776-479-556/c
; Sequence 556, Application US/09776479
; Publication No. US20030087848A1

; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 556
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-556

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 122
US-09-776-479-556/c
; Sequence 556, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 556
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-556

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 123
US-09-776-479-560
; Sequence 560, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the

; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 560
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-560

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 124

US-09-776-479-560
; Sequence 560, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 560
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-560

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 125

US-09-976-601A-55
; Sequence 55, Application US/09976601A
; Publication No. US20030124528A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-116

; CURRENT APPLICATION NUMBER: US/09/976,601A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-976-601A-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 126

US-09-975-059A-55
; Sequence 55, Application US/09975059A
; Publication No. US20030143538A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-115
; CURRENT APPLICATION NUMBER: US/09/975,059A
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-975-059A-55

RESULT 130

US-09-994-701B-6/c
; Sequence 6, Application US/09994701B
; Publication No. US20040152076A1
; GENERAL INFORMATION:

; APPLICANT: Richard C. Willson and Jason C. Murphy
; TITLE OF INVENTION: NUCLEIC ACID SEPARATION USING IMMOBILIZED METAL AFFINITY CHROMATOGRAPHY

; FILE REFERENCE: 96605/13UTL

; CURRENT APPLICATION NUMBER: US/09/994,701B

; CURRENT FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: 60/246292

; PRIOR FILING DATE: 2000-11-06

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide Sequence

US-09-994-701B-6

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

|||||

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 131

US-09-916-369A-1/c

; Sequence 1, Application US/09916369A

; Publication No. US20020058802A1

; GENERAL INFORMATION:

; APPLICANT: Dellinger, Douglas J

; APPLICANT: Perbost, Michael GM

; APPLICANT: Caruthers, Marvin H

; APPLICANT: Betley, Jason R

; TITLE OF INVENTION: Synthesis of Polynucleotides Using Combined Oxidation/Deprotection

; FILE REFERENCE: 10003869-1

; CURRENT APPLICATION NUMBER: US/09/916,369A

; CURRENT FILING DATE: 2001-07-21

; PRIOR APPLICATION NUMBER: US 09/627,249

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 20

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic sequence

US-09-916-369A-1

Query Match

Best Local Similarity 1.1%; Score 20; DB 1; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

|||||

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 132

US-09-975-498-55

; Sequence 55, Application US/09975498

; Publication No. US20020160381A1

; GENERAL INFORMATION:

; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elgharian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-i14
; CURRENT APPLICATION NUMBER: US/09/975,498
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-09-975-498-55

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 133

US-10-181-200-10/c

; Sequence 10, Application US/10181200

; Publication No. US20030212267A1

; GENERAL INFORMATION:

; APPLICANT: Cole, Douglas L.

; APPLICANT: Ravikumar, Vasulinga T.

; APPLICANT: Cheruvallath, Zacharia S.

; TITLE OF INVENTION: IMPROVED SYNTHESIS OF SULFURIZED OLIGONUCLEOTIDES

; FILE REFERENCE: ISIS-4709

; CURRENT APPLICATION NUMBER: US/10/181,200

; CURRENT FILING DATE: 2002-12-12

; PRIOR APPLICATION NUMBER: PCT/US01/00715

; PRIOR FILING DATE: 2001-01-10

; PRIOR APPLICATION NUMBER: US 09/481,486

; PRIOR FILING DATE: 2000-01-11

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 10

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: 2'-O-methoxyethyl

; FEATURE:

; NAME/KEY: misc_feature

```
; LOCATION: (1)..(20)
; OTHER INFORMATION: phosphorothioate 20-mer
US-10-181-200-10

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 134
US-10-181-200-15/c
; Sequence 15, Application US/10181200
; Publication No. US20030212267A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Douglas L.
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Cheruvallath, Zacharia S.
; TITLE OF INVENTION: IMPROVED SYNTHESIS OF SULFURIZED OLIGONUCLEOTIDES
; FILE REFERENCE: ISIS-4709
; CURRENT APPLICATION NUMBER: US/10/181,200
; CURRENT FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: PCT/US01/00715
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 09/481,486
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: phosphorothioate 20-mer
US-10-181-200-15

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 135
US-10-314-578-226/c
; Sequence 226, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
```

```
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 226
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-226

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 136
US-10-314-578-556/c
; Sequence 556, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 556
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-556

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 137
US-10-314-578-560
; Sequence 560, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
```

```
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 560
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-560

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 138
US-10-208-357-26
; Sequence 26, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence.
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-26

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 139
US-10-051-643-83
; Sequence 83, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
```

```
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-051-643-83

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 140
US-10-176-055-11
; Sequence 11, Application US/10176055
; Publication No. US20030013109A1
; GENERAL INFORMATION:
; APPLICANT: Evident Technologies
; TITLE OF INVENTION: Hairpin Sensors Using Quenchable Fluorescing Agents
; FILE REFERENCE: 11739/26
; CURRENT APPLICATION NUMBER: US/10/176,055
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,460
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Target sequence
; OTHER INFORMATION: Target sequence that is desired to be detected and
; OTHER INFORMATION: that has a nucleotide sequence that is
; OTHER INFORMATION: complementary to the sequence of complementary
; OTHER INFORMATION: probe of hairpin loop assembly
US-10-176-055-11

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 141
US-10-117-267-1/c
; Sequence 1, Application US/10117267
; Publication No. US20030045698A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Ph.D., Martin A.
; TITLE OF INVENTION: Compounds, Processes And Intermediates For Synthesis Of Mixed Backl
; TITLE OF INVENTION: Oligomeric Compounds
; FILE REFERENCE: ISIS-5039
; CURRENT APPLICATION NUMBER: US/10/117,267
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/726,096
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/250,075
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
```



```
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: 2'-methoxyethoxy (MOE)
US-10-117-267-1

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 142
US-10-112-653-218/c
; Sequence 218, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 218
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-218

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 143
US-10-112-653-533/c
; Sequence 533, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 533
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-533

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 144
US-10-112-653-537
; Sequence 537, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 537
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-537

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 145
US-10-077-383-5
; Sequence 5, Application US/10077383
; Publication No. US20030050444A1
; GENERAL INFORMATION:
; APPLICANT: Haydock, Paul V.
; APPLICANT: U'Ren, Jack
; APPLICANT: Saigene Corporation
; TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and
; FILE REFERENCE: 018048-001710US
; CURRENT APPLICATION NUMBER: US/10/077,383
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/296,812
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: (A)-12-20
; OTHER INFORMATION: homopolymer spacer sequence
; FEATURE:
; NAME/KEY: modified_base
```

```
; LOCATION: (13)..(20)
; OTHER INFORMATION: a at positions 13-20 may be present or absent
US-10-077-383-5

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 146
US-10-077-383-6/c
; Sequence 6, Application US/10077383
; Publication No. US2003005044A1
; GENERAL INFORMATION:
; APPLICANT: Haydock, Paul V.
; APPLICANT: U'Ren, Jack
; APPLICANT: Saigene Corporation
; TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and
; FILE REFERENCE: DNA/RNA Mixed Polymer Intermediate Products
; CURRENT APPLICATION NUMBER: US/10/077,383
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/296,812
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:(T)-12-20
; NAME/KEY: modified base
; LOCATION: (13)..(20)
; OTHER INFORMATION: t at positions 13-20 may be present or absent
US-10-077-383-6

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 147
US-10-017-995-226/c
; Sequence 226, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 226
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-226
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 148
US-10-017-995-556/c
; Sequence 556, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 556
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-556
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 149
US-10-017-995-560
; Sequence 560, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 560
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-560
```

```
Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 150
```

US-10-194-138-32
; Sequence 32, Application US/10194138
; Publication No. US20030082588A1
; GENERAL INFORMATION:
; APPLICANT: Nanosphere, Inc.
; APPLICANT: Garimella, Viswanadham
; TITLE OF INVENTION: Method for Immobilizing Molecules onto Surfaces
; FILE REFERENCE: 01-897-B
; CURRENT APPLICATION NUMBER: US/10/194,138
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/363472
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/305369
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: "a20" oligonucleotide probe
US-10-194-138-32

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 151
US-10-008-978-55
; Sequence 55, Application US/10008978
; Publication No. US20030087242A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; APPLICANT: Garimella, Viswanadham
; APPLICANT: Li, Zhi
; APPLICANT: Park, So-Jung
; APPLICANT: Lu, Gang
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-1272-C
; CURRENT APPLICATION NUMBER: US/10/008,978
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/927,777
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/820,279
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/760,500
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/176,409
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/192,699
; PRIOR FILING DATE: 2000-03-28

; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/213,906
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/224,631
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/254,392
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/254,418
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/255,235
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: 60/255,236
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: 60/282,640
; PRIOR FILING DATE: 2000-04-01
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-10-008-978-55

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 152
US-10-008-978-70
; Sequence 70, Application US/10008978
; Publication No. US20030087242A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; APPLICANT: Garimella, Viswanadham
; APPLICANT: Li, Zhi
; APPLICANT: Park, So-Jung
; APPLICANT: Lu, Gang
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-1272-C
; CURRENT APPLICATION NUMBER: US/10/008,978
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/927,777
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/820,279
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/760,500
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/176,409
; PRIOR FILING DATE: 2000-03-28

```
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/192,699
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/213,906
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/224,631
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/254,392
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/254,418
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/255,235
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: 60/255,236
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: 60/282,640
; PRIOR FILING DATE: 2000-04-01
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-10-008-978-70
```

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
      |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
```

```
RESULT 153
US-10-188-404-66/c
; Sequence 66, Application US/10188404
; Publication No. US20030105286A1
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; APPLICANT: Coull, James M.
; APPLICANT: Kiely, John
; APPLICANT: Griffith, Michael
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS5042
; CURRENT APPLICATION NUMBER: US/10/188,404
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/275,951
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/765,798
; PRIOR FILING DATE: 1997-04-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(11)
; OTHER INFORMATION: Amino Hexanoic Acid, Amino Ethyl Glycine,
; OTHER INFORMATION: Acetyl, Amino Hexanoic Acid Linkage
```

US-10-188-404-66

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
      |||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
```

RESULT 154

```
US-10-234-764-10/c
; Sequence 10, Application US/10234764
; Publication No. US20030113769A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Lonnberg, Harri
; APPLICANT: Salo, Harri
; APPLICANT: Virta, Pasi
; TITLE OF INVENTION: Aminoxy Functionalized Oligomers
; FILE REFERENCE: ISIS5089
; CURRENT APPLICATION NUMBER: US/10/234,764
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 09/344,260
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; OTHER INFORMATION: Synthetic construct
US-10-234-764-10
```

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
      |||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
```

RESULT 155

```
US-10-008-789-4
; Sequence 4, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-008-789-4
```

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1001 GCTGCGGAGAGATGTGGTT 1020
      |||||
```

```
Db      1  GCTGCGGAGAGATGTGGTT 20

RESULT 156
US-10-008-789-12/c
; Sequence 12, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-12

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      46  GCCAGAAAAAGTTTCTTTT 65
      |||||
Db      20  GCCAGAAAAAGTTTCTTTT 1

RESULT 157
US-10-008-789-13/c
; Sequence 13, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-13

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      124  TTCAAGACCGCTGTCTGGAG 143
      |||||
Db      20  TTCAAGACCGCTGTCTGGAG 1

RESULT 158
US-10-008-789-14/c
; Sequence 14, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
```

```
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-14

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      152  TCCAGGCCATGTCGGGGCCC 171
      |||||
Db      20  TCCAGGCCATGTCGGGGCCC 1

RESULT 159
US-10-008-789-15/c
; Sequence 15, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-15

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      259  CACGAGCAGCACTCCAGCC 278
      |||||
Db      20  CACGAGCAGCACTCCAGCC 1

RESULT 160
US-10-008-789-16/c
; Sequence 16, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-16

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      365  TGGGTCCCATGGAGTACTC 384
      |||||
Db      20  TGGGTCCCATGGAGTACTC 1
```

```
RESULT 161
US-10-008-789-17/c
; Sequence 17, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-17

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 ACTCCAGCACACGCGGGC 400
Db 20 ACTCCAGCACACGCGGGC 1

RESULT 162
US-10-008-789-18/c
; Sequence 18, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-18

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 GCACAGCAGCGGGCTCCCTG 406
Db 20 GCACAGCAGCGGGCTCCCTG 1

RESULT 163
US-10-008-789-19/c
; Sequence 19, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 19
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-19

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 GGCCTTCGCCCTGGAAGCCT 437
Db 20 GGCCTTCGCCCTGGAAGCCT 1

RESULT 164
US-10-008-789-20/c
; Sequence 20, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-20

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 443 CCGAGATAGACTTGCTGAGC 462
Db 20 CCGAGATAGACTTGCTGAGC 1

RESULT 165
US-10-008-789-21/c
; Sequence 21, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-21

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 457 CTGAGCACCACGCTGGCCAA 476
Db 20 CTGAGCACCACGCTGGCCAA 1
```



```
RESULT 166
US-10-008-789-22/c
; Sequence 22, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-22
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      552 CCGCACGGGCTCCCTGAAGC 571
Db      20 CCGCACGGGCTCCCTGAAGC 1

RESULT 167
US-10-008-789-23/c
; Sequence 23, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-23
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      568 AAGCCAAATCCAGCTCGCC 587
Db      20 AAGCCAAATCCAGCTCGCC 1

RESULT 168
US-10-008-789-24/c
; Sequence 24, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 24
; LENGTH: 20
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-24
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      714 GCGGGAGCCTCTCAGGCTT 733
Db      20 GCGGGAGCCTCTCAGGCTT 1

RESULT 169
US-10-008-789-25/c
; Sequence 25, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-25
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      720 AGCCTCTCAGGCTTCTGGGC 739
Db      20 AGCCTCTCAGGCTTCTGGGC 1

RESULT 170
US-10-008-789-26/c
; Sequence 26, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-26
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      788 GGCCTGGCTATAGGACCCAG 807
Db      20 GGCCTGGCTATAGGACCCAG 1
```

```
RESULT 171
US-10-008-789-27/c
; Sequence 27, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-27
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      797 ATAGGAGCCAGAGAGGCCA 816
      |||||
Db      20 ATAGGAGCCAGAGAGGCCA 1

RESULT 172
US-10-008-789-28/c
; Sequence 28, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-28
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      830 AAGAGGAAGCTGCTGGGTC 849
      |||||
Db      20 AAGAGGAAGCTGCTGGGTC 1

RESULT 173
US-10-008-789-29/c
; Sequence 29, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-29
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      899 CCCTGAGCCAGCCTCCAGAG 918
      |||||
Db      20 CCCTGAGCCAGCCTCCAGAG 1

RESULT 174
US-10-008-789-30/c
; Sequence 30, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-30
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      973 AGCGGGGAGTACTTTGGCCA 992
      |||||
Db      20 AGCGGGGAGTACTTTGGCCA 1

RESULT 175
US-10-008-789-31/c
; Sequence 31, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-31
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      985 TTGGCCAGTGTGGTGGCTG 1004
      |||||
Db      20 TTGGCCAGTGTGGTGGCTG 1

RESULT 176
```

```
US-10-008-789-32/c
; Sequence 32, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-32
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1030 GCTGGGTTGTGGCCCTTGA 1049
Db 20 GCTGGGTTGTGGCCCTTGA 1
RESULT 177
US-10-008-789-33/c
; Sequence 33, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-33
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1054 GTCCTTCACGTGGCTGCTT 1073
Db 20 GTCCTTCACGTGGCTGCTT 1
RESULT 178
US-10-008-789-34/c
; Sequence 34, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-34
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1063 GTGGGCTGCTTTGTATGTTTC 1082
Db 20 GTGGGCTGCTTTGTATGTTTC 1
RESULT 179
US-10-008-789-35/c
; Sequence 35, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-35
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1073 TTGTATGTTCTACATGCCGG 1092
Db 20 TTGTATGTTCTACATGCCGG 1
RESULT 180
US-10-008-789-36/c
; Sequence 36, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-36
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1091 GGGCCAGCTTCGGCCAG 1110
Db 20 GGGCCAGCTTCGGCCAG 1
RESULT 181
US-10-008-789-37/c
```

```
; Sequence 37, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-37

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1103 GCGGCCAGCATTTCTACGCC 1122
      |||||
Db 20 GCGGCCAGCATTTCTACGCC 1

RESULT 182
US-10-008-789-38/c
; Sequence 38, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-38

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 GCTACGTGGCCACCTGGAG 1170
      |||||
Db 20 GCTACGTGGCCACCTGGAG 1

RESULT 183
US-10-008-789-39/c
; Sequence 39, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-39

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1156 GTGGCCACCCTGGAGAAATG 1175
      |||||
Db 20 GTGGCCACCCTGGAGAAATG 1

RESULT 184
US-10-008-789-40/c
; Sequence 40, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-40

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1164 CCTGGAGAAATGTGCCACGT 1183
      |||||
Db 20 CCTGGAGAAATGTGCCACGT 1

RESULT 185
US-10-008-789-41/c
; Sequence 41, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-41

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 AGCCCATCCTGGACCGGATC 1209
      |||||
Db 20 AGCCCATCCTGGACCGGATC 1

RESULT 186
US-10-008-789-42/c
; Sequence 42, Application US/10008789
```

Publication No. US20030125276A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
FILE REFERENCE: RTS-0333
CURRENT APPLICATION NUMBER: US/10/008,789
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 42
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-42

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1201 GACCGGATCCTGCGGGCTAT 1220
Db 20 GACCGGATCCTGCGGGCTAT 1

RESULT 187
US-10-008-789-43/c
Sequence 43, Application US/10008789
Publication No. US20030125276A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
FILE REFERENCE: RTS-0333
CURRENT APPLICATION NUMBER: US/10/008,789
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 43
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-43

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1247 TCACCTGCGTGGTGTGTCTAC 1266
Db 20 TCACCTGCGTGGTGTGTCTAC 1

RESULT 188
US-10-008-789-44/c
Sequence 44, Application US/10008789
Publication No. US20030125276A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
FILE REFERENCE: RTS-0333
CURRENT APPLICATION NUMBER: US/10/008,789
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 44
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide

US-10-008-789-44

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1255 GTGGTGTGTACCCGCGCCT 1274
Db 20 GTGGTGTGTACCCGCGCCT 1

RESULT 189
US-10-008-789-45/c
Sequence 45, Application US/10008789
Publication No. US20030125276A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
FILE REFERENCE: RTS-0333
CURRENT APPLICATION NUMBER: US/10/008,789
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 45
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-45

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1292 CAGTGGATGCTACGAGCCAG 1311
Db 20 CAGTGGATGCTACGAGCCAG 1

RESULT 190
US-10-008-789-46/c
Sequence 46, Application US/10008789
Publication No. US20030125276A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
FILE REFERENCE: RTS-0333
CURRENT APPLICATION NUMBER: US/10/008,789
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 46
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-46

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1308 CCAGATCCACTGTATTGAGG 1327
Db 20 CCAGATCCACTGTATTGAGG 1

RESULT 191
US-10-008-789-47/c
Sequence 47, Application US/10008789
Publication No. US20030125276A1

```
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-47

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1320 TATTGAGGACTTTCACAGGA 1339
Db      20 TATTGAGGACTTTCACAGGA 1

RESULT 192
US-10-008-789-48/c
; Sequence 48, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-48

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1328 ACTTTCACAGGAAGTTGCC 1347
Db      20 ACTTTCACAGGAAGTTGCC 1

RESULT 193
US-10-008-789-49/c
; Sequence 49, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-49
```

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1358 CAGTGTGCGGTGGGGCCATA 1377
Db      20 CAGTGTGCGGTGGGGCCATA 1

RESULT 194
US-10-008-789-50/c
; Sequence 50, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-50

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1367 GTGGGGCCATAATGCCTGAG 1386
Db      20 GTGGGGCCATAATGCCTGAG 1

RESULT 195
US-10-008-789-51/c
; Sequence 51, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-51

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1372 GCCATAATGCCTGAGCCAGG 1391
Db      20 GCCATAATGCCTGAGCCAGG 1

RESULT 196
US-10-008-789-52/c
; Sequence 52, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
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```
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-52

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1384 GAGCCAGGTCAGGAGGAGAC 1403
      |||||
Db 20 GAGCCAGGTCAGGAGGAGAC 1

RESULT 197
US-10-008-789-53/c
; Sequence 53, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-53

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1397 AGGAGACTGTGAGAATTGTT 1416
      |||||
Db 20 AGGAGACTGTGAGAATTGTT 1

RESULT 198
US-10-008-789-54/c
; Sequence 54, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-54
```

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1405 GTGAGAATTGTTGCTCTGGA 1424
      |||||
Db 20 GTGAGAATTGTTGCTCTGGA 1

RESULT 199
US-10-008-789-55/c
; Sequence 55, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-55

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AATTGTTGCTCTGGATCGAA 1429
      |||||
Db 20 AATTGTTGCTCTGGATCGAA 1

RESULT 200
US-10-008-789-56/c
; Sequence 56, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-56

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1416 TGCTCTGGATCGAAGTTTC 1435
      |||||
Db 20 TGCTCTGGATCGAAGTTTC 1

RESULT 201
US-10-008-789-57/c
; Sequence 57, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
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; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-57

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1427 GAAGTTTTCACATTGGCTGT 1446
Db 20 GAAGTTTTCACATTGGCTGT 1

RESULT 202
US-10-008-789-58/c
; Sequence 58, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-58

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1469 TGCTGCTCTCCTCTGAGGGC 1488
Db 20 TGCTGCTCTCCTCTGAGGGC 1

RESULT 203
US-10-008-789-59/c
; Sequence 59, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-59

Query Match      1.1%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1497 GGGCTGTACCCGCTGGATG 1516
Db 20 GGGCTGTACCCGCTGGATG 1

RESULT 204
US-10-008-789-60/c
; Sequence 60, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-60

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 CTGCTACCCGCTGGATGGC 1519
Db 20 CTGCTACCCGCTGGATGGC 1

RESULT 205
US-10-008-789-61/c
; Sequence 61, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-61

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 CCGCTGGATGGGCACATCTT 1526
Db 20 CCGCTGGATGGGCACATCTT 1

RESULT 206
US-10-008-789-62/c
; Sequence 62, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
```

```
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-62

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CGCTGGATGGGCACATCTTG 1527
Db 20 CGCTGGATGGGCACATCTTG 1

RESULT 207
US-10-008-789-63/c
; Sequence 63, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-63

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1513 GATGGGCACATCTTGTGCAA 1532
Db 20 GATGGGCACATCTTGTGCAA 1

RESULT 208
US-10-008-789-64/c
; Sequence 64, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-64

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 TCTTGTGCAAGGCCTGCAGC 1542
Db 20 TCTTGTGCAAGGCCTGCAGC 1

RESULT 209
US-10-008-789-65/c
; Sequence 65, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-65

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1543 GCCTGGCGCATCCAGGAGCT 1562
Db 20 GCCTGGCGCATCCAGGAGCT 1

RESULT 210
US-10-008-789-66/c
; Sequence 66, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-66

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1558 GAGCTCTCAGCCACCGTCAC 1577
Db 20 GAGCTCTCAGCCACCGTCAC 1

RESULT 211
US-10-008-789-67/c
; Sequence 67, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
```

; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-67

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 GCCACCGTCACCACTGACTG 1586
Db 20 GCCACCGTCACCACTGACTG 1

RESULT 212

US-10-008-789-68/c
; Sequence 68, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP

; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-68

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1571 CCGTCACCACTGACTGCTGA 1590
Db 20 CCGTCACCACTGACTGCTGA 1

RESULT 213

US-10-008-789-69/c
; Sequence 69, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP

; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-69

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1579 ACTGACTGCTGAGTCTTCCT 1598
Db 20 ACTGACTGCTGAGTCTTCCT 1

RESULT 214

US-10-008-789-70/c
; Sequence 70, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP

; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-70

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1594 TTCCTAGAGTACCTGCTGG 1613
Db 20 TTCCTAGAGTACCTGCTGG 1

RESULT 215

US-10-008-789-71/c
; Sequence 71, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP

; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-71

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1608 TGCTGGGTTCTCAGTTCCAG 1627
Db 20 TGCTGGGTTCTCAGTTCCAG 1

RESULT 216

US-10-008-789-72/c
; Sequence 72, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP

; FILE REFERENCE: RTS-0333

; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 72
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-72

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1623 TCCAGTCCCATCCTTTGAT 1642
Db 20 TCCAGTCCCATCCTTTGAT 1

RESULT 217
US-10-008-789-73/c
; Sequence 73, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-73

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1636 CTTTGATTGATCACTCTCCC 1655
Db 20 CTTTGATTGATCACTCTCCC 1

RESULT 218
US-10-008-789-74/c
; Sequence 74, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 74
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-74

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1664 ACCTGTATGACTTTGTCCAC 1683
Db 20 ACCTGTATGACTTTGTCCAC 1

RESULT 219
US-10-008-789-75/c
; Sequence 75, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-75

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1683 CAAATGCTGTCTTCTTTC 1702
Db 20 CAAATGCTGTCTTCTTTC 1

RESULT 220
US-10-008-789-76/c
; Sequence 76, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-76

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1708 TCAAGAAATAATAATCCCTC 1727
Db 20 TCAAGAAATAATAATCCCTC 1

RESULT 221
US-10-008-789-77/c
; Sequence 77, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789

; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 77
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-77

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1712 GAAATAATAATCCCTCGAGT 1731
Db 20 GAAATAATAATCCCTCGAGT 1

RESULT 222

US-10-008-789-78/c

; Sequence 78, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-78

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 ATCCCTCGAGTTTACAAAAA 1740.
Db 20 ATCCCTCGAGTTTACAAAAA 1

RESULT 223

US-10-255-434-14/c

; Sequence 14, Application US/10255434
; Publication No. US20030129626A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Kirsten V.
; APPLICANT: Hyldig-Nielsen, Jens J.
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly
; TITLE OF INVENTION: Distributed Repeat Sequences In Genomic Nucleic Acid
; FILE REFERENCE: BP0101-US
; CURRENT APPLICATION NUMBER: US/10/255,434
; CURRENT FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic
; OTHER INFORMATION: Oligomer Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe

; OTHER INFORMATION: Sequence
US-10-255-434-14

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 224

US-10-255-434-26

; Sequence 26, Application US/10255434
; Publication No. US20030129626A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Kirsten V.
; APPLICANT: Hyldig-Nielsen, Jens J.
; APPLICANT: Williams, Brett F.
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly
; TITLE OF INVENTION: Distributed Repeat Sequences In Genomic Nucleic Acid
; FILE REFERENCE: BP0101-US
; CURRENT APPLICATION NUMBER: US/10/255,434
; CURRENT FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic
; OTHER INFORMATION: Oligomer Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe
; OTHER INFORMATION: Sequence
US-10-255-434-26

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 225

US-10-278-047-1/c

; Sequence 1, Application US/10278047
; Publication No. US20030143591A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Martin
; APPLICANT: Bruce, Ian
; APPLICANT: Wolter, Andreas
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHODS TO DETECT AND/OR QUANTIFY NUCLEIC
; TITLE OF INVENTION: ACID ANALYTES
; FILE REFERENCE: PRO.07
; CURRENT APPLICATION NUMBER: US/10/278,047
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 60/336,432
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Nucleic Acid Probe
; FEATURE:


```
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
US-10-278-047-1

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 226
US-10-371-066-16/c
; Sequence 16, Application US/10371066
; Publication No. US20030162214A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; MICROELECTRONIC SYSTEMS AND DEVICES FOR
; MOLECULAR BIOLOGICAL ANALYSIS AND
; DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/371,066
; FILING DATE: 21-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,504
; FILING DATE: No. US20030162214A1ember 1, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 203/218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-371-066-16

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 227
US-10-410-324-55
; Sequence 55, Application US/10410324
; Publication No. US20030180783A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storchhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-126
; CURRENT APPLICATION NUMBER: US/10/410,324
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 09/961,949
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-10-410-324-55

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 228
US-10-266-983-55
; Sequence 55, Application US/10266983
; Publication No. US20030207296A1
; GENERAL INFORMATION:
; APPLICANT: Park, So-Jung
; APPLICANT: Taton, Thomas Andrew
; APPLICANT: Mirkin, Chad A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 01-1565-A
; CURRENT APPLICATION NUMBER: US/10/266,983
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: 09/927,777
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/820,279
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/760,500
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
```

```
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/176,409
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/192,699
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-10-266-983-55

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
      |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 229
US-10-266-983-70
; Sequence 70, Application US/10266983
; Publication No. US20030207296A1
; GENERAL INFORMATION:
; APPLICANT: Park, So-Jung
; APPLICANT: Taton, Thomas Andrew
; APPLICANT: Mirkin, Chad A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 01-1565-A
; CURRENT APPLICATION NUMBER: US/10/266,983
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: 09/927,777
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/820,279
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/760,500
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/176,409
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/192,699
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-10-266-983-70
```

Query Match

1.1%; Score 20; DB 1; Length 20;

```
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
      |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 230
US-10-431-341-31
; Sequence 31, Application US/10431341
; Publication No. US20040086897A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad
; APPLICANT: Cao, Yun-Wei
; APPLICANT: Jin, Rongchao
; TITLE OF INVENTION: Nanoparticle Probes with Raman Spectroscopic Fingerprints for Anal
; TITLE OF INVENTION: Detection
; FILE REFERENCE: 02-338-C
; CURRENT APPLICATION NUMBER: US/10/431,341
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/378,538
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/383,630
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US 10/172,428
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: Synthetic target sequence
US-10-431-341-31

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
      |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 231
US-10-653-416-25/c
; Sequence 25, Application US/10653416
; Publication No. US20040110201A1
; GENERAL INFORMATION:
; APPLICANT: RASHTCHIAN, AYOUB
; APPLICANT: SCHUSTER, DAVID M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CDNA SYNTHESIS
; FILE REFERENCE: 38266-0011
; CURRENT APPLICATION NUMBER: US/10/653,416
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: 60/407,248
; PRIOR FILING DATE: 2002-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-653-416-25
```

Query Match

1.1%; Score 20; DB 1; Length 20;

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-178

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 232
US-10-716-829-55
; Sequence 55, Application US/10716829
; Publication No. US20040110220A1
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-715-A
; CURRENT APPLICATION NUMBER: US/10/716,829
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US/09/760,500A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
US-10-716-829-55

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 233
US-10-671-395-178/c
; Sequence 178, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-178

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 234
US-10-671-395-179/c
; Sequence 179, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-179

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 235
US-10-671-395-180/c
; Sequence 180, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
```

US-10-671-395-180

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 236

US-10-671-395-181/c
; Sequence 181, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 181
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-181

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 237

US-10-671-395-182/c
; Sequence 182, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 182
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-182

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 238

US-10-671-395-183/c
; Sequence 183, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 183
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-183

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 239

US-10-671-395-184/c
; Sequence 184, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 184
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-184

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 240

US-10-671-395-185/c
; Sequence 185, Application US/10671395

```
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 185
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-185

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 241
US-10-671-395-186/c
; Sequence 186, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 186
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-186

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 242
US-10-671-395-187/c
; Sequence 187, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
```

```
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 187
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-187

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 243
US-10-671-395-188/c
; Sequence 188, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 188
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-188

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 244
US-10-671-395-189/c
; Sequence 189, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 189
```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-189

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 245

US-10-671-395-190/c
; Sequence 190, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:

; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 190
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-190

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 246

US-10-671-395-191/c
; Sequence 191, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:

; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 191
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-191

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 247

US-10-671-395-192/c
; Sequence 192, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:

; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-192

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 248

US-10-671-395-193/c
; Sequence 193, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:

; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-193

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1


```

RESULT 249
US-10-671-395-194/c
; Sequence 194, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 194
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-194

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 250
US-10-671-395-195/c
; Sequence 195, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-195

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 251
US-10-671-395-196/c
; Sequence 196, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:

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; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 196
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2-antisense
US-10-671-395-196

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 252
US-10-671-395-197/c
; Sequence 197, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-197

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 253
US-10-671-395-198/c
; Sequence 198, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25

```

; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-198

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 254

US-10-671-395-199/c
; Sequence 199, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 199
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-199

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 255

US-10-671-395-200/c
; Sequence 200, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 20
; TYPE: DNA

; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-200

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 256

US-10-671-395-201/c
; Sequence 201, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 201
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-201

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 257

US-10-671-395-202/c
; Sequence 202, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 202
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-202

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 258
US-10-671-395-203/c
; Sequence 203, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 203
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-203

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 259
US-10-671-395-204/c
; Sequence 204, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 204
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-204

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 260
US-10-671-395-205/c
; Sequence 205, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 205
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-205

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 261
US-10-671-395-206/c
; Sequence 206, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-206

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 262
US-10-671-395-207/c
; Sequence 207, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K

```
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-207

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 263
US-10-671-395-208/c
; Sequence 208, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 208
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-208

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 264
US-10-671-395-262/c
; Sequence 262, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
```

```
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 262
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-262

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 265
US-10-671-395-274/c
; Sequence 274, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-274

Query Match          1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 266
US-10-671-395-275/c
; Sequence 275, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 275
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
```

; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-275

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 267

US-10-671-395-276/c
; Sequence 276, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 276
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense

US-10-671-395-276
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 268

US-10-671-395-277/c
; Sequence 277, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 277
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense

US-10-671-395-277
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 269

US-10-671-395-311/c
; Sequence 311, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 311
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense

US-10-671-395-311
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 270

US-10-671-395-338/c
; Sequence 338, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 338
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense

US-10-671-395-338
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 271

US-10-671-395-376/c

```
; Sequence 376, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 376
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-376

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 272
US-10-671-395-403/c
; Sequence 403, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 403
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-403

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 273
US-10-671-395-427/c
; Sequence 427, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
```

```
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 427
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-427

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 274
US-10-671-395-433/c
; Sequence 433, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 433
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-433

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
Db 20 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 275
US-10-671-395-444/c
; Sequence 444, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
```



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; SEQ ID NO 444
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-444

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 276
US-10-671-395-487/c
; Sequence 487, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: EXPRESSION
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 487
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-487

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 277
US-10-671-395-575/c
; Sequence 575, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: EXPRESSION
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 575
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-575
```

```
; Query Match      1.1%; Score 20; DB 1; Length 20;
; Best Local Similarity 100.0%; Pred. No. 89;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 278
US-09-888-326-840/c
; Sequence 840, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 840
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-840

Query Match      1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 279
US-09-912-014-2
; Sequence 2, Application US/09912014
; Publication No. US2003005929A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; MICROELECTRONIC SYSTEMS AND DEVICES FOR
; MOLECULAR BIOLOGICAL ANALYSIS AND
; DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/912,014
; FILING DATE: 24-Jul-2001
; CLASSIFICATION: <Unknown>
```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/146,504
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 203/218
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-912-014-2

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 280

US-09-997-672-41/c
; Sequence 41, Application US/09997672
; Publication No. US20030061632A1
; GENERAL INFORMATION:
; APPLICANT: Weterings, Koen
; APPLICANT: Apuya, Nestor R.
; APPLICANT: Tatarinova, Tatiana
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; APPLICANT: Ceres, Inc.
; TITLE OF INVENTION: Polynucleotides Useful for Modulating Transcription
; FILE REFERENCE: 023070-115810US
; CURRENT APPLICATION NUMBER: US/09/997,672
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,672
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:dt-20dn
; NAME/KEY: modified_base
; LOCATION: (21)
; OTHER INFORMATION: n = G, C, A or T
US-09-997-672-41

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 281

US-09-776-479-912/c
; Sequence 912, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:

;; APPLICANT: Bratzler, Robert L.
;; APPLICANT: Petersen, Deanna M.
;; APPLICANT: Fouron, Yves
;; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;; TITLE OF INVENTION: Treatment of Asthma and Allergy
;; FILE REFERENCE: C1037/7013 (HCL/MAT)
;; CURRENT APPLICATION NUMBER: US/09/776,479
;; CURRENT FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: US 60/179,991
;; PRIOR FILING DATE: 2000-02-03
;; NUMBER OF SEQ ID NOS: 1093
;; SOFTWARE: FastSEQ for Windows Version 3.0
;; SEQ ID NO 912
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-912

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 282

US-09-776-479-912/c
; Sequence 912, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 912
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-912

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 283

US-10-144-179A-41/c
; Sequence 41, Application US/10144179A
; Publication No. US20030211483A1
; GENERAL INFORMATION:
; APPLICANT: Schroeder, Benjamin
; APPLICANT: Chen, Caifu
; APPLICANT: Schroth, Gary
; TITLE OF INVENTION: Methods for the Enrichment of
; TITLE OF INVENTION: Low-Abundance Polynucleotides

```
; FILE REFERENCE: ABIOS.005A
; CURRENT APPLICATION NUMBER: US/10/144,179A
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligo-dT primer
US-10-144-179A-41

Query Match          1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 284
US-10-314-578-912/c
; Sequence 912, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 912
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-912

Query Match          1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 285
US-10-096-221-4
; Sequence 4, Application US/10096221
; Publication No. US20020164628A1
; GENERAL INFORMATION:
; APPLICANT: Kurn, Nurith
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; FILE REFERENCE: 49269200700
; CURRENT APPLICATION NUMBER: US/10/096,221
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US 60/274,236
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 4

; FILE REFERENCE: ABIOS.005A
; CURRENT APPLICATION NUMBER: US/10/144,179A
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: n = A,T,C or G
US-10-096-221-4

Query Match          1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 2 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 286
US-10-112-653-881/c
; Sequence 881, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 881
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-881

Query Match          1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    |||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 287
US-10-017-995-912/c
; Sequence 912, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 912
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
```


Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 291

US-10-410-031-188/c

; Sequence 188, Application US/10410031

; Publication No. US20040010817A1

; GENERAL INFORMATION:

; APPLICANT: Shocke, Jay M.

; APPLICANT: Schnurr, Judy

; APPLICANT: Browse, John A.

; TITLE OF INVENTION: Plant Acyl-CoA Synthetases

; FILE REFERENCE: DOW-07654

; CURRENT APPLICATION NUMBER: US/10/410,031

; CURRENT FILING DATE: 2003-04-09

; NUMBER OF SEQ ID NOS: 191

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 188

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-410-031-188

Query Match 1.1%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 292

US-10-410-031-189/c

; Sequence 189, Application US/10410031

; Publication No. US20040010817A1

; GENERAL INFORMATION:

; APPLICANT: Shocke, Jay M.

; APPLICANT: Schnurr, Judy

; APPLICANT: Browse, John A.

; TITLE OF INVENTION: Plant Acyl-CoA Synthetases

; FILE REFERENCE: DOW-07654

; CURRENT APPLICATION NUMBER: US/10/410,031

; CURRENT FILING DATE: 2003-04-09

; NUMBER OF SEQ ID NOS: 191

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 189

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-410-031-189

Query Match 1.1%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 293

US-10-435-489-41/c

; Sequence 41, Application US/10435489

; Publication No. US20040014105A1

; GENERAL INFORMATION:

; APPLICANT: Schroeder, Benjamin

; APPLICANT: Chen, Caifu

; APPLICANT: Schroth, Gary

; TITLE OF INVENTION: Methods for the Enrichment of

; TITLE OF INVENTION: Low-Abundance Polynucleotides

; FILE REFERENCE: ABIOS.005CP1

; CURRENT APPLICATION NUMBER: US/10/435,489

; CURRENT FILING DATE: 2003-05-09

; PRIOR APPLICATION NUMBER: 10/144,179

; PRIOR FILING DATE: 2002-05-09

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 41

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: oligo-dt primer

US-10-435-489-41

Query Match 1.1%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 294

US-10-278-760-2/c

; Sequence 2, Application US/10278760

; Publication No. US20040081962A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Caifu

; APPLICANT: Schroeder, Ben

; APPLICANT: Brandis, John

; APPLICANT: Schroth, Gary

; APPLICANT: Applied Biosystems

; TITLE OF INVENTION: Methods for Synthesizing Complementary DNA

; FILE REFERENCE: 1560.012US1

; CURRENT APPLICATION NUMBER: US/10/278,760

; CURRENT FILING DATE: 2002-10-23

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: A control primer.

US-10-278-760-2

Query Match 1.1%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 295

US-10-401-520-118

; Sequence 118, Application US/10401520

; Publication No. US20040009506A1

; GENERAL INFORMATION:

; APPLICANT: Stephen, Jean-Philippe F.

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wong, Wai Lee Tan

; APPLICANT: Billeci, Todd

; TITLE OF INVENTION: Methods and Compositions for Detection and

; TITLE OF INVENTION: Quantitation of Nucleic Acid Analytes

; FILE REFERENCE: P1806R1US

; CURRENT APPLICATION NUMBER: US/10/401,520

; CURRENT FILING DATE: 2003-03-28

Elizabeth H. Blackburn
Nam Woo Kim
Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,927A
FILING DATE: 29-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-232-927A-32
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGGCTGGGGTTGTGG 1042
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24
RESULT 299
US-10-232-927A-34
Sequence 34, Application US/10232927A
Publication No. US20030190638A1
GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF

CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,927A
FILING DATE: 29-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-232-927A-34
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGGCTGGGGTTGTGG 1042
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24
RESULT 300
US-10-118-854-29
Sequence 29, Application US/10118854
Publication No. US20030194754A1
GENERAL INFORMATION:
APPLICANT: Bates, Paula J
APPLICANT: Miller, Donald M
APPLICANT: Trent, John O
APPLICANT: Xu, Xiaohua
TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF MALIGNANT
DISEASES
FILE REFERENCE: 9799910-
CURRENT APPLICATION NUMBER: US/10/118,854
CURRENT FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.2
SEQ ID NO 29
LENGTH: 24
TYPE: DNA
ORGANISM: artificial sequence

```
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-118-854-29

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1019 TTGGGATGGGGCTGGGTTGTGG 1042
          ||||| ||||| ||||| ||||| ||
Db       1 TTGGGTTGGGTTGGGTTGGG 24

RESULT 301
US-10-607-455-29
; Sequence 29, Application US/10607455
; Publication No. US20040132049A1
; GENERAL INFORMATION:
; APPLICANT: Bates, Paula J
; APPLICANT: Mi, Yingchang
; TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF MALIGNANT
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 0979910-0034
; CURRENT APPLICATION NUMBER: US/10/607,455
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 60/392,143
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 24
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-607-455-29

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1019 TTGGGATGGGGCTGGGTTGTGG 1042
          ||||| ||||| ||||| ||||| ||
Db       1 TTGGGTTGGGTTGGGTTGGG 24

RESULT 302
US-09-917-138-1/c
; Sequence 1, Application US/09917138
; Patent No. US20020031776A1
; GENERAL INFORMATION:
; APPLICANT: TULLIS, Richard
; APPLICANT: STEIFFEL, Jerome
; TITLE OF INVENTION: ENZYMATIC LABELING AND DETECTION OF DNA
; TITLE OF INVENTION: HYBRIDIZATION PROBES
; FILE REFERENCE: 24730-2207B
; CURRENT APPLICATION NUMBER: US/09/917,138
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/580,358
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/136,545
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotinylation at the 5' end

; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Combined DNA/RNA
US-09-917-138-1

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1754
          ||||| ||||| ||||| ||||| ||
Db       19 AAAAAAAAAAAAAAAAAA 1

RESULT 303
US-09-901-484A-515/c
; Sequence 515, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T11XC3D2
; CURRENT APPLICATION NUMBER: US/09/901,484A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 515
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: potential microsequencing oligo for 4-4-187.mis2
US-09-901-484A-515

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1754
          ||||| ||||| ||||| ||||| ||
Db       19 AAAAAAAAAAAAAAAAAA 1

RESULT 304
US-09-853-526-515/c
; Sequence 515, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CP1CP
; CURRENT APPLICATION NUMBER: US/09/853,526
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/338,907
; PRIOR FILING DATE: 1999-06-23
```



```

; Publication No. US20020182687A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
;
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
;
; FILE REFERENCE: 50036/031002
;
; CURRENT APPLICATION NUMBER: US/10/208,357
;
; CURRENT FILING DATE: 2002-07-30
;
; PRIOR APPLICATION NUMBER: US/09/619,103
;
; PRIOR FILING DATE: 2000-07-19
;
; PRIOR APPLICATION NUMBER: 60/145,834
;
; PRIOR FILING DATE: 1999-07-27
;
; NUMBER OF SEQ ID NOS: 26
;
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 25
;
; LENGTH: 19
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-25

```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 1 AAAAAAAAAAAAAAAAAA 19

```

RESULT 309
US-10-123-597-1/c
; Sequence 1, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-aminoxyethoxy
US-10-123-597-1

```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 310
US-10-123-597-2/c
; Sequence 2, Application US/10123597

```

; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
; US-10-123-597-2

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

```

RESULT 311
US-10-123-597-3/c
; Sequence 3, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-methoxyethoxy
US-10-123-597-3

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

```
RESULT 312
US-10-123-597-4/c
; Sequence 4, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-10-123-597-4
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 313
US-10-123-597-5/c
; Sequence 5, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
US-10-123-597-5
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
```

```
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 314
US-10-123-597-6/c
; Sequence 6, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-O-propyl
US-10-123-597-6
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 315
US-10-123-597-7/c
; Sequence 7, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-10-123-597-7
Query Match          1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
          |||||
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1
          |||||

RESULT 316
US-10-123-597-8/c
; Sequence 8, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc.feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: 5-methyl-2'-methoxyethoxy
US-10-123-597-8

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
          |||||
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1
          |||||

RESULT 317
US-10-123-597-12/c
; Sequence 12, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc.feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-10-123-597-12
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
          |||||
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1
          |||||

RESULT 318
US-10-123-597-14/c
; Sequence 14, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc.feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-10-123-597-14
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1754
          |||||
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1
          |||||

RESULT 319
US-10-123-597-15/c
; Sequence 15, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc.feature
; LOCATION: (16)..(19)
```



```
; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-10-123-597-15

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 320
US-10-123-597-25/c
; Sequence 25, Application US/10123597
; Publication No. US20030078415A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Kawasaki, Andrew M
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Prakash, Thazha P
; APPLICANT: Fraser, Allister S
; TITLE OF INVENTION: Regioselective Synthesis of 2'-O-Modified Nucleosides
; FILE REFERENCE: ISIS5040
; CURRENT APPLICATION NUMBER: US/10/123,597
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/227,782
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic construct
; NAME/KEY: misc feature
; LOCATION: (15)..(18)
; OTHER INFORMATION: 2'-methyleneiminoxyethoxy
US-10-123-597-25

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 321
US-10-100-321-24
; Sequence 24, Application US/10100321
; Publication No. US20030087251A1
; GENERAL INFORMATION:
; APPLICANT: Kurn, Nurith
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES
; FILE REFERENCE: 492692000500
; CURRENT APPLICATION NUMBER: US/10/100,321
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/274,550
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-100-321-24
```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 322
US-10-232-881-1/c
; Sequence 1, Application US/10232881
; Publication No. US2003008088A1
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Capaldi, Daniel
; APPLICANT: Krotz, Achim
; APPLICANT: Cole, Douglas
; APPLICANT: Guzaev, Andrei
; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric
; TITLE OF INVENTION: Compounds
; FILE REFERENCE: ISIS3380
; CURRENT APPLICATION NUMBER: US/10/232,881
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/288,679
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/118,564
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. US2003008088A1el Sequence
US-10-232-881-1

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 323
US-10-247-893-3/c
; Sequence 3, Application US/10247893
; Publication No. US20030092046A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Philip Dan
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Guanidinium Functionalized Oligomers And Methods
; FILE REFERENCE: Isis-4406
; CURRENT APPLICATION NUMBER: US/10/247,893
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/612,531
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/349,040
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: T*=2'-O-[2-(guanidinium)ethyl]
US-10-247-893-3

Query Match      1.1%  Score 19;  DB 1;  Length 19;
Best Local Similarity 100.0%;  Pred. No. 1.2e+02;
Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
    |||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 324
US-10-247-893-7/c
; Sequence 7, Application US/10247893
; Publication No. US20030092046A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Philip Dan
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Guanidinium Functionalized Oligomers And Methods
; FILE REFERENCE: Isis-4406
; CURRENT APPLICATION NUMBER: US/10/247,893
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/612,531
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/349,040
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: T*=2'-O-[2-(guanidinium)ethyl]
US-10-247-893-7

Query Match      1.1%  Score 19;  DB 1;  Length 19;
Best Local Similarity 100.0%;  Pred. No. 1.2e+02;
Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
    |||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 325
US-10-247-893-13/c
; Sequence 13, Application US/10247893
; Publication No. US20030092046A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Philip Dan
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Guanidinium Functionalized Oligomers And Methods
; FILE REFERENCE: Isis-4406
; CURRENT APPLICATION NUMBER: US/10/247,893
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/612,531
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/349,040
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(17)
; OTHER INFORMATION: 3' - O-MOE linkage
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 3' - O-MOE linkage
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 3' - O-MOE linkage
US-10-098-816-15

Query Match      1.1%  Score 19;  DB 1;  Length 19;
Best Local Similarity 100.0%;  Pred. No. 1.2e+02;
Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
    |||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 326
US-10-098-816-15/c
; Sequence 15, Application US/10098816
; Publication No. US20030105311A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Oligonucleotides Having A DNA Form And B-DNA Form
; FILE REFERENCE: ISIS3310
; CURRENT APPLICATION NUMBER: US/10/098,816
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/303,586
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Oligonucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(17)
; OTHER INFORMATION: 3' - O-MOE linkage
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 3' - O-MOE linkage
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 3' - O-MOE linkage
US-10-098-816-15

Query Match      1.1%  Score 19;  DB 1;  Length 19;
Best Local Similarity 100.0%;  Pred. No. 1.2e+02;
Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
    |||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 327
```


Matches	19;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy 1736 AAAAAAAAAAAAAAAAAA 1754
| | | | | | | | | | | | | | | | | |
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 330

```

US-10-098-816-26/c
; Sequence 26, Application US/10098816
; Publication No. US20030105311A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Mohan, Venkatraman
; TITLE OF INVENTION: Oligonucleotides Having A DNA Form And B-DNA Form
; TITLE OF INVENTION: Confirmation Geometry
; FILE REFERENCE: ISIS3310
; CURRENT APPLICATION NUMBER: US/10/098,816
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/303,586
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 19

```

Query Match . 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
D'b 19 AAAAAAAAAAAAAAAAAA 1

RESULT 331

```

US-10-322-242-1/c
; Sequence 1, Application US/10322242
; Publication No. US20030139586A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Martin
; APPLICANT: An, Haoyun
; TITLE OF INVENTION: C3'-Methylene Hydrogen
; FILE REFERENCE: ISIS-3312
; CURRENT APPLICATION NUMBER: US/10/322,242
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/349,033
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 12

```

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Sequence
US-10-322-242-1

```

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 332

```

US-10-371-600-14
; Sequence 14, Application US/10371600
; Publication No. US20030180776A1
; GENERAL INFORMATION:
; APPLICANT: WU, MING
; APPLICANT: ULLMAN, EDWIN F.
; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION
; FILE REFERENCE: 3817.10-2
; CURRENT APPLICATION NUMBER: US/10/371,600
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/359,223
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/379,360
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-371-600-14

```

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Dbb 1 AAAAAAAAAAAAAAAAAA 19

RESULT 333

US-10-170-172-16/c
; Sequence 16, Application US/10170172
; Publication No. US20030190632A1
; GENERAL INFORMATION:
; APPLICANT: SOSNOWSKI, RONALD G
; APPLICANT: BUTLER, WILLIAM F
; APPLICANT: TU, EUGENE
; APPLICANT: NERENBERG, MICHAEL I
; APPLICANT: HELLER, MICHAEL J
; APPLICANT: EDMAN, CARL F
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING MICROELECTRONIC
; TITLE OF INVENTION: INTEGRATED SYSTEMS, COMPONENT DEVICES, MECHANISMS
; TITLE OF INVENTION: METHODS, AND PROCEDURES FOR MOLECULAR BIOLOGICAL
; TITLE OF INVENTION: ANALYSIS AND DIAGNOSTICS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 227/194
; CURRENT APPLICATION NUMBER: US/10/170,172
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US/08/986,065
; PRIOR FILING DATE: 1997-12-05

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 338
US-10-359-328-26/c
; Sequence 26, Application US/10359328
; Publication No. US2004000938A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; TITLE OF INVENTION: METHODS OF ENHANCING RENAL UPTAKE OF OLIGONUCLEOTIDES
; FILE REFERENCE: ISIS-5140
; CURRENT APPLICATION NUMBER: US/10/359,328
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 09/370,625
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 09/130,566
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(19)
; OTHER INFORMATION: 2'-O-(2-(2-N,N-dimethylaminoethyl)oxyethyl)-5-methyl uridine
; OTHER INFORMATION: sub-T)
US-10-359-328-26

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 339
US-10-387-346B-154/c
; Sequence 154, Application US/10387346B
; Publication No. US20040117869A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Cloning of Cytochrome P450 Genes from
; FILE REFERENCE: 78623
; CURRENT APPLICATION NUMBER: US/10/387,346B
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 10/293,252
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/340,861
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/363,684
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/347,444
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/337,684
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 154
; LENGTH: 19

TYPE: DNA
ORGANISM: Nicotiana
US-10-387-346B-154

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 340
US-09-005-243-32/c
; Sequence 32, Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,243
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/34465
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear


```

; MOLECULE TYPE: DNA
US-09-005-243-32

Query Match      1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 341
US-09-224-683-32/c
; Sequence 32, Application US/09224683
; Patent No. US20020031491A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor: Composition Claims
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,683
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
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```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-224-683-32

Query Match      1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 342
US-09-916-369A-3
; Sequence 3, Application US/09916369A
; Publication No. US20020058802A1
; GENERAL INFORMATION:
; APPLICANT: Dellinger, Douglas J
; APPLICANT: Perbost, Michael GM
; APPLICANT: Caruthers, Marvin H
; APPLICANT: Betley, Jason R
; TITLE OF INVENTION: Synthesis of Polynucleotides Using Combined Oxidation/Deprotector
; FILE REFERENCE: 10003869-1
; CURRENT APPLICATION NUMBER: US/09/916,369A
; CURRENT FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: US 09/627,249
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-09-916-369A-3

Query Match      1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 2 AAAAAAAAAAAAAAAAAA 20

RESULT 343
US-10-671-395-654/c
; Sequence 654, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 654
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-654
```

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1753
Db 19 CAAAAA...AAAAA 1

RESULT 344
US-10-182-434-1/c
; Sequence 1, Application US/10182434
; Publication No. US20030190633A1
; GENERAL INFORMATION:
; APPLICANT: TANGA, Michifumi
; APPLICANT: OKAMURA, Hiroshi
; APPLICANT: TAKAGI, Kenichi
; APPLICANT: TAKAHASHI, Kojiro
; TITLE OF INVENTION: SUPPORT FOR FIXING NUCLEOTIDE AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: TANGAS
; CURRENT APPLICATION NUMBER: US/10/182,434
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: JP 2000-019301
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-182-434-1

Query Match 1.1%; Score 19; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1753
Db 24 CAAAAA...AAAAA 6

RESULT 345
US-09-754-853A-686
; Sequence 686, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 686
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 318013_region_A3_151839_17_Reverse_Primer_Seq
US-09-754-853A-686

Query Match 1.1%; Score 19; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 CAGGAAGAGGAGAGGAGG 878
Db 1 CAGGAAGAGGAGAGGAGG 19

RESULT 346
US-10-396-551-15/c
; Sequence 15, Application US/10396551
; Publication No. US20040053816A1
; GENERAL INFORMATION:
; APPLICANT: BHATTACHARYA, Samir
; APPLICANT: ROY, Sib Sankar
; APPLICANT: DASGUPTA, Subrata
; APPLICANT: MUKHERJEE, Mohua
; TITLE OF INVENTION: AN ADIPOCYTE INSULIN ADPINSL WITH INSULIN A AND B CHAINS AND AN
; TITLE OF INVENTION: EFFECTIVE METHOD OF TREATING TYPE 2 DIABETES IN A SUBJECT USING
; TITLE OF INVENTION: ADIPOCYTE INSULIN
; FILE REFERENCE: 112402
; CURRENT APPLICATION NUMBER: US/10/396,551
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US 60/367,212
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligo (dT) primer
US-10-396-551-15

Query Match 1.1%; Score 19; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA...AAAAA 1754
Db 25 AAAAAA...AAAAA 7

RESULT 347
US-10-309-775A-20/c
; Sequence 20, Application US/10309775A
; Publication No. US20040006032A1
; GENERAL INFORMATION:
; APPLICANT: LOPEZ, Ricardo A.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 2901/OM327
; CURRENT APPLICATION NUMBER: US/10/309,775A
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: CA 2,388,049
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-309-775A-20

Query Match 1.1%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 AAAAAA...AAAAA 1755
Db 24 AAAAAA...AAAAA 3

RESULT 348

US-10-309-775A-27/c
; Sequence 27, Application US/10309775A
; Publication No. US20040006032A1
; GENERAL INFORMATION:
; APPLICANT: LOPEZ, Ricardo A.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 2901/OM327
; CURRENT APPLICATION NUMBER: US/10/309,775A
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: CA 2,388,049
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-309-775A-27

Query Match 1.1%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
||||| |||||||||
Db 22 ACAAAATGAAAAAAAAAAAAAAAA 1

RESULT 349
US-10-309-775A-28/c
; Sequence 28, Application US/10309775A
; Publication No. US20040006032A1
; GENERAL INFORMATION:
; APPLICANT: LOPEZ, Ricardo A.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 2901/OM327
; CURRENT APPLICATION NUMBER: US/10/309,775A
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: CA 2,388,049
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-309-775A-28

Query Match 1.1%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
||||| |||||||||
Db 24 ACAAAATGAAAAAAAAAAAAAAAA 3

RESULT 350
US-09-005-243-33/c
; Sequence 33, Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,243
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/34465
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-005-243-33

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
||||| |||||||||
Db 20 CTAATAAAAAAAAAAAAAAAAAA 1

RESULT 351
US-09-005-243-34/c
; Sequence 34, Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-005-243-34

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
DB 20 CGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 352
US-09-224-683-33/c
Sequence 33, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-224-683-33

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
DB 20 CTAATAAAAAAAAAAAAAAAAAA 1

RESULT 353
US-09-224-683-34/c
Sequence 34, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,683
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-224-683-34

Query Match          1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1735 CAAAAAAGAAAAAAAAAAAAA 1754
      | | | | | | | | | | | | | | | |
Db      20 CGAAAAAAGAAAAAAAAAAAAA 1

RESULT 354
US-10-728-399-87/c
; Sequence 87, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Colca, Jerry
; TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
```

```
;
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-87

Query Match          1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1755
      | | | | | | | | | | | | | | | |
Db      20 AAACAAAAAAGAAAAAAAAA 1

RESULT 355
US-10-418-182-106/c
; Sequence 106, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-106

Query Match          1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1755
      | | | | | | | | | | | | | | | |
Db      21 AAAAAAAGAAAAAAGAAAAA 2

RESULT 356
US-09-995-898A-27/c
; Sequence 27, Application US/09995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20030027253Alak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR 2CYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/09/995,898A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
```

```
; SEQ ID NO 27
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC37681
US-09-995-898A-27

Query Match          1.0%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 863 GAAGAGGAAGAGGCGGAG 882
Db 21 GAGGAGGAAGAGGCGGAG 2

RESULT 357
US-10-420-034A-27/c
; Sequence 27, Application US/10420034A
; Publication No. US20040029228A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20040029228A1ak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Klucher, Kevin M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; FILE REFERENCE: 02-10
; CURRENT APPLICATION NUMBER: US/10/420,034A
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,813
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC37681
US-10-420-034A-27

Query Match          1.0%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 863 GAAGAGGAAGAGGCGGAG 882
Db 21 GAGGAGGAAGAGGCGGAG 2

RESULT 358
US-10-309-775A-21/c
; Sequence 21, Application US/10309775A
; Publication No. US20040006032A1
; GENERAL INFORMATION:
; APPLICANT: LOPEZ, Ricardo A.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 2901/OM327
; CURRENT APPLICATION NUMBER: US/10/309,775A
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: CA 2,388,049
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: PCR primer
US-10-309-775A-21

Query Match          1.0%; Score 18.4; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAACAAAA 5

RESULT 359
US-09-371-307-85/c
; Sequence 85, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-371-307-85

Query Match          1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
Db 19 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 360
US-10-176-884-44/c
; Sequence 44, Application US/10176884
; Publication No. US20030126642A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert
; APPLICANT: Kinoshita, Tetsu
; APPLICANT: Yadegari, Ramin
; APPLICANT: Gehring, Mary
; APPLICANT: Okamuro, Jack
; APPLICANT: Dang, Van-Dinh
; APPLICANT: The Regents of the University of California
; APPLICANT: Ceres, Inc.
; TITLE OF INVENTION: Compositions and Methods for Modulating Plant
; FILE REFERENCE: 023070-116710US
; CURRENT APPLICATION NUMBER: US/10/176,884
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/300,506
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 19
```



```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo(dT)-18
; OTHER INFORMATION: primer, oligo dT
US-10-176-884-44

Query Match          1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1753
Db 19 BAAAAA..... 1

RESULT 361
US-10-177-478-1/c
; Sequence 1, Application US/10177478
; Publication No. US20030165903A1
; GENERAL INFORMATION:
; APPLICANT: Dang, Van-Dinh
; APPLICANT: Okamuro, Jack
; TITLE OF INVENTION: Chimeric Histone Acetyltransferase
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 11696-037001
; CURRENT APPLICATION NUMBER: US/10/177,478
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: U.S. 60/300,135
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-177-478-1

Query Match          1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1753
Db 19 BAAAAA..... 1

RESULT 362
US-10-182-230-196/c
; Sequence 196, Application US/10182230
; Publication No. US20030215817A1
; GENERAL INFORMATION:
; APPLICANT: Leonardi, Amedeo
; APPLICANT: Sartani, Abraham
; APPLICANT: Glass, James R.
; APPLICANT: Sutcliffe, J. Gregor
; APPLICANT: Hasel, Karl W.
; TITLE OF INVENTION: Modulation of Gene Expression in Formation of Fatty Atherosclerosis
; TITLE OF INVENTION: Lesions
; FILE REFERENCE: 216019-143
; CURRENT APPLICATION NUMBER: US/10/182,230
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/177,963
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: 3' sequencing primer for dire
; OTHER INFORMATION: ct sequencing
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: v stands for a, c, or g
US-10-182-230-196

Query Match          1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1753
Db 19 BAAAAA..... 1

RESULT 363
US-10-401-321-85/c
; Sequence 85, Application US/10401321
; Publication No. US20030233679A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Pillar, Kenneth J.
; APPLICANT: Kilshore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; APPLICANT: Baerson, Scott R.
; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
; FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1)
; CURRENT APPLICATION NUMBER: US/10/401,321
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-401-321-85

Query Match          1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1753
Db 19 BAAAAA..... 1

RESULT 364
US-09-809-545A-84/c
; Sequence 84, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS.017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Oligos corresponding to polylinker sequence.
US-09-809-545A-84

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 365

US-09-888-326-837/c
; Sequence 837, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 837
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-837

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 366

US-09-994-311-6/c
; Sequence 6, Application US/09994311
; Publication No. US20030082556A1
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Feng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/09/994,311
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/637,751
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-6

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAA 1751
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 367

US-09-776-479-913/c
; Sequence 913, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-913

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 368

US-09-776-479-913/c
; Sequence 913, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-913

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 369

US-09-776-479-939/c
; Sequence 939, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 939
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-939

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 370

US-09-776-479-939/c
; Sequence 939, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 939
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-939

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 371

US-09-370-541-14/c
; Sequence 14, Application US/09370541
; Publication No. US20030088079A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Nucleosidic Compounds And Oligomeric
; TITLE OF INVENTION: Compounds Prepared Therefrom
; FILE REFERENCE: ISIS3993
; CURRENT APPLICATION NUMBER: US/09/370,541
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: 09/130,973
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 09/016,520
; EARLIER FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 09/344,260
; EARLIER FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-370-541-14

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 372

US-09-979-275A-7/c
; Sequence 7, Application US/09979275A
; Publication No. US20040110919A1
; GENERAL INFORMATION:
; APPLICANT: NAGAI, HIROSHI
; APPLICANT: KURODA, KYOKO
; APPLICANT: NAKAJIMA, TERUMI
; TITLE OF INVENTION: NOVEL PROTEINS HAVING HEMOLYTIC ACTIVITY AND GENES
; TITLE OF INVENTION: ENCODING THE PROTEIN
; FILE REFERENCE: 037181.50611US
; CURRENT APPLICATION NUMBER: US/09/979,275A
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: PCT/JP01/02209
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: JP 2000-78967
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; OTHER INFORMATION: this sequence may encompass 12-18 nucleotides
US-09-979-275A-7

Query Match 1.0%; Score 18; DB 1; Length 18;

```
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
|||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 373

US-10-389-417-97/c
; Sequence 97, Application US/10389417
; Publication No. US20040049014A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; Co, Man Sung
; Schneider, William P.
; Landolfi, Nicholas F.
; Coelingh, Kathleen L.
; Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
18 AAAAAAAAAAAAAAAAAA 1

RESULT 374

```

US-10-292-088-144/c
; Sequence 144, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-292-088-144

```

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
 |||||
 pb 18 AAAAAAAAAAAAAAAAAA 1

RESULT 375

US-10-314-578-913/c
; Sequence 913, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-913


```
RESULT 379
US-10-112-653-882/c
; Sequence 882, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 882
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-882

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1753
      |||||
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 380
US-10-017-995-913/c
; Sequence 913, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 913
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-913

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1753
      |||||
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 381
US-10-017-995-939/c
; Sequence 939, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
```

```
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 939
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-939

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1753
      |||||
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 382
US-10-206-613-4/c
; Sequence 4, Application US/10206613
; Publication No. US20030104432A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Zhidong
; APPLICANT: Jablons, David
; APPLICANT: You, Liang
; APPLICANT: He, Biao
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods of Amplifying Long Sense Strand RNA
; FILE REFERENCE: 023070-119510US
; CURRENT APPLICATION NUMBER: US/10/206,613
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 60/308,190
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo dt-18
US-10-206-613-4

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1753
      |||||
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 383
US-10-056-479A-15/c
; Sequence 15, Application US/10056479A
; Publication No. US20030175678A1
; GENERAL INFORMATION:
; APPLICANT: Bowen, Benjamin A.
; APPLICANT: Deakin, Edward
; APPLICANT: Goldsmith, Neil
; APPLICANT: Haudenschild, Christian
; APPLICANT: Houck, David
; APPLICANT: McAlpine, James B.
; APPLICANT: Neilsen, Soren
; APPLICANT: Pazoles, Christopher
; APPLICANT: Spencer, Marget E.
; APPLICANT: Stafford, Angela
```


;; TITLE OF INVENTION: Methods for Identifying Genes Regulating
;; TITLE OF INVENTION: Desired Cell Phenotypes
;; FILE REFERENCE: 50273/005002
;; CURRENT APPLICATION NUMBER: US/10/056,479A
;; CURRENT FILING DATE: 2003-02-07
;; PRIOR APPLICATION NUMBER: US 60/263,807
;; PRIOR FILING DATE: 2001-01-24
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 15
;; LENGTH: 18
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-056-479A-15

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 384
US-10-352-704-12/c
; Sequence 12, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; STATE: D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,704
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..18
;; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-352-704-12

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 385
US-10-352-704-18
; Sequence 18, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; STATE: D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,704
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..18
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-352-704-18

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 386

US-10-075-335-9/c
; Sequence 9, Application US/10075335
; Publication No. US20030186237A1
; GENERAL INFORMATION:
; APPLICANT: Ginsberg, Stephen
; APPLICANT: Che, Shaoli
; TITLE OF INVENTION: Methods and Compositions of Amplifying RNA
; FILE REFERENCE: HO-P02202US2
; CURRENT APPLICATION NUMBER: US/10/075,335
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/268,664
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/348,242
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/268,645
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/344,557
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/306,216
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/350,176
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-075-335-9

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 387

US-10-389-155-97/c
; Sequence 97, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; Co, Man Sung
; Schneider, William P.
; Landolfi, Nicholas F.
; Coelingh, Kathleen L.
; Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:
NAME/KEY: modified_base
LOCATION: 13..18
OTHER INFORMATION: /mod base= OTHER
/note= "T at positions 13-18 may be
present or absent"

SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-389-155-97

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 388
US-10-271-602B-84
; Sequence 84, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
; APPLICANT: Alice Xiang Li
; APPLICANT: Ghazala Hashmi
; APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; TITLE OF INVENTION: BY CONCURRENT INTERROGATION AND ENZYME-MEDIATED DETECTION
; FILE REFERENCE: eMAP-US
; CURRENT APPLICATION NUMBER: US/10/271,602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 60/364,416
; PRIOR FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according
; OTHER INFORMATION: to the specification as filed
US-10-271-602B-84

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 389
US-10-334-143-204/c
; Sequence 204, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 204
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; OTHER INFORMATION: this sequence may encompass 12-18 nucleotides in length
US-10-334-143-204

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 390
US-10-653-416-26/c
; Sequence 26, Application US/10653416
; Publication No. US20040110201A1
; GENERAL INFORMATION:
; APPLICANT: RASHTCHIAN, AYOUN
; APPLICANT: SCHUSTER, DAVID M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CDNA SYNTHESIS
; FILE REFERENCE: 38266-0011
; CURRENT APPLICATION NUMBER: US/10/653,416
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: 60/407,248
; PRIOR FILING DATE: 2002-09-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; OTHER INFORMATION: this sequence may encompass 12-18 nucleotides according
; OTHER INFORMATION: to the specification as filed
US-10-653-416-26

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 391
US-10-785-744-15/c
; Sequence 15, Application US/10785744
; Publication No. US20040133941A1
; GENERAL INFORMATION:
; APPLICANT: Bowen, Benjamin A.
; APPLICANT: Deakin, Edward
; APPLICANT: Goldsmith, Neil
; APPLICANT: Haudenschield, Christian
; APPLICANT: Houck, David
; APPLICANT: McAlpine, James B.
; APPLICANT: Neilson, Soren
; APPLICANT: Pazoles, Christopher
; APPLICANT: Spencer, Marget E.
; APPLICANT: Stafford, Angela
; TITLE OF INVENTION: Methods for Identifying Genes Regulating
; TITLE OF INVENTION: Desired Cell Phenotypes
; FILE REFERENCE: 50273/005002
; CURRENT APPLICATION NUMBER: US/10/785,744
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US/10/056,479
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/263,807
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-785-744-15

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 392
US-09-917-138-2
; Sequence 2, Application US/09917138
; Patent No. US20020031776A1
; GENERAL INFORMATION:
; APPLICANT: TULLIS, Richard
; APPLICANT: STEIFFEL, Jerome
; TITLE OF INVENTION: ENZYMIC LABELING AND DETECTION OF DNA
; TITLE OF INVENTION: HYBRIDIZATION PROBES
; FILE REFERENCE: 24730-2207B

```
; CURRENT APPLICATION NUMBER: US/09/917,138
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/580,358
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/136,545
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: Combined DNA/RNA
US-09-917-138-2
```

```
Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18
```

RESULT 393

```
US-09-996-292A-54/c
; Sequence 54, Application US/09996292A
; Publication No. US20030158403A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Martin A.
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Rajeev, Kallanthottathil Gopalan
; TITLE OF INVENTION: Nuclease Resistant Chimeric Oligonucleotides
; FILE REFERENCE: ISIS-4804
; CURRENT APPLICATION NUMBER: US/09/996,292A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: N= phenoxazine
US-09-996-292A-54
```

```
Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1
```

RESULT 394

```
US-09-996-292A-55/c
; Sequence 55, Application US/09996292A
; Publication No. US20030158403A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Martin A.
; APPLICANT: Prakash, Thazha P.
; APPLICANT: Rajeev, Kallanthottathil Gopalan
```

```
; TITLE OF INVENTION: Nuclease Resistant Chimeric Oligonucleotides
; FILE REFERENCE: ISIS-4804
; CURRENT APPLICATION NUMBER: US/09/996,292A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: N= G-clamp modification
US-09-996-292A-55
```

```
Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1
```

RESULT 395

```
US-10-096-221-3
; Sequence 3, Application US/10096221
; Publication No. US20020164628A1
; GENERAL INFORMATION:
; APPLICANT: Kurn, Nurith
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; FILE REFERENCE: 492692000700
; CURRENT APPLICATION NUMBER: US/10/096,221
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US 60/274,236
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: n = A,T,C or G
US-10-096-221-3
```

```
Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 2 AAAAAAAAAAAAAAAAAA 19
```

RESULT 396

```
US-10-100-321-22
; Sequence 22, Application US/10100321
; Publication No. US20030087251A1
; GENERAL INFORMATION:
; APPLICANT: Kurn, Nurith
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; FILE REFERENCE: 492692000500
; CURRENT APPLICATION NUMBER: US/10/100,321
```

; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/274,550
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: n = A,T,C or G
US-10-100-321-22

Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 2 AAAAAAAAAAAAAAAAAA 19

RESULT 397
US-10-013-295-54/c
; Sequence 54, Application US/10013295
; Publication No. US20030175906A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Nuclease Resistant Chimeric Oligonucleotides
; FILE REFERENCE: ISIS4948
; CURRENT APPLICATION NUMBER: US/10/013,295
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/302,682
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030175906A1el Sequence
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: N= phenoxazine
US-10-013-295-54

Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 398
US-10-013-295-55/c
; Sequence 55, Application US/10013295
; Publication No. US20030175906A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Nuclease Resistant Chimeric Oligonucleotides
; FILE REFERENCE: ISIS4948
; CURRENT APPLICATION NUMBER: US/10/013,295
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/302,682
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030175906A1el Sequence
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: N= G-clamp modification
US-10-013-295-55

Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 399
US-10-671-395-558/c
; Sequence 558, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 558
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-558

Query Match 1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAA 1

RESULT 400
US-09-955-410-4
; Sequence 4, Application US/09955410
; Patent No. US20020146718A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
; FILE REFERENCE: ISIS4800
; CURRENT APPLICATION NUMBER: US/09/955,410
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 09/686,114
; PRIOR FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US200201467i8A1e1 Sequence
US-09-955-410-4

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
||||| |||||||||
Db 1 AAAAAAGAAAAAAAAAAAAA 19

RESULT 401

US-10-154-890-4
; Sequence 4, Application US/10154890
; Publication No. US20030180734A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/10/154,890
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US/08/108,591
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030180734A1e1 Sequence
US-10-154-890-4

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
||||| |||||||||
Db 1 AAAAAAGAAAAAAAAAAAAA 19

RESULT 402

US-10-728-399-141/c
; Sequence 141, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Colca, Jerry
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitONEET antisense
US-10-728-399-141

Query Match 1.0%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1754
||||| |||||||||
Db 19 AAAAAAGAAAAAAAAAAAAA 1

RESULT 403

US-09-776-479-61/c
; Sequence 61, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-61

Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAA 1755
||||| |||||||||
Db 22 AAAAAACAAAAAAAAACAAAAA 1

RESULT 404

US-09-776-479-61/c
; Sequence 61, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-61

Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAA 1755
||||| |||||||||

Db 22 AAAACAAAAAAACAAAAAAA 1

RESULT 405

US-10-314-578-61/c
; Sequence 61, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence

US-10-314-578-61

Query Match 1.0%; Score 17.2; DB 1; Length 22;

Best Local Similarity 86.4%; Pred. No. 2.5e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 ACAAAAAA 1755

Db 22 AAAACAAAAAAACAAAAAAA 1

RESULT 406

US-10-112-653-55/c
; Sequence 55, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide

Query Match 1.0%; Score 17.2; DB 1; Length 22;

Best Local Similarity 86.4%; Pred. No. 2.5e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 ACAAAAAA 1755

Db 22 AAAACAAAAAAACAAAAAAA 1

RESULT 407

US-10-017-995-61/c
; Sequence 61, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence

US-10-017-995-61

Query Match 1.0%; Score 17.2; DB 1; Length 22;

Best Local Similarity 86.4%; Pred. No. 2.5e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 ACAAAAAA 1755

Db 22 AAAACAAAAAAACAAAAAAA 1

RESULT 408

US-09-843-676-132/c
; Sequence 132, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429

```

; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-843-676-132

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1752
Db      17 AAAAAAAAAAAAAAAAAA 1

RESULT 409
US-09-766-253-132/c
; Sequence 132, Application US/09766253
; Publication No.: US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; LINGNER, JOACHIM
; NAKAMURA, TORU
; CHAPMAN, KAREN B.
; MORIN, GREGG B.
; HARLEY, CALVIN
; ANDREWS, WILLIAM H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-766-253-132
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```

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1752
Db      17 AAAAAAAAAAAAAAAAAA 1

RESULT 410
US-09-438-486-132/c
; Sequence 132, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-438-486-132

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 411
US-10-208-357-23
; Sequence 23, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-23

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 412
US-10-053-758-132/c
; Sequence 132, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 413
US-10-054-295-132/c
; Sequence 132, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-053-758-132
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 413
US-10-054-295-132/c
; Sequence 132, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-054-295-132

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 414
US-10-117-267-5/c
; Sequence 5, Application US/10117267
; Publication No. US20030045698A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Ph.D., Martin A.
; TITLE OF INVENTION: Compounds, Processes And Intermediates For Synthesis Of Mixed Back
; TITLE OF INVENTION: Oligomeric Compounds
; FILE REFERENCE: ISIS-5039
; CURRENT APPLICATION NUMBER: US/10/117,267
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/726,096
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/250,075
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(19)
; OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate
; OTHER INFORMATION: internucleoside linkage
US-10-117-267-5
```

```
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1
```

```
RESULT 415
US-10-054-611-132/c
; Sequence 132, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
```

```
;
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-054-611-132
```

```
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1
```

```
RESULT 416
US-10-324-409B-16
; Sequence 16, Application US/10324409B
; Publication No. US20040086880A1
; GENERAL INFORMATION:
; APPLICANT: Sampson, et al.
; TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced
; TITLE OF INVENTION: Secondary Structure
; FILE REFERENCE: 200309-0028
; CURRENT APPLICATION NUMBER: US/10/324,409B
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Anneal Primer
US-10-324-409B-16

```

```
Query Match          1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. NO. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 417

```

US-09-994-311-5/c
; Sequence 5, Application US/09994311
; Publication No. US20030082556A1
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Feng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/09/994,311
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/637,751
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Se
US-09-994-311-5

```

```
Query Match      1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1735 CAAAAAAAAAAAAA 1751
|||
Db 17 CAAAAAAAAAAAAA 1

RESULT 418

US-10-671-395-616/c
; Sequence 616, Application US/10671395
; Publication No. US20040132063A1
: GENERAL INFORMATION:

```

; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 616
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-616

```

Query Match

```

Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0;

```

Qy 1735 CAAAAA AAAAAA 1751
Db 17 CAAAAA AAAAAA 1

RESULT 419

```

US-09-263-959-849
; Sequence 849, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
;   APPLICANT: Hood, Leroy E.
;   APPLICANT: Rowen, Lee
;   APPLICANT: Koop, Ben F.
;   TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC C
;   NUMBER OF SEQUENCES: 1279
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Seed and Berry LLP
;   STREET: 6300 Columbia Center, 701 Fifth Avenue
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: US
;   ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/263,959
;   FILING DATE: 05-MAR-1999
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: McMasters, David D.
;   REGISTRATION NUMBER: 33,963
;   REFERENCE/DOCKET NUMBER: 920010.426C2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 849:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-09-263-959-849

```

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18: Conservative 0; Mismatches 2; Indels

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
 ||||| ||||| ||||| ||||| |||||
 Db 1 AAAGAAAAAAAAAAAAAAAA 20

RESULT 420

US-10-181-846-68/c
; Sequence 68, Application US/10181846
; Publication No. US20030083297A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RTSP-0363
; CURRENT APPLICATION NUMBER: US/10/181,846
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US01/01416
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/490,692
; PRIOR FILING DATE: 2000-01-24

```

; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-846-68

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      859 GCAGGAAGAGGAGGAGGAGG 878
Db      20 GGAGGAAGAAGAGGAGGAGG 1

RESULT 421
US-10-728-399-199/c
; Sequence 199, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Colca, Jerry
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 199
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-199

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1732 TTACAAAAAATAAAAAAAAAA 1751
Db      20 TTAACAAAAAATAAAAAAAAAA 1

RESULT 422
US-10-728-399-273/c
; Sequence 273, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Colca, Jerry
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-273

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1731 TTTACAAAAAATAAAAAAAAAA 1750
Db      20 TTTAAACAAAAAATAAAAAAAAAA 1

RESULT 423
US-10-728-399-400/c
; Sequence 400, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Colca, Jerry
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 400
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-400

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1730 GTTTACAAAAAATAAAAAAAAAA 1749
Db      20 GTTTAAACAAAAAATAAAAAAAAAA 1

RESULT 424
US-09-775-479-9/c
; Sequence 9, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: LECLERC, Guy
; APPLICANT: MARTEL, R.mi
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 12168-1US-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-9

Query Match      0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1731 TTTACAAAAAATAAAAAAAAAA 1748
Db      18 TTTAAACAAAAAATAAAAAAAAAA 1

RESULT 425
US-10-333-461-18/c
```

```

QY      1731 TTTACAAAAAATAAAAAAAAAA 1750
Db      20 TTTAAACAAAAAATAAAAAAAAAA 1

RESULT 423
US-10-728-399-400/c
; Sequence 400, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Colca, Jerry
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 400
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-400

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1730 GTTTACAAAAAATAAAAAAAAAA 1749
Db      20 GTTTAAACAAAAAATAAAAAAAAAA 1

RESULT 424
US-09-775-479-9/c
; Sequence 9, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: LECLERC, Guy
; APPLICANT: MARTEL, R.mi
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 12168-1US-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-9

Query Match      0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1731 TTTACAAAAAATAAAAAAAAAA 1748
Db      18 TTTAAACAAAAAATAAAAAAAAAA 1

RESULT 425
US-10-333-461-18/c
```


; Sequence 18, Application US/10333461

; Publication No. US20030165952A1

; GENERAL INFORMATION:

; APPLICANT: Global Genomics AB

; APPLICANT: Linnarsson, Sten

; APPLICANT: Ernfors, Patrik

; APPLICANT: Bauren, Goran

; TITLE OF INVENTION: Methods for analysis and identification of transcribed

; TITLE OF INVENTION: genes, and fingerprinting

; FILE REFERENCE: smwfp5941752

; CURRENT APPLICATION NUMBER: US/10/333,461

; CURRENT FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: GB 0018016.6

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/219,925

; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 18

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Double-stranded product DNA

US-10-333-461-18

Query Match

Best Local Similarity 0.9%; Score 16.4; DB 1; Length 18;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAAAAAA 1752

Db 18 CGAAAA AAAAAAAAAA 1

RESULT 426

US-10-352-253A-18/c

; Sequence 18, Application US/10352253A

; Publication No. US20030175908A1

; GENERAL INFORMATION:

; APPLICANT: Linnarsson, Sten

; APPLICANT: Ernfors, Patrik

; APPLICANT: Bauren, Goran

; APPLICANT: Metsis, Ats

; APPLICANT: Pihlak, Arno

; APPLICANT: Montelius, Andreas

; TITLE OF INVENTION: Methods And Means For Manipulating Nucleic Acid

; FILE REFERENCE: 620-234

; CURRENT APPLICATION NUMBER: US/10/352,253A

; CURRENT FILING DATE: 2003-01-28

; PRIOR APPLICATION NUMBER: US 60/352,215

; PRIOR FILING DATE: 2002-01-29

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 18

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Double-stranded product DNA

US-10-352-253A-18

Query Match

Best Local Similarity 0.9%; Score 16.4; DB 1; Length 18;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAAAAAA 1752

Db 18 CGAAAA AAAAAAAAAA 1

```
; SEQ ID NO 991
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-665-951-991

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1621 GTTCCAGTTCCCATCCTT 1638
    ||||| ||||| ||||| |||||
Db 18 GTTCCGGTTCCCATCCTT 1

RESULT 429
US-10-665-951-1315
; Sequence 1315, Application US/10665951
; Publication No. US20040138163A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/131 (MBHB02-742-F)
; CURRENT APPLICATION NUMBER: US/10/665,951
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1315
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-665-951-1315

Query Match          0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 10; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1621 GTTCCAGTTCCCATCCTT 1638
    ||||| ||||| ||||| |||||
Db 2 GUUCCGGUUCUCCAUCCUU 19

RESULT 430
```

```
US-10-275-080A-6/c
; Sequence 6, Application US/10275080A
; Publication No. US20040053214A1
; GENERAL INFORMATION:
; APPLICANT: Schroder, Klaus Hobe
; APPLICANT: Schubler, Andrea
; APPLICANT: Koike, Katsuro
; TITLE OF INVENTION: Method of Diagnosing HBV Infection Stages
; FILE REFERENCE: 012627-033
; CURRENT APPLICATION NUMBER: US/10/275,080A
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/EP01/04918
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: EP 00 109 436.6
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-275-080A-6

Query Match          0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAAATAAAAAA 1750
    ||||| ||||| ||||| |||||
Db 18 TTCAAAAAAATAAAAAA 1

RESULT 431
US-10-289-762-2140/c
; Sequence 2140, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2140
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2140

Query Match          0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 137 TCTGGAGTCCCTTTCC 154
    ||||| ||||| ||||| |||||
Db 18 TCTGGAGTCCCTTTCC 1

RESULT 432
US-09-775-479-17
; Sequence 17, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: Leclerc, Guy
; APPLICANT: Martel, R.mi
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 12168-IUS-2
```

; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-17

Query Match 0.9%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1748
Db 1 TTTAAAAA 18

RESULT 433
US-10-252-155-511
; Sequence 511, Application US/10252155
; Publication No. US20040068096A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS IN ORGANIC ANION TRANSPORT
; TITLE OF INVENTION: MULTI-DRUG RESISTANT PROTEINS
; FILE REFERENCE: D0152 NP
; CURRENT APPLICATION NUMBER: US/10/252,155
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/324,172
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/333,700
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 511
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-252-155-511

Query Match 0.9%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1323 TGAGGACTTTCACAGGAA 1340
Db 4 TGAGGACATTCACAGGAA 21

RESULT 434
US-10-252-155-512
; Sequence 512, Application US/10252155
; Publication No. US20040068096A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS IN ORGANIC ANION TRANSPORT
; TITLE OF INVENTION: MULTI-DRUG RESISTANT PROTEINS
; FILE REFERENCE: D0152 NP
; CURRENT APPLICATION NUMBER: US/10/252,155
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/324,172
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/333,700
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 783

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 512
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-252-155-512

Query Match 0.9%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1323 TGAGGACTTTCACAGGAA 1340
Db 4 TGAGGACATTCACAGGAA 21

RESULT 435
US-10-418-182-128
; Sequence 128, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-128

Query Match 0.9%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 861 AGGAAGAGGAAGAGGAGG 878
Db 2 AGGAAGAGGAAGAGAGG 19

RESULT 436
US-09-981-397A-1/c
; Sequence 1, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axxima Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Matthias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
; TITLE OF INVENTION: Inhibition
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981,397A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/240,750
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polyT primer

```
; NAME/KEY: misc feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: n = a,c,g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: v = a,g or c
US-09-981-397A-1

Query Match          0.9%; Score 16.2; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1751
Db 17 BAAAAA..... 1

RESULT 437
US-10-103-614A-4
; Sequence 4, Application US/10103614A
; Publication No. US20030059796A1
; GENERAL INFORMATION:
; APPLICANT: SALMAN AL-MAHMOOD
; TITLE OF INVENTION: METHOD FOR IDENTIFYING NOVEL GENES INVOLVED IN THE
; TITLE OF INVENTION: REGULATION OF ANGIOGENESIS, STUDY OF SAID GENES AND USE
; TITLE OF INVENTION: THEREOF FOR THERAPEUTIC PURPOSES
; FILE REFERENCE: 1071-02
; CURRENT APPLICATION NUMBER: US/10/103,614A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: PCT/FR00/02607
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: FR 99/11790
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: a, t, c or g
; NAME/KEY: modified_base
; LOCATION: (19)
; OTHER INFORMATION: a, t, c or g
US-10-103-614A-4

Query Match          0.9%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.1e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1751
Db 2 VAAAAA..... 18

RESULT 438
US-09-739-928-2/c
; Sequence 2, Application US/09739928
; Patent No. US20020052482A1
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamber, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
```

```
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-928-2

Query Match          0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAA..... 1751
Db 16 AAAAAA..... 1

RESULT 439
US-09-152-059-70/c
; Sequence 70, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-70

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAA 1751
| | | | | | | | | | | | | | | | | |
Db 16 AAAAAAAAAAAAAAA 1

RESULT 440
US-09-805-296D-9/c
; Sequence 9, Application US/09805296D
; Patent No. US20020155989A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakcheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1US
; CURRENT APPLICATION NUMBER: US/09/805,296D
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
US-09-805-296D-9

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAA 1751
| | | | | | | | | | | | | | | | | |
Db 16 AAAAAAAAAAAAAAA 1

RESULT 441
US-09-843-676-131
; Sequence 131, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin

; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-843-676-131

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAA 1751
| | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAA 16

RESULT 442
US-09-766-253-131
; Sequence 131, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America

```
;
;
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-766-253-131
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 443
US-09-438-486-131
; Sequence 131, Application US/09438486
; Publication No. US2003009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US2003009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
```

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;
;
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-438-486-131
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 444
US-09-895-585-9/c
; Sequence 9, Application US/09895585
; Publication No. US20020081725A1
; GENERAL INFORMATION:
; APPLICANT: Tsang, Wen-Ghih
; APPLICANT: Zheng, Tianli
; APPLICANT: Huang, Chang Jiang
; APPLICANT: AmCyt, Inc.
; TITLE OF INVENTION: Culturing Pancreatic Stem Cells Having a Specified,
; FILE REFERENCE: 021164-000100US
; CURRENT APPLICATION NUMBER: US/09/895,585
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/215,634
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,306
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US 60/291,787
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo-(dT)-16
US-09-895-585-9
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAAAAAA 16
```


Db 16 AAAAAAAAAAAAAA 1

RESULT 445

US-10-208-357-22

; Sequence 22, Application US/10208357

; Publication No. US20020182687A1

; GENERAL INFORMATION:

; APPLICANT: Kurz, Markus

; APPLICANT: Lohse, Peter

; APPLICANT: Wagner, Richard

; TITLE OF INVENTION: Peptide Acceptor Ligation Methods

; FILE REFERENCE: 50036/031002

; CURRENT APPLICATION NUMBER: US/10/208,357

; CURRENT FILING DATE: 2002-07-30

; PRIOR APPLICATION NUMBER: US/09/619,103

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 60/145,834

; PRIOR FILING DATE: 1999-07-27

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 22

; LENGTH: 16

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: designed sequence for nucleic acid purification

US-10-208-357-22

Query Match 0.9%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751

Db 1 AAAAAAAAAAAAAA 16

RESULT 446

US-10-053-758-131

; Sequence 131, Application US/10053758

; Publication No. US20030032075A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. US20030032075A1el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/053,758

; FILING DATE: 18-Jan-2002

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 131:

US-10-053-758-131

Query Match 0.9%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751

Db 1 AAAAAAAAAAAAAA 16

RESULT 447

US-10-054-295-131

; Sequence 131, Application US/10054295

; Publication No. US20030044953A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. US20030044953A1el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/054,295

; FILING DATE: 18-Jan-2002

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/854,050

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

```
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-054-295-131

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1751
Db      1 AAAAAAAAAAAAAAAAAA 16

RESULT 448
US-10-054-611-131
; Sequence 131, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-054-611-131

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1751
Db      1 AAAAAAAAAAAAAAAAAA 16

RESULT 449
US-10-072-975-9/c
; Sequence 9, Application US/10072975
; Publication No. US20030059789A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakcheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1.IUS
; CURRENT APPLICATION NUMBER: US/10/072,975
; CURRENT FILING DATE: 2002-02-09
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/805,296
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/0811
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
US-10-072-975-9

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAA 1751
Db      16 AAAAAAAAAAAAAAAAAA 1

RESULT 450
US-10-227-001-21/c
; Sequence 21, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
; APPLICANT: Dempcy, Robert O.
; APPLICANT: Afonina, Irina Aleksandrovna
; APPLICANT: Vermeulen, Nicolaas M.J.
; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: Hybridization-Triggered Fluorescent
; TITLE OF INVENTION: Detection of Nucleic Acids
; FILE REFERENCE: 17682A-004210US
; CURRENT APPLICATION NUMBER: US/10/227,001
```

```
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 09/428,236
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: R2 (ODN) of fluorophore-MGB-ODN
; OTHER INFORMATION: conjugate
US-10-227-001-21

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
Db      16 AAAAAAAAAAAAAAAAAA 1

RESULT 451
US-10-008-029-70/c
; Sequence 70, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-70

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
Db      16 AAAAAAAAAAAAAAAAAA 1

RESULT 452
US-10-051-436-9/c
; Sequence 9, Application US/10051436
```

```
; Publication No. US20030138045A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1US
; CURRENT APPLICATION NUMBER: US/10/051,436
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
US-10-051-436-9

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
Db      16 AAAAAAAAAAAAAAAAAA 1

RESULT 453
US-10-208-650-70/c
; Sequence 70, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 16
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-208-650-70
Query Match          0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAA 1

RESULT 454
US-10-203-780-9/c
; Sequence 9, Application US/10203780
; Publication No. US20030165914A1
; GENERAL INFORMATION:
; APPLICANT: CUZIN, MARC
; APPLICANT: PELTIE, PHILIPPE
; APPLICANT: FONTECAVE, MARC
; APPLICANT: DECOUT, JEAN-LUC
; APPLICANT: DUEYMES, CECILE
; TITLE OF INVENTION: ANALYSIS OF BIOLOGICAL TARGETS USING A BIOCHIP COMPRISING A FLUOR
; FILE REFERENCE: 226286USOXPCT
; CURRENT APPLICATION NUMBER: US/10/203,780
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/FR01/00516
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: FR 00 02236
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
; NAME/KEY: modified_base
; LOCATION: (1)...(1)
; OTHER INFORMATION: t is modified with a covalent linkage to flavin
US-10-203-780-9

Query Match          0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAA 1

RESULT 455
US-10-360-275-9/c
; Sequence 9, Application US/10360275
; Publication No. US20040014644A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Choob, Mikhail
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: AM102.P.1.1.IUS
; CURRENT APPLICATION NUMBER: US/10/360,275
; CURRENT FILING DATE: 2003-02-07
```

```
; PRIOR APPLICATION NUMBER: US 10/072,975
; PRIOR FILING DATE: 2002-02-09
; PRIOR APPLICATION NUMBER: US 09/805,296
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
US-10-360-275-9

Query Match          0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAA 1

RESULT 456
US-10-611-629-4/c
; Sequence 4, Application US/10611629
; Publication No. US20040091905A1
; GENERAL INFORMATION:
; APPLICANT: GUO, BAOCHUAN
; TITLE OF INVENTION: METHOD FOR DETECTING MUTATED POLYNUCLEOTIDES WITHIN A
; FILE REFERENCE: 27433/04012
; CURRENT APPLICATION NUMBER: US/10/611,629
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 60/392,251
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 4
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-611-629-4

Query Match          0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGGAAAAAAAAAAAGCC 48
Db 16 AGGAAAAAAAAAAAGCC 1

RESULT 457
US-10-776-099-9/c
; Sequence 9, Application US/10776099
; Publication No. US20040141957A1
; GENERAL INFORMATION:
; APPLICANT: Tsang, Wen-Ghih
; APPLICANT: Zheng, Tianli
; APPLICANT: Huang, Chang Jiang
; APPLICANT: AmCyt, Inc.
; TITLE OF INVENTION: Culturing Pancreatic Stem Cells Having a Specified,
; FILE REFERENCE: 021164-000100US
; CURRENT FILING DATE: 2003-02-07
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; CURRENT APPLICATION NUMBER: US/10/776,099
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US/09/895,585
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/215,634
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/246,306
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US 60/291,787
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo-(dT)-16
US-10-776-099-9

Query Match          0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 458
US-09-788-362-3/c
; Sequence 3, Application US/09788362
; Patent No. US20020009731A1
; GENERAL INFORMATION:
; APPLICANT: Muramatsu, Takamichi
; APPLICANT: Fujita, Takeshi
; APPLICANT: Kiyama, Masaharu
; APPLICANT: Irie, Takashi
; TITLE OF INVENTION: PREPARATION METHOD OF NUCLEIC ACID SAMPLE FOR RARE
; TITLE OF INVENTION: EXPRESSED GENES AND ANALYZING METHOD USING THE PREPARED
; FILE REFERENCE: NIT-129-03
; CURRENT APPLICATION NUMBER: US/09/788,362
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 09/313,637
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: JP 10-153651
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
US-09-788-362-3

Query Match          0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2

RESULT 459
US-09-090-672B-106/c
; Sequence 106, Application US/09090672B
; Patent No. US20020068707A1
; GENERAL INFORMATION:
; APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
```

```
; APPLICANT: Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
; APPLICANT: Shigemasa; Takei, Masami
; TITLE OF INVENTION: Iga Nephropathy-Related Genes
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
US-09-090-672B-106

Query Match          0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2

RESULT 460
US-09-788-338-3/c
; Sequence 3, Application US/09788338
; Patent No. US20020102561A1
; GENERAL INFORMATION:
; APPLICANT: MURAMATSU, TAKAMICHI
; APPLICANT: FUJITA, TAKESHI
; APPLICANT: KIYAMA, MASAHARU
; APPLICANT: IRIE, TAKASHI
; TITLE OF INVENTION: PREPARATION METHOD OF NUCLEIC ACID SAMPLE FOR RARE
; TITLE OF INVENTION: EXPRESSED GENES AND ANALYZING METHOD USING THE PREPARED
; TITLE OF INVENTION: NUCLEIC ACID SAMPLES THEREBY
; FILE REFERENCE: NIT-129-02
; CURRENT APPLICATION NUMBER: US/09/788,338
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 09/313,637
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: JP 10-153651
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-788-338-3

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2

RESULT 461
US-09-848-754A-906
; Sequence 906, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 906
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-906

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 907 CAGCCTCCAGAGGATG 922
Db 2 CAGCCUCCAGAGGAUG 17

RESULT 462
US-09-848-754A-907
; Sequence 907, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 907
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-907

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 907 CAGCCTCCAGAGGATG 922
Db 1 CAGCCUCCAGAGGAUG 16

RESULT 463
US-09-730-559B-108/c
; Sequence 108, Application US/09730559B
```

```

; Publication No. US20030207828A1
; GENERAL INFORMATION:
; APPLICANT: ISHIWATA, TETSUYOSHI
; APPLICANT: SAKURADA, MIKIO
; APPLICANT: KAWABATA, AYAKO
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: NISHI, TATSUNARI
; APPLICANT: KUGA, TETSURO
; APPLICANT: SAWADA, SHIGEMASA
; APPLICANT: TAKEI, MASAMI
; APPLICANT: SHIBATA, KENJI
; APPLICANT: FURUYA, AKIKO
; TITLE OF INVENTION: IGA NEPHROPATHY-ASSOCIATED GENE
; FILE REFERENCE: 766.21 CIP
; CURRENT APPLICATION NUMBER: US/09/730,559B
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-730-559B-108

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2

RESULT 464
US-10-380-254-5/c
; Sequence 5, Application US/10380254
; Publication No. US20040038252A1
; GENERAL INFORMATION:
; APPLICANT: Sugita et al.
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
; FILE REFERENCE: 6235-64773
; CURRENT APPLICATION NUMBER: US/10/380,254
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08246
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: JP 2000-291318
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized primer sequence
US-10-380-254-5

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2

RESULT 465
US-10-398-885A-4/c
; Sequence 4, Application US/10398885A
; Publication No. US20040053282A1
```


GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; APPLICANT: Takahashi, Eiki
; TITLE OF INVENTION: Method of Testing For Allergic Diseases
; FILE REFERENCE: SHIMIZU-07907
; CURRENT APPLICATION NUMBER: US/10/398,895A
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08937
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-885A-4

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAA 1750
|||||
Db 17 CAAAAAAAAAAAAAAAA 2

RESULT 466

US-10-398-877-20/c
; Sequence 20, Application US/10398877
; Publication No. US20040058351A1
; GENERAL INFORMATION:

; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: Method of Testing for Allergic Diseases
; FILE REFERENCE: SHIMIZU-07906
; CURRENT APPLICATION NUMBER: US/10/398,877
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08574
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-877-20

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAA 1750
|||||
Db 17 CAAAAAAAAAAAAAAAA 2

RESULT 467
US-10-291-808-64/c
; Sequence 64, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-64

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAA 1750
|||||
Db 17 CAAAAAAAAAAAAAAAA 2

RESULT 468

US-10-333-461-24/c
; Sequence 24, Application US/10333461
; Publication No. US20030165952A1
; GENERAL INFORMATION:

; APPLICANT: Global Genomics AB
; APPLICANT: Linnarsson, Sten
; APPLICANT: Ernfors, Patrik
; APPLICANT: Bauren, Goran
; TITLE OF INVENTION: Methods for analysis and identification of transcribed
; TITLE OF INVENTION: genes, and fingerprinting
; FILE REFERENCE: smwfp5941752
; CURRENT APPLICATION NUMBER: US/10/333,461
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: GB 0018016.6
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/219,925
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Double-stranded product DNA
US-10-333-461-24

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 469

US-10-352-253A-24/c
; Sequence 24, Application US/10352253A
; Publication No. US20030175908A1
; GENERAL INFORMATION:
; APPLICANT: Linnarsson, Sten
; APPLICANT: Ernfors, Patrik
; APPLICANT: Bauren, Goran
; APPLICANT: Metsis, Ats
; APPLICANT: Pihlak, Arno
; APPLICANT: Montelius, Andreas
; TITLE OF INVENTION: Methods And Means For Manipulating Nucleic Acid
; FILE REFERENCE: 620-234
; CURRENT APPLICATION NUMBER: US/10/352,253A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,215
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Double-stranded product DNA
US-10-352-253A-24

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 470

US-10-220-373-9/c
; Sequence 9, Application US/10220373
; Publication No. US20030180743A1
; GENERAL INFORMATION:
; APPLICANT: NAGASU, Takeshi
; APPLICANT: OSHIDA, Tadahiyo
; APPLICANT: OBAYASHI, Izumi
; APPLICANT: MATSUI, Keiko
; APPLICANT: SAITO, Hirohisa
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
; FILE REFERENCE: SHZ-010US
; CURRENT APPLICATION NUMBER: US/10/220,373
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-61832
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificially
; OTHER INFORMATION: Synthesized Primer Sequence
US-10-220-373-9

Query Match. 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2

RESULT 471

US-10-352-255A-24/c
; Sequence 24, Application US/10352255A
; Publication No. US20030215839A1
; GENERAL INFORMATION:
; APPLICANT: LONNERBERG, Peter
; APPLICANT: OLDIN, Mats
; APPLICANT: LINNARSSON, Sten
; APPLICANT: ERNFORS, Patrik
; TITLE OF INVENTION: Methods and Means for Identification of Gene Features
; FILE REFERENCE: 620-235
; CURRENT APPLICATION NUMBER: US/10/352,255A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,245
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Double-stranded product DNA
US-10-352-255A-24

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 472

US-10-380-255-8/c
; Sequence 8, Application US/10380255
; Publication No. US20040023263A1
; GENERAL INFORMATION:
; APPLICANT: Sugita et al.
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
; FILE REFERENCE: 6235-64935
; CURRENT APPLICATION NUMBER: US/10/380,255
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08247
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: JP 2000-293021
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:an artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-380-255-8

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2

```
RESULT 473
US-10-138-674-1074/c
; Sequence 1074, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1074

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
Db      17 AAAAAAAAAAAAAAAAAA 2

RESULT 474
US-10-138-674-1075/c
; Sequence 1075, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1075

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
Db      16 AAAAAAAAAAAAAAAAAA 1

RESULT 475
US-10-287-949A-1074/c
; Sequence 1074, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
```

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1074

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
Db      17 AAAAAAAAAAAAAAAAAA 2

RESULT 476
US-10-287-949A-1075/c
; Sequence 1075, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1075
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1075

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
Db      16 AAAAAAAAAAAAAAAAAA 1

RESULT 477
US-09-994-311-7/c
; Sequence 7, Application US/09994311
; Publication No. US20030082556A1
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Feng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/09/994,311
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/637,751
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-994-311-7

Query Match 0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 478
US-10-275-080A-5/c
; Sequence 5, Application US/10275080A
; Publication No. US20040053214A1
; GENERAL INFORMATION:
; APPLICANT: Schroder, Klaus Hobe
; APPLICANT: Schubler, Andrea
; APPLICANT: Koike, Katsuro
; TITLE OF INVENTION: Method of Diagnosing HBV Infection Stages
; FILE REFERENCE: 012627-033
; CURRENT APPLICATION NUMBER: US/10/275,080A
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/EP01/04918
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: EP 00 109 436.6
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-275-080A-5

Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
|||||
Db 16 CAAAAAAAAAAAAAAAAA 1

RESULT 479
US-10-363-198-47
; Sequence 47, Application US/10363198
; Publication No. US20040023908A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF A20 EXPRESSION
; FILE REFERENCE: RTS-0141
; CURRENT APPLICATION NUMBER: US/10/363,198
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 09/658,687
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide
US-10-363-198-47

Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 TTTCTGGAGTCCCAAA 78
|||||
Db 1 TTTCTGGAGTCCCAAA 16

RESULT 480
US-10-671-395-990/c
; Sequence 990, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 990
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-990

Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1750
|||||
Db 16 CAAAAAAAAAAAAAAAAA 1

RESULT 481
US-09-982-262B-57/c
; Sequence 57, Application US/09982262B
; Publication No. US20030077565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Christopher K. Mirabelli
; TITLE OF INVENTION: OLIGONUCLEOTIDE MODULATION OF CELL ADHESION
; FILE REFERENCE: ISPH-0612
; CURRENT APPLICATION NUMBER: US/09/982,262B
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/659,288
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/128,496
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: 08/440,740
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/063,167
; PRIOR FILING DATE: 1993-05-17
; PRIOR APPLICATION NUMBER: 07/969,151
; PRIOR FILING DATE: 1993-02-10
; PRIOR APPLICATION NUMBER: 08/007,997
; PRIOR FILING DATE: 1993-01-21
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-982-262B-57

Query Match          0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      839 CTGCTGGGGTCTCTGGCCC 857
Db      19 CTCCTCGGGTCTCTGGCCC 1

RESULT 482
US-09-899-440-1
; Sequence 1, Application US/09899440
; Publication No. US20030092158A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Cy
; TITLE OF INVENTION: PHOSPHOROTHIOATE ANTISENSE HEPARANASE OLIGONUCLEOTIDES
; FILE REFERENCE: 0575/63180
; CURRENT APPLICATION NUMBER: US/09/899,440
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..(7)
; OTHER INFORMATION: anitsense oligonucleotide LB63
US-09-899-440-1

Query Match          0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      166 GGGCCACCTGGCTGCCCC 184
Db      2 GGGCTACCTGGCTGCTCC 20

RESULT 483
US-09-915-814-96/c
; Sequence 96, Application US/09915814
; Publication No. US20030096771A1
; GENERAL INFORMATION:
; APPLICANT: Madeline M. Butler
; APPLICANT: Andrew T. Watt
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
; FILE REFERENCE: ISPH-0587
; CURRENT APPLICATION NUMBER: US/09/915,814
; CURRENT FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 96
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-915-814-96

Query Match          0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      167 GGGCCACCTGGCTGCCCC 185
Db      19 GGCCTACCTGGCTGCCCTC 1
```

```
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-454-663-57/c
; Sequence 57, Application US/10454663
; Publication No. US20040033977A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Christopher K. Mirabelli
; TITLE OF INVENTION: OLIGONUCLEOTIDE MODULATION OF CELL ADHESION
; FILE REFERENCE: ISPH-0744
; CURRENT APPLICATION NUMBER: US/10/454,663
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 09/982,262
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/659,288
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/128,496
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: 08/440,740
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/063,167
; PRIOR FILING DATE: 1993-05-17
; PRIOR APPLICATION NUMBER: 07/969,151
; PRIOR FILING DATE: 1993-02-10
; PRIOR APPLICATION NUMBER: 08/007,997
; PRIOR FILING DATE: 1993-01-21
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-454-663-57

Query Match          0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      839 CTGCTGGGTCTCTGGCCC 857
Db      19 CTCCTCGGGTCTCTGGCCC 1

RESULT 485
US-10-006-430-26/c
; Sequence 26, Application US/10006430
; Publication No. US20030113914A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD81 EXPRESSION
; FILE REFERENCE: RTS-0341
; CURRENT APPLICATION NUMBER: US/10/006,430
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-430-26

Query Match          0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1146 GGGCTGCTACGTGGCCACC 1164
Db      19 GGGCTGCTACGGGGCCATC 1
```


US-09-964-261-73

Query Match 0.9%; Score 15.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 182 CCCGAGACGCGGAGCCCG 202
||||| :|||
Db 1 CCCGAGACGCGGAGCYCCG 21

RESULT 491
US-10-349-143-10471/c
; Sequence 10471, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10471
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-12181 for SEQ 2606, in complete
US-10-349-143-10471

Query Match 0.9%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 289 GTCAATTTTGGCCCTTC 307
||||| :|||
Db 19 GTCAATTTTGGCTCTTC 1

RESULT 492
US-10-301-764-17/c
; Sequence 17, Application US/10301764
; Publication No. US20040039184A1
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-No. US20040039184A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-301-764-17

Query Match 0.9%; Score 15.6; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.4e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA 1751
: ||||| :|||
Db 17 SNA 1

RESULT 493
US-10-146-474-17/c
; Sequence 17, Application US/10146474
; Publication No. US20030023061A1
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,474
FILING DATE: 14-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-146-474-17

Query Match      0.9%; Score 15.6; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.4e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA
Db 17 SNA
RESULT 494
US-09-780-533A-2364
; Sequence 2364, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2364
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2364

Query Match      0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 861 AGGAAGAGGAGAGGAG 877
Db 1 AGGAGGAGGAGAGGAG 17

RESULT 495
US-10-156-306-521/c
; Sequence 521, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 521
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-521

Query Match      0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAA

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Db 17 AAAAAA
RESULT 496
US-10-156-306-524/c
; Sequence 524, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 524
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-524

Query Match      0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA
Db 17 TTTAAAAA
RESULT 497
US-09-808-602-46
; Sequence 46, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:32125243 S7
US-09-808-602-46

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1532 AGGCCTGCAGCGCCTGG 1548
Db 2 AGGCCTGCACACGCTGG 18

```

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RESULT 498
US-09-808-602-47/c
; Sequence 47, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:32125243 S8
US-09-808-602-47

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1532 AGGCCTGCAGCGCCTGG 1548
Db      17 AGGCCTGCAACGCCTGG 1

RESULT 499
US-09-994-177-7
; Sequence 7, Application US/09994177
; Publication No. US20030158379A1
; GENERAL INFORMATION:
; APPLICANT: CELESTE, ANTHONY J.
; APPLICANT: MURRAY, BETH L.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN-16
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/994,177
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/328,775
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, STEVEN R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5275-DIV
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 665-8260
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-994-177-7

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1479 CTCTGAGGGCGAGTGTC 1495
Db      1 CTGTGAGGGCGAGTGTC 17

RESULT 500
US-10-275-080A-7/c
; Sequence 7, Application US/10275080A
; Publication No. US20040053214A1
; GENERAL INFORMATION:
; APPLICANT: Schroder, Klaus Hobe
; APPLICANT: Schubler, Andrea
; APPLICANT: Koike, Katsuro
; TITLE OF INVENTION: Method of Diagnosing HBV Infection Stages
; FILE REFERENCE: 012627-033
; CURRENT APPLICATION NUMBER: US/10/275,080A
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/EP01/04918
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: EP 00 109 436.6
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-275-080A-7

Query Match          0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1735 CAAAAAIAAAAAAAAAA 1751
Db      17 CTAIAAAAAAAAAAIAA 1

RESULT 501
US-10-216-484-94
; Sequence 94, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
```

; FILE REFERENCE: ISIS5042
; CURRENT APPLICATION NUMBER: US/10/188,404
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/275,951
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/765,798
; PRIOR FILING DATE: 1997-04-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequencing
; OTHER INFORMATION: primer for a DNA encoding the heavy chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-10-216-484-94

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 TTAGGGGGGAAGAGGAA 37
||| ||||| ||||| |||||
Db 3 TTTGGGGGAAGAGGAA 19

RESULT 502

US-10-216-484-98/c
; Sequence 98, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 98
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequencing
; OTHER INFORMATION: primer for a DNA encoding the heavy chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-10-216-484-98

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 TTAGGGGGGAAGAGGAA 37
||| ||||| ||||| |||||
Db 18 TTTGGGGGAAGAGGAA 2

RESULT 503

US-10-188-404-49/c
; Sequence 49, Application US/10188404
; Publication No. US20030105286A1
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; APPLICANT: Coull, James M.
; APPLICANT: Kiely, John
; APPLICANT: Griffith, Michael
; TITLE OF INVENTION: Linked Peptide Nucleic Acids

; FILE REFERENCE: ISIS5042
; CURRENT APPLICATION NUMBER: US/10/188,404
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/275,951
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/765,798
; PRIOR FILING DATE: 1997-04-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(11)
; OTHER INFORMATION: Ethylene Glycol, Ethylene Glycol,
; OTHER INFORMATION: Ethylene Glycol Linkage
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: N is Pseudoisocytosine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: N is Pseudoisocytosine
US-10-188-404-49

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
||||| ||||| ||||| |||||
Db 19 AAAAAAAAAAAGAAAAA 2

RESULT 504

US-10-026-106E-3
; Sequence 3, Application US/10026106E
; Publication No. US20030158100A1
; GENERAL INFORMATION:
; APPLICANT: Renauld, Jean-Christophe
; APPLICANT: Fickensicher, Helmut
; APPLICANT: Dumoutier, Laure
; APPLICANT: Hor, Simon
; TITLE OF INVENTION: Isolated Cytokine Receptor LICR-2
; FILE REFERENCE: LUD 5752 NDH
; CURRENT APPLICATION NUMBER: US/10/026,106E
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-026-106E-3

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 155 AGGCCATGCGGGGCC 171
||||| ||||| ||||| |||||
Db 2 AGGCCATGCGGGGCC 18

RESULT 505

US-10-384-933-94
; Sequence 94, Application US/10384933
; Publication No. US20030170817A1

GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 94
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequencing
; OTHER INFORMATION: primer for a DNA encoding the heavy chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-10-384-933-94

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 TTAGGGGGAAGAGGAA 37
|||
Db 3 TTTGGGGGAAGAGGAA 19

RESULT 506

US-10-384-933-98/c
; Sequence 98, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 98
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequencing
; OTHER INFORMATION: primer for a DNA encoding the heavy chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-10-384-933-98

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 TTAGGGGGAAGAGGAA 37
|||
Db 18 TTTGGGGGAAGAGGAA 2

RESULT 507

US-09-790-264-26/c

; Sequence 26, Application US/09790264

US-10-380-596A-5/c
; Sequence 5, Application US/10380596A
; Publication No. US20040053275A1
; GENERAL INFORMATION:
; APPLICANT: Shafer, David A.
; TITLE OF INVENTION: Systems and Methods to Quantify and Amplify
; TITLE OF INVENTION: Both Signaling and Probes for cDNA Chips and
; TITLE OF INVENTION: Gene Expression Microarrays
; FILE REFERENCE: D6430
; CURRENT APPLICATION NUMBER: US/10/380,596A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/US01/07508
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: random_base
; LOCATION: 16...17
; OTHER INFORMATION: Modified poly-T primer; v=a, c, or g at position 16;
; OTHER INFORMATION: n=a, c, g, or t at position 17
US-10-380-596A-5

Query Match 0.9%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.9e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAGAAAAA 1750
:|||||
Db 16 BAAAAAAGAAAAA 1

RESULT 508

US-10-015-593-2/c
; Sequence 2, Application US/10015593
; Publication No. US20020090636A1
; GENERAL INFORMATION:
; APPLICANT: Kozian, Detlef
; APPLICANT: Reuner, Birgit
; TITLE OF INVENTION: Two-color differential display as a method for
; TITLE OF INVENTION: detecting regulated genes
; FILE REFERENCE: 2481-1635
; CURRENT APPLICATION NUMBER: US/10/015,593
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/390,324
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(17)
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: "V=A,C,G; N=A,C,G,T"
US-10-015-593-2

Query Match 0.9%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.9e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAGAAAAA 1750
:|||||
Db 16 BAAAAAAGAAAAA 1

```
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
US-09-790-264-26
```

```
Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 681 GGCACAGCCAGTGAGGGGCT 700
Db 20 GGCACAGGCCATGAGGGGCT 1
```

```
RESULT 510
US-09-823-634A-18
; Sequence 18, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: MISMATCHES USING RNASE H
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02025
US-09-823-634A-18
```

```
Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAATTATAAAAAA 20
```

```
RESULT 511
US-09-823-647B-18
; Sequence 18, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02025
US-09-823-647B-18
```

```
Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAATTATAAAAAA 20
```

```
RESULT 512
US-09-263-959-894
; Sequence 894, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 894:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```



```
; TOPOLOGY: linear
US-09-263-959-894

Query Match          0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1734 ACAAAAAAAAAAAAAAAAAAAAAA 1753
Db      1 AGAAAGAAAAAAAAAAGAAAAA 20

RESULT 513
US-09-964-261-36
; Sequence 36, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelles
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGJ-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-36

Query Match          0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      728 AGGCTTCTGGGCCCTCCCG 747
Db      1 AGGCGCCTGGGCCTCTCCCG 20

RESULT 514
US-09-916-369A-9/c
; Sequence 9, Application US/09916369A
; Publication No. US20020058802A1
; GENERAL INFORMATION:
; APPLICANT: Dellinger, Douglas J
; APPLICANT: Perbost, Michael GM
; APPLICANT: Caruthers, Marvin H
; APPLICANT: Betley, Jason R
; TITLE OF INVENTION: Synthesis of Polynucleotides Using Combined Oxidation/Deprotection
; FILE REFERENCE: 10003869-1
; CURRENT APPLICATION NUMBER: US/09/916,369A
; CURRENT FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: US 09/627,249
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-09-916-369A-9

Query Match          0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
```

```
; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      26 GGGGAAGAGGAAAAAAAAAAAA 45
Db      20 GGGGGGGGGGAAAAAAAAAAAA 1

RESULT 515
US-10-113-824-6
; Sequence 6, Application US/10113824
; Publication No. US20030050269A1
; GENERAL INFORMATION:
; APPLICANT: Escary, Jean-Louis
; TITLE OF INVENTION: NEW POLYNUCLEOTIDES AND POLYPEPTIDES OF THE ERYTHROPOIETIN GENE
; FILE REFERENCE: 021349/0037
; CURRENT APPLICATION NUMBER: US/10/113,824
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: FR 0104603
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/343163
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/345,440
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/358,598
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-113-824-6

Query Match          0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1644 GATCACTCTCCCTGACATCC 1663
Db      1 GATCATCTCCCTTTCATCC 20

RESULT 516
US-10-269-353-26/c
; Sequence 26, Application US/10269353
; Publication No. US20030104447A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI2000-5380MNICN1M
; CURRENT APPLICATION NUMBER: US/10/269,353
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 09/790,264
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
US-10-269-353-26

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 681 GGCACAGCCAGTGAGGGGCT 700
Db 20 GGCACAGGCCATGAGGGGCT 1

RESULT 517

US-10-001-863-7
; Sequence 7, Application US/10001863
; Publication No. US20030125272A1
; GENERAL INFORMATION:

; APPLICANT: James Karras
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF TOLL-LIKE RECEPTOR 4 EXPRESSION
; FILE REFERENCE: ISPH-0618
; CURRENT APPLICATION NUMBER: US/10/001,863
; CURRENT FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-863-7

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 101 GGTGAAGGCCAGAGGCTCGG 120
Db 1 GGTGAAGGGCTGAGGCTCCG 20

RESULT 518

US-10-367-470-18
; Sequence 18, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:

; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02025
US-10-367-470-18

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAATTATAAAAAA 20

RESULT 519

US-10-114-544-12
; Sequence 12, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-12

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1176 TGCCACGTGCTCCAGCCCA 1195
Db 1 TGCCACGTCTCTCCAGCCCA 20

RESULT 520

US-10-159-834-26/c
; Sequence 26, Application US/10159834
; Publication No. US20030228688A1
; GENERAL INFORMATION:

; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ISOPRENYLCYSTEINE CARBOXYL METHYLTRANSFERASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0299
; CURRENT APPLICATION NUMBER: US/10/159,834
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-834-26

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1436 ACATTGGCTGTACAAGTGC 1455
Db 20 ACTTTGGCTGGTACATGTGC 1

RESULT 521

US-10-388-329-9
; Sequence 9, Application US/10388329
; Publication No. US20040002093A1
; GENERAL INFORMATION:
; APPLICANT: SHI, LIANG
; TITLE OF INVENTION: NUCLEIC ACID DETECTION METHOD
; FILE REFERENCE: 109845.191US2; TMRI-020US
; CURRENT APPLICATION NUMBER: US/10/388,329
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: 60/364,230
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-388-329-9

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 862 GGAAGAGGAAGAGGAGCGCA 881
Db 1 GGAGGAGGAGGAGGAGGAGA 20
|||||

RESULT 522

US-10-349-143-6563
; Sequence 6563, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6563
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-12356 for SEQ 2629,
US-10-349-143-6563

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1014 TGTGTTGGGATGGGGCTG 1033
Db 1 TCTGATTGGGATGGGGCTG 20
|||||

RESULT 523

US-10-349-143-10187/c
; Sequence 10187, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10187
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-10438 for SEQ 2322, in compleme
US-10-349-143-10187

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 564 CCTGAAGCCAAATCCAGCCT 583
Db 20 CCTGAAGCCAAACACACCCT 1
|||||

RESULT 524

US-10-188-470-21/c
; Sequence 21, Application US/10188470
; Publication No. US20040005707A1
; GENERAL INFORMATION:
; APPLICANT: Scott Cooper
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA 5 EXPRESSION
; FILE REFERENCE: PTS-0024
; CURRENT APPLICATION NUMBER: US/10/188,470
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-470-21

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 808 AGAGAGCCAGGCCAGGGGC 827
Db 20 AGTGAGCCTGGGCCAGGAGC 1
|||||

RESULT 525

US-10-309-775A-72/c
; Sequence 72, Application US/10309775A
; Publication No. US20040006032A1
; GENERAL INFORMATION:

```
; APPLICANT: LOPEZ, Ricardo A.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 2901/OM327
; CURRENT APPLICATION NUMBER: US/10/309,775A
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: CA 2,388,049
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-309-775A-72

Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAACAAATGAAAA 1

RESULT 526
US-10-240-403-7/c
; Sequence 7, Application US/10240403
; Publication No. US20040092712A1
; GENERAL INFORMATION:
; APPLICANT: FURUSAKO, Shoji et al.
; TITLE OF INVENTION: TLR/CD14 BINDING INHIBITOR
; FILE REFERENCE: 1110-0311P
; CURRENT APPLICATION NUMBER: US/10/240,403
; CURRENT FILING DATE: 2003-05-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sense primer 1
US-10-240-403-7

Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1687 TGCTGCTTCTCTTCTTCTCCA 1706
Db 20 TGGTGCTTCTCTTCTCTCTCGA 1

RESULT 527
US-10-671-395-924/c
; Sequence 924, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 924
; LENGTH: 20
```

```
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-924

Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1730 GTTACAAAAAAAAAAAAAA 1749
Db 20 GTCTGCCAAAAAAAAAAAAAA 1

RESULT 528
US-10-671-395-938/c
; Sequence 938, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 938
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-938

Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 TTTACAAAAAAAAAAAAAA 1750
Db 20 TCTGCCAAAAAAAAAAAAAA 1

RESULT 529
US-09-504-231A-22/c
; Sequence 22, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 22
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-22

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 530
US-09-930-218-5/c
; Sequence 5, Application US/09930218
; Patent No. US20020034810A1
; GENERAL INFORMATION:
; APPLICANT: goldshmidt, orit
; APPLICANT: pecker, iris
; APPLICANT: vlodavsky, israel
; APPLICANT: israel, michal
; TITLE OF INVENTION: AVIAN AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE H
; TITLE OF INVENTION: HEPARANASE ACTIVITY
; FILE REFERENCE: 01/22335
; CURRENT APPLICATION NUMBER: US/09/930,218
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/666,390
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide
US-09-930-218-5

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 531
US-09-274-553D-22/c
; Sequence 22, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: tpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
```

```
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-22

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 532
US-09-776-874A-5/c
; Sequence 5, Application US/09776874A
; Patent No. US20020102560A1
; GENERAL INFORMATION:
; APPLICANT: pecker, iris
; APPLICANT: vlodavsky, israel
; APPLICANT: feinstein, elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22603
; CURRENT APPLICATION NUMBER: US/09/776,874A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-776-874A-5

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 533
US-09-955-410-17/c
; Sequence 17, Application US/09955410
; Patent No. US20020146718A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
; FILE REFERENCE: ISIS4800
; CURRENT APPLICATION NUMBER: US/09/955,410
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 09/686,114
```

; PRIOR FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020146718A1e1 Sequence
US-09-955-410-17

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 534

US-09-955-410-18
; Sequence 18, Application US/09955410
; Patent No. US20020146718A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
; FILE REFERENCE: ISIS4800
; CURRENT APPLICATION NUMBER: US/09/955,410
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 09/686,114
; PRIOR FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020146718A1e1 Sequence
US-09-955-410-18

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 535

US-09-805-296D-10/c
; Sequence 10, Application US/09805296D
; Patent No. US20020155989A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakmakhecheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1US
; CURRENT APPLICATION NUMBER: US/09/805,296D

; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: SyntheticConstruct
US-09-805-296D-10

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 536

US-09-983-210-19/c
; Sequence 19, Application US/09983210
; Patent No. US20020160383A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/983,210
; FILING DATE: 2001-OCT-23
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150156
; FILING DATE: 1994-APR-05
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-09-983-210-19

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAAAAAA 1

RESULT 537

```

US-09-983-210-20
; Sequence 20, Application US/09983210
; Patent No. US20020160383A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEOTIDE SEQUENCES IN THE DIAGNOSIS AND TREATMENT OF HIV INFECTION
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR HIV INFECTION
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 09/983,210
; FILING DATE: 2001-OCT-23
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150156
; FILING DATE: 1994-APR-05
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/0122
; FILING DATE: 22-MAY-1992
; US-09-983-210-20

```

```
Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. NO. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAAAAAA 15

RESULT 538

```

US-09-850-982B-4/c
; Sequence 4, Application US/09850982B
; Patent No. US20020166145A1
; GENERAL INFORMATION:
; APPLICANT: Nestec S.A.
; TITLE OF INVENTION: COFFEE MANNANASE
; FILE REFERENCE: 88265-4025
; CURRENT APPLICATION NUMBER: US/09/850,982B
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotides provided by Eurogentec (Parc Scientifi
; OTHER INFORMATION: que due Sart Tilman [Sart Tilman Scientific Park]-4102 Seraing-Be
; OTHER INFORMATION: lguim).
US-09-850-982B-4

```

```

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

	1736	1750
Qy	AAAAAAAAAAAAAA	AAAAAAAAAAAAAA
Db	15 AAAAAAAAAAAAAA	1 AAAAAAAAAAAAAA

RESULT 539

US-09-988-113-5/c
; Sequence 5, Application US/09988113
; Patent No. US20020168749A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodaysky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-988-113-5

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	1736	1750
Qy	AAAAAAAAAAAAAA	AAAAAAAAAAAA
D _b	15 AAAAAAAAAAAAAA	1 AAAAAAAAAAAAAA

RESULT 540

US-09-793-146-54/c
; Sequence 54, Application US/09793146
; Publication No. US20030203359A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13

```
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-54

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
   |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 541
US-09-793-146-55/c
; Sequence 55, Application US/09793146
; Publication No. US20030203359A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-55

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
   |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 542
US-10-433-005-4/c
; Sequence 4, Application US/10433005
; Publication No. US20040072289A1
; GENERAL INFORMATION:
; APPLICANT: Hwang, Inhwan
; APPLICANT: Piao, Hai Lan
; TITLE OF INVENTION: Novel Transcriptional Factor Enhancing the Resistance
; FILE REFERENCE: 012679-089
; CURRENT APPLICATION NUMBER: US/10/433,005
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: PCT/KR01/00364
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: KR 10-2000-72720
; PRIOR FILING DATE: 2000-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
```

```
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3' primer for construction of subtraction library of osmotic
; OTHER INFORMATION: stress genes
US-10-433-005-4

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
   |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 543
US-10-637-935-9/c
; Sequence 9, Application US/10637935
; Publication No. US20040033525A1
; GENERAL INFORMATION:
; APPLICANT: Monforte, Joseph A.
; APPLICANT: Becker, Christopher H.
; APPLICANT: Pollart, Daniel J.
; APPLICANT: Shaler, Thomas A.
; TITLE OF INVENTION: Releasable No. US20040033525A1volatile Mass-Label Molecules
; FILE REFERENCE: 24736-2057E
; CURRENT APPLICATION NUMBER: US/10/637,935
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 10/202,189
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 08/988,024
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: US 60/033,037
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: US 60/046,719
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-637-935-9

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
   |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 544
US-10-239-655A-4/c
; Sequence 4, Application US/10239655A
; Publication No. US20040048816A1
; GENERAL INFORMATION:
; APPLICANT: ZOHLNHOFFER, DIETLIND
; APPLICANT: BAUERLE, PATRICK
; APPLICANT: KLEIN, CHRISTOPH
; APPLICANT: NEUMANN, FRANZ-JOSEF
; TITLE OF INVENTION: RESTENOSIS TREATMENT
; FILE REFERENCE: 029976/0103
; CURRENT APPLICATION NUMBER: US/10/239,655A
; CURRENT FILING DATE: 2003-02-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03312
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00106468.2
```

```
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-239-655A-4
```

```
Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1750
          |||||
Db      15 AAAAAAAAAAAAAA 1
```

RESULT 545

```
US-10-291-808-68/c
; Sequence 68, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-68
```

```
Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1750
          |||||
Db      15 AAAAAAAAAAAAAA 1
```

RESULT 546

```
US-10-208-357-21
; Sequence 21, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
```

```
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-21
```

```
Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1750
          |||||
Db      1 AAAAAAAAAAAAAA 15
```

RESULT 547

```
US-10-176-055-9
; Sequence 9, Application US/10176055
; Publication No. US20030013109A1
; GENERAL INFORMATION:
; APPLICANT: Evident Technologies
; TITLE OF INVENTION: Hairpin Sensors Using Quenchable Fluorescing Agents
; FILE REFERENCE: 11739/26
; CURRENT APPLICATION NUMBER: US/10/176,055
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,460
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Target sequence
; OTHER INFORMATION: Target sequence that is desired to be detected and
; OTHER INFORMATION: that has a nucleotide sequence that is
; OTHER INFORMATION: complementary to the sequence of complementary
; OTHER INFORMATION: probe of hairpin loop assembly
US-10-176-055-9
```

```
Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1750
          |||||
Db      1 AAAAAAAAAAAAAA 15
```

RESULT 548

```
US-10-202-189-9/c
; Sequence 9, Application US/10202189
; Publication No. US20030022225A1
; GENERAL INFORMATION:
; APPLICANT: Monforte, Joseph A.
; APPLICANT: Becker, Christopher H.
; APPLICANT: Pollart, Daniel J.
; APPLICANT: Shaler, Thomas A.
; TITLE OF INVENTION: Releasable No. US20030022225A1volatile Mass-Label Molecules
; FILE REFERENCE: 24736-2057D
; CURRENT APPLICATION NUMBER: US/10/202,189
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER:
; PRIOR APPLICATION NUMBER: US 08/988,024
```

```

; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: US 60/033,037
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: US 60/046,719
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-202-189-9

```

```
Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1736	AAAAAAAAAAAAAAA	1750
Db	15	AAAAAAAAAAAAAAA	1

RESULT 549

US-10-072-975-10/c
; Sequence 10, Application US/10072975
; Publication No. US20030059789A1
; GENERAL INFORMATION:

```

, APPLICANT: Active Motif
, APPLICANT: Efimov, Vladimir
, APPLICANT: Fernandez, Joseph
, APPLICANT: Archdeacon, Dorothy
, APPLICANT: Archdeacon, John
, APPLICANT: Chakhmakcheau, Oksana
, APPLICANT: Buryakova, Alla
, APPLICANT: Choob, Mikhail
, APPLICANT: Hondorp, Kyle
, TITLE OF INVENTION: OLIGONUCLEOTID
, FILE REFERENCE: AM102.P.1.1.US
, CURRENT APPLICATION NUMBER: US/10/
, CURRENT FILING DATE: 2002-02-09
, PRIOR APPLICATION NUMBER: US 60/18
, PRIOR FILING DATE: 2000-03-14
, PRIOR APPLICATION NUMBER: US 60/25
, PRIOR FILING DATE: 2000-11-30
, PRIOR APPLICATION NUMBER: 09/805,2
, PRIOR FILING DATE: 2001-03-13
, PRIOR APPLICATION NUMBER: PCT/US01
, PRIOR FILING DATE: 2001-03-23

```

```
Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
```

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 550
US-10-227-001-23/c

```

; Sequence 23, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
; APPLICANT: Dempcy, Robert O.
; APPLICANT: Afonina, Irina Aleksandrovna
; APPLICANT: Vermeulen, Nicolaas M.J.
; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: Hybridization-Triggered Fluorescent
; TITLE OF INVENTION: Detection of Nucleic Acids
; FILE REFERENCE: 17682A-004210US
; CURRENT APPLICATION NUMBER: US/10/227,001
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 09/428,236
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: R2 (ODN) of fluorophore-MGB-ODN
; OTHER INFORMATION: conjugate
; US-10-227-001-23

```

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 551

```

US-10-051-436-10/c
; Sequence 10, Application US/10051436
; Publication No. US20030138045A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakmakhcheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGS
; FILE REFERENCE: AM102.P.LUS
; CURRENT APPLICATION NUMBER: US/10/051,436
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: SyntheticConstruct
US-10-051-436-10

```

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels

Qy 1736 AAAAAAAAAAAAAA 1750

Db 15 AAAAAAAAAAAAAA 1

RESULT 552

US-10-341-582-5/c

; Sequence 5, Application US/10341582

; Publication No. US20030161823A1

; GENERAL INFORMATION:

; APPLICANT: Neta Ilan

; APPLICANT: Israel Vlodavsky

; APPLICANT: Oron Yacoby-Zeevi

; APPLICANT: Iris Pecker

; TITLE OF INVENTION: THERAPEUTIC AND COSMETIC USES OF HEPARANASES

; FILE REFERENCE: 25449

; CURRENT APPLICATION NUMBER: US/10/341,582

; CURRENT FILING DATE: 2003-01-14

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide

US-10-341-582-5

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

Db 15 AAAAAAAAAAAAAA 1

RESULT 553

US-10-106-749-1/c

; Sequence 1, Application US/10106749

; Publication No. US20030165879A1

; GENERAL INFORMATION:

; APPLICANT: Inscent, Inc.

; APPLICANT: Woods, Daniel

; APPLICANT: Dimitrios, Spiros

; TITLE OF INVENTION: EFFICIENT METHODS FOR ISOLATING FUNCTIONAL G-PROTEIN COUPLED RECE

; TITLE OF INVENTION: AND IDENTIFYING ACTIVE EFFECTORS AND EFFICEINT METHODS TO ISOLAT

; TITLE OF INVENTION: INVOLVED IN OLFACTION AND IDENTIFYING ACTIVE EFFECTORS

; FILE REFERENCE: INS-00101.P.1.1

; CURRENT APPLICATION NUMBER: US/10/106,749

; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 60/279,168

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 60/353,392

; PRIOR FILING DATE: 2002-01-31

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-106-749-1

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

Db 15 AAAAAAAAAAAAAA 1

RESULT 554

US-10-106-749-5/c

; Sequence 5, Application US/10106749

; Publication No. US20030165879A1

; GENERAL INFORMATION:

; APPLICANT: Inscent, Inc.

; APPLICANT: Woods, Daniel

; APPLICANT: Dimitrios, Spiros

; TITLE OF INVENTION: EFFICIENT METHODS FOR ISOLATING FUNCTIONAL G-PROTEIN COUPLED RECEI

; TITLE OF INVENTION: AND IDENTIFYING ACTIVE EFFECTORS AND EFFICEINT METHODS TO ISOLATI

; TITLE OF INVENTION: INVOLVED IN OLFACTION AND IDENTIFYING ACTIVE EFFECTORS

; FILE REFERENCE: INS-00101.P.1.1

; CURRENT APPLICATION NUMBER: US/10/106,749

; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 60/279,168

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 60/353,392

; PRIOR FILING DATE: 2002-01-31

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-106-749-5

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

Db 15 AAAAAAAAAAAAAA 1

RESULT 555

US-10-384-451-5/c

; Sequence 5, Application US/10384451

; Publication No. US20030170860A1

; GENERAL INFORMATION:

; APPLICANT: Pecker, Iris

; APPLICANT: Vlodavsky, Israel

; APPLICANT: Feinstein, Elena

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY I

; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

; FILE REFERENCE: 25718

; CURRENT APPLICATION NUMBER: US/10/384,451

; CURRENT FILING DATE: 2003-03-10

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide

US-10-384-451-5

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

Db 15 AAAAAAAAAAAAAA 1

RESULT 556

US-10-269-031A-54/c

; Sequence 54, Application US/10269031A

; Publication No. US20030175749A1

; GENERAL INFORMATION:


```
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-352-704-16

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1750
Db      1 AAAAAAAAAAAAAAAAAA 15

RESULT 559
US-10-154-890-17/c
; Sequence 17, Application US/10154890
; Publication No. US20030180734A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/10/154,890
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US/08/108,591
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030180734A1el Sequence
US-10-154-890-17

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAAAAAA 1

RESULT 560
US-10-154-890-18
; Sequence 18, Application US/10154890
; Publication No. US20030180734A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/10/154,890
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US/08/108,591
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030180734A1el Sequence
US-10-154-890-18

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
```

```
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1750
Db      1 AAAAAAAAAAAAAAAAAA 15

RESULT 561
US-10-431-438-5/c
; Sequence 5, Application US/10431438
; Publication No. US20030180788A1
; GENERAL INFORMATION:
; APPLICANT: goldshmidt, orit
; APPLICANT: pecker, iris
; APPLICANT: vlodavsky, israel
; APPLICANT: israel, michal
; TITLE OF INVENTION: AVIAN AND REPTILE DERIVED POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HU
; FILE REFERENCE: 26013
; CURRENT APPLICATION NUMBER: US/10/431,438
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide
US-10-431-438-5

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAAAAAA 1

RESULT 562
US-10-091-231-2/c
; Sequence 2, Application US/10091231
; Publication No. US20030181712A1
; GENERAL INFORMATION:
; APPLICANT: NELSON, Jeffrey S.
; TITLE OF INVENTION: REAGENTS FOR OLIGONUCLEOTIDE CLEAVAGE AND DEPROTECTION
; FILE REFERENCE: 4688US
; CURRENT APPLICATION NUMBER: US/10/091,231
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/274,309
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-10-091-231-2

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAAAAAA 1

RESULT 563
US-10-384-450-5/c
```

```
; Sequence 5, Application US/10384450
; Publication No. US20030190737A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 25717
; CURRENT APPLICATION NUMBER: US/10/384,450
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-384-450-5

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 564
US-10-371-218A-5/c
; Sequence 5, Application US/10371218A
; Publication No. US20030217375A1
; GENERAL INFORMATION:
; APPLICANT: Zcharia, Eyal
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Metzger, Shula
; APPLICANT: Pecker, Iris
; APPLICANT: Ilan, Neta
; APPLICANT: Chajek-Shaul, Tova
; APPLICANT: Goldshmidt, Orit
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING HEPARANASE AND USES THEREOF
; FILE REFERENCE: 25783
; CURRENT APPLICATION NUMBER: US/10/371,218A
; CURRENT FILING DATE: 2003-07-01
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-371-218A-5

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 565
US-10-045-674-622/c
; Sequence 622, Application US/10045674
; Publication No. US2003023233A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
```

```
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: US/10/045,674
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 09/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: nucleotide sequence
US-10-045-674-622

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 566
US-10-456-573-5/c
; Sequence 5, Application US/10456573
; Publication No. US20030236215A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 25677
; CURRENT APPLICATION NUMBER: US/10/456,573
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US 09/435,739
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: US 09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-10-456-573-5

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
```

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FEATURE:
; OTHER INFORMATION: Sample oligo
US-10-344-092-2

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
   |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 569
US-10-785-116-5/c
; Sequence 5, Application US/10785116
; Publication No. US20040142427A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 27674
; CURRENT APPLICATION NUMBER: US/10/785,116
; CURRENT FILING DATE: 2004-02-25
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-785-116-5

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
   |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 570
US-09-739-928-3/c
; Sequence 3, Application US/09739928
; Patent No. US20020052482A1
; GENERAL INFORMATION:
; APPLICANT: Kutuyavin, Igor V.
;               Lukhtanov, Eugeny A.
;               Gamber, Howard B.
;               Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
;               Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod base= OTHER
; /note= "N = thymidine modified by 6-aminohexanoic acid
; (-NH(CH-2)-6COOH)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-739-928-3

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 571
US-09-739-928-4/c
; Sequence 4, Application US/09739928
; Patent No. US20020052482A1
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamper, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
```

```
;
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod base= OTHER
; /note= "N = thymidine modified by minor groove binder moiety
; represented by X, where m = one
; 4-amino-N-methylpyrrol-2-carboxylic acid residue"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-739-928-4

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 572
US-09-739-928-5/c
; Sequence 5, Application US/09739928
; Patent No. US20020052482A1
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamper, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
```

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod_base= OTHER
; /note= "N = thymidine modified by minor groove binder moiety
; represented by X, where m = two
; 4-amino-N-methylpyrrol-2-carboxylic acid residues"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-739-928-5

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 573
US-09-739-928-6/c
; Sequence 6, Application US/09739928
; Patent No. US20020052482A1
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamber, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

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;
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod_base= OTHER
; /note= "N = thymidine modified by minor groove binder moiety
; represented by X, where m = three
; 4-amino-N-methylpyrrol-2-carboxylic acid residues"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-739-928-6

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 574
US-09-739-928-7/c
; Sequence 7, Application US/09739928
; Patent No. US20020052482A1
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamber, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

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```
;
;
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod base= OTHER
; /note= "N = thymidine modified by minor groove binder moiety
; represented by X, where m = four
; 4-amino-N-methylpyrrol-2-carboxylic acid residues"
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-739-928-7

Query Match      0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 575
US-09-739-928-8/c
; Sequence 8, Application US/09739928
; Patent No. US20020052482A1
; GENERAL INFORMATION:
; APPLICANT: Kutuyavin, Igor V.
; Lukhtanov, Eugeny A.
; Gamper, Howard B.
; Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod base= OTHER
; /note= "N = thymidine modified by minor groove binder moiety
```

```
;
;
; represented by X, where m = five
; 4-amino-N-methylpyrrol-2-carboxylic acid residues"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-739-928-8

Query Match      0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 576
US-10-227-001-20/c
; Sequence 20, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
; APPLICANT: Dempcy, Robert O.
; APPLICANT: Afonina, Irina Aleksandrovna
; APPLICANT: Vermeulen, Nicolaas M.J.
; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: Hybridization-Triggered Fluorescent
; DETECTION OF NUCLEIC ACIDS
; FILE REFERENCE: 17682A-004210US
; CURRENT APPLICATION NUMBER: US/10/227,001
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 09/428,236
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polydT-MGB-
; OTHER INFORMATION: (2-dimethylaminonaphthalene-6-sulfonamide)
; OTHER INFORMATION: conjugate
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: n = thymine modified by MGB-
; OTHER INFORMATION: (2-dimethylaminonaphthalene-6-sulfonamide)
; US-10-227-001-20

Query Match      0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 577
US-10-164-915-2
; Sequence 2, Application US/10164915
; Publication No. US20030148391A1
; GENERAL INFORMATION:
; APPLICANT: Salafsky, Joshua S.
; TITLE OF INVENTION: Method Using a Surface-Selective No. US20030148391A1linear Optical
; DETECTION OF INTERACTIONS INVOLVING A CONFORMATIONAL CHANGE
; FILE REFERENCE: 11100-035-999
; CURRENT APPLICATION NUMBER: US/10/164,915
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/253,862
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/260,249
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/265,775
; PRIOR FILING DATE: 2001-02-01
```


; PRIOR APPLICATION NUMBER: 60/278,941
; PRIOR FILING DATE: 2001-01-27
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2

; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide structure for
; OTHER INFORMATION: molecular beacon
US-10-164-915-2

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 2 AAAAAAAAAAAAAA 16

RESULT 578

US-09-090-672B-105/c
; Sequence 105, Application US/09090672B
; Patent No. US20020068707A1

GENERAL INFORMATION:

; APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
; APPLICANT: Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
; APPLICANT: Shigemasa; Takei, Masami
; TITLE OF INVENTION: Iga Nephropathy-Related Genes
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112-3801

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC

; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997

; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:

; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200

; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA

US-09-090-672B-105

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||

Db 16 AAAAAAAAAAAAAA 2

RESULT 579

US-09-090-672B-107/c
; Sequence 107, Application US/09090672B
; Patent No. US20020068707A1

GENERAL INFORMATION:

; APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
; APPLICANT: Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
; APPLICANT: Shigemasa; Takei, Masami
; TITLE OF INVENTION: Iga Nephropathy-Related Genes
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112-3801

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC

; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997

; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:

; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200

; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA

US-09-090-672B-107

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||

Db 16 AAAAAAAAAAAAAA 2

RESULT 580

US-09-848-754A-35
; Sequence 35, Application US/09848754A
; Publication No. US20030073207A1

GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

; FILE REFERENCE: MEHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 17

Qy 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | |
Db 16 AAAAAAAAAAAAAA 2

RESULT 585
US-10-380-254-4/c
; Sequence 4, Application US/10380254
; Publication No. US20040038252A1
; GENERAL INFORMATION:
; APPLICANT: Sugita et al.
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
; FILE REFERENCE: 6235-64773
; CURRENT APPLICATION NUMBER: US/10/380,254
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08246
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: JP 2000-291318
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:an artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-380-254-4

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | |
Db 16 AAAAAAAAAAAAAA 2

RESULT 586
US-10-398-885A-2/c
; Sequence 2, Application US/10398885A
; Publication No. US20040053282A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; APPLICANT: Takahasi, Eiki
; TITLE OF INVENTION: Method of Testing For Allergic Diseases
; FILE REFERENCE: SHIMIZU-07907
; CURRENT APPLICATION NUMBER: US/10/398,885A
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08937
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-885A-2

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | |
Db 16 AAAAAAAAAAAAAA 2

RESULT 587
US-10-398-885A-3/c
; Sequence 3, Application US/10398885A
; Publication No. US20040053282A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; APPLICANT: Takahasi, Eiki
; TITLE OF INVENTION: Method of Testing For Allergic Diseases
; FILE REFERENCE: SHIMIZU-07907
; CURRENT APPLICATION NUMBER: US/10/398,885A
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08937
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-885A-3

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | |
Db 16 AAAAAAAAAAAAAA 2

RESULT 588
US-10-398-877-18/c
; Sequence 18, Application US/10398877
; Publication No. US20040058351A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: Method of Testing for Allergic Diseases
; FILE REFERENCE: SHIMIZU-07906
; CURRENT APPLICATION NUMBER: US/10/398,877
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08574
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-877-18

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 589

US-10-398-877-19/c
; Sequence 19, Application US/10398877
; Publication No. US20040058351A1
; GENERAL INFORMATION:
; APPLICANT: Sugita, Yuji
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Ogawa, Kaoru
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Obayashi, Masaya
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: Method of Testing for Allergic Diseases
; FILE REFERENCE: SHIMIZU-07906
; CURRENT APPLICATION NUMBER: US/10/398,877
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08574
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: JP 2000-314093
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-398-877-19

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 590

US-10-291-808-63/c
; Sequence 63, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-63

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 591

US-10-408-025-5/c
; Sequence 5, Application US/10408025
; Publication No. US20030224423A1
; GENERAL INFORMATION:
; APPLICANT: Matsumoto, Yoshiko
; APPLICANT: Imai, Yukiho
; APPLICANT: Yoshida, Nei
; APPLICANT: Oshida, Tadashi
; APPLICANT: Sugita, Yuji
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: Method of Testing for Allergic Diseases
; FILE REFERENCE: SHIMIZU-07914
; CURRENT APPLICATION NUMBER: US/10/408,025
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 2002-100908
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: PCT/JP03/02047
; PRIOR FILING DATE: 2003-02-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-408-025-5

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 592

US-10-061-201-1503/c
; Sequence 1503, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/328,205
 ; PRIOR FILING DATE: 2001-10-10
 ; NUMBER OF SEQ ID NOS: 4162
 ; SOFTWARE: Aeomica Sequence Listing Engine
 ; SEQ ID NO 1503
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-061-201-1503

Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 897 GCCCCTGAGCCAGCC 911
 Db 17 GCCCCTGAGCCAGCC 3

RESULT 593
 US-10-061-201-1504/c
 ; Sequence 1504, Application US/10061201
 ; Publication No. US20030166229A1
 ; GENERAL INFORMATION:

; APPLICANT: Shannon, Mark
 ; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
 ; FILE REFERENCE: PB0178
 ; CURRENT APPLICATION NUMBER: US/10/061,201
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/328,205
 ; PRIOR FILING DATE: 2001-10-10
 ; NUMBER OF SEQ ID NOS: 4162
 ; SOFTWARE: Aeomica Sequence Listing Engine
 ; SEQ ID NO 1504
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-061-201-1504

Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 897 GCCCCTGAGCCAGCC 911
 Db 16 GCCCCTGAGCCAGCC 2

RESULT 594
 US-10-061-201-1505/c
 ; Sequence 1505, Application US/10061201
 ; Publication No. US20030166229A1
 ; GENERAL INFORMATION:

; APPLICANT: Shannon, Mark
 ; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
 ; FILE REFERENCE: PB0178
 ; CURRENT APPLICATION NUMBER: US/10/061,201
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/328,205
 ; PRIOR FILING DATE: 2001-10-10
 ; NUMBER OF SEQ ID NOS: 4162
 ; SOFTWARE: Aeomica Sequence Listing Engine
 ; SEQ ID NO 1505
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-061-201-1505

Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 897 GCCCCTGAGCCAGCC 911
 Db 15 GCCCCTGAGCCAGCC 1

RESULT 595
 US-10-309-152A-3/c
 ; Sequence 3, Application US/10309152A
 ; Publication No. US20030175759A1
 ; GENERAL INFORMATION:

; APPLICANT: Hitachi LTD.
 ; TITLE OF INVENTION: A method for prediction of genes and a method for providing a list
 ; FILE REFERENCE: H02001031A
 ; CURRENT APPLICATION NUMBER: US/10/309,152A
 ; CURRENT FILING DATE: 2002-12-04
 ; PRIOR APPLICATION NUMBER: JP 2002-047297
 ; PRIOR FILING DATE: 2002-02-25
 ; NUMBER OF SEQ ID NOS: 10
 ; SEQ ID NO 3
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:

; OTHER INFORMATION: Oligo-d(T) primer by Nippon Flour Mills
 US-10-309-152A-3

Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750

Db 16 AAAAAAAAAAAAAAA 2
|||||

RESULT 596
US-10-220-373-7/c
; Sequence 7, Application US/10220373
; Publication No. US20030180743A1
; GENERAL INFORMATION:
; APPLICANT: NAGASU, Takeshi
; APPLICANT: OSHIDA, Tadashi
; APPLICANT: OBAYASHI, Izumi
; APPLICANT: MATSUI, Keiko
; APPLICANT: SAITO, Hirohisa
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
; FILE REFERENCE: SHZ-010US
; CURRENT APPLICATION NUMBER: US/10/220,373
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-61832
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificially
; OTHER INFORMATION: Synthesized Primer Sequence
US-10-220-373-7

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1750
|||||

Db 16 AAAAAAAAAAAAAAA 2

RESULT 597
US-10-220-373-8/c
; Sequence 8, Application US/10220373
; Publication No. US20030180743A1
; GENERAL INFORMATION:
; APPLICANT: NAGASU, Takeshi
; APPLICANT: OSHIDA, Tadashi
; APPLICANT: OBAYASHI, Izumi
; APPLICANT: MATSUI, Keiko
; APPLICANT: SAITO, Hirohisa
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE
; FILE REFERENCE: SHZ-010US
; CURRENT APPLICATION NUMBER: US/10/220,373
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-61832
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificially
; OTHER INFORMATION: Synthesized Primer Sequence
US-10-220-373-8

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1750
|||||

Db 16 AAAAAAAAAAAAAAA 2

RESULT 598
US-10-380-255-6/c
; Sequence 6, Application US/10380255
; Publication No. US20040023263A1
; GENERAL INFORMATION:
; APPLICANT: Sugita et al.
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
; FILE REFERENCE: 6235-64935
; CURRENT APPLICATION NUMBER: US/10/380,255
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08247
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: JP 2000-293021
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:an artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-380-255-6

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1750
|||||

Db 16 AAAAAAAAAAAAAAA 2

RESULT 599
US-10-380-255-7/c
; Sequence 7, Application US/10380255
; Publication No. US20040023263A1
; GENERAL INFORMATION:
; APPLICANT: Sugita et al.
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES
; FILE REFERENCE: 6235-64935
; CURRENT APPLICATION NUMBER: US/10/380,255
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08247
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: JP 2000-293021
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:an artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-380-255-7

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1750
|||||

Db 16 AAAAAAAAAAAAAAA 2

RESULT 600
US-10-138-674-1073/c


```
; Sequence 1073, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1073

Query Match          0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAAAAAA 3

RESULT 601
US-10-138-674-1076/c
; Sequence 1076, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1076

Query Match          0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 602
US-10-287-949A-1073/c
; Sequence 1073, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
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; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1073
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1073

Query Match          0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAAAAAA 3

RESULT 603
US-10-287-949A-1076/c
; Sequence 1076, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1076

Query Match          0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 604
US-09-904-744-1
; Sequence 1, Application US/09904744
; Patent No. US20020150905A1
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
; FILE REFERENCE: B-73
; CURRENT APPLICATION NUMBER: US/09/904,744
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/437076
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/107828
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
```

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-09-904-744-1

Query Match          0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
    |||||
Db 4 AAAAAAAAAAAAAA 18

RESULT 605
US-09-904-744-2/c
; Sequence 2, Application US/09904744
; Patent No. US20020150905A1
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
; TITLE OF INVENTION: dendrimers in a signal amplification system
; FILE REFERENCE: B-73
; CURRENT APPLICATION NUMBER: US/09/904,744
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/437076
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/107828
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-09-904-744-2

Query Match          0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
    |||||
Db 18 AAAAAAAAAAAAAA 4

RESULT 606
US-09-775-479-8
; Sequence 8, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: LECLERC, Guy
; APPLICANT: MARTEL, R.mi
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 12168-1US-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 18
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-8

Query Match          0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
    |||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 607
US-10-618-540-3/c
; Sequence 3, Application US/10618540
; Publication No. US20040052771A1
; GENERAL INFORMATION:
; APPLICANT: Lim, Sai K.
; TITLE OF INVENTION: Hemangioblast Progenitor Cells
; FILE REFERENCE: 4810-66314
; CURRENT APPLICATION NUMBER: US/10/618,540
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: 10/197,189
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/426,789
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-618-540-3

Query Match          0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GAGGAAGAGGAGCG 880
    |||||
Db 16 GAGGAAGAGGAGCG 2

RESULT 608
US-10-164-915-1
; Sequence 1, Application US/10164915
; Publication No. US20030148391A1
; GENERAL INFORMATION:
; APPLICANT: Salafsky, Joshua S.
; TITLE OF INVENTION: Method Using a Surface-Selective No. US20030148391A1linear Optical
; TITLE OF INVENTION: for Detection of Interactions Involving a Conformational Change
; FILE REFERENCE: 11100-035-999
; CURRENT APPLICATION NUMBER: US/10/164,915
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/253,862
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/260,249
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/265,775
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/278,941
; PRIOR FILING DATE: 2001-01-27
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide structure for
; OTHER INFORMATION: molecular beacon
```

US-10-164-915-1

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 609

US-10-167-241-11/c
; Sequence 11, Application US/10167241
; Publication No. US20030165895A1
; GENERAL INFORMATION:
; APPLICANT: CZERNIAK, BOGDAN
; APPLICANT: JOHNSTON, DENNIS
; TITLE OF INVENTION: METHODS OF DETECTING, DIAGNOSING AND TREATING CANCER
; TITLE OF INVENTION: AND IDENTIFYING NEOPLASTIC PROGRESSION
; FILE REFERENCE: UTSC:712US
; CURRENT APPLICATION NUMBER: US/10/167,241
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/297,813
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-167-241-11

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 857 CTGCAGGAAGAGGAA 871
Db 15 CTGCAGGAAGAGGAA 1

RESULT 610

US-10-407-078-51
; Sequence 51, Application US/10407078
; Publication No. US20030195154A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Kenneth
; APPLICANT: Xiong, Fei
; TITLE OF INVENTION: Use of Transthyretin Peptide/Protein Fusions to Increase the Serum
; FILE REFERENCE: A-813A
; CURRENT APPLICATION NUMBER: US/10/407,078
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: A-813
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-407-078-51

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 GGGGGAAGAGGAAA 39
Db 1 GGGGGAAGAGGAAA 15

RESULT 611
US-10-380-931-116/c
; Sequence 116, Application US/10380931
; Publication No. US20030215944A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTSP-0187
; CURRENT APPLICATION NUMBER: US/10/380,931
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/676,610
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-931-116

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 907 CAGCCTCCAGAGGAT 921
Db 15 CAGCCTCCAGAGGAT 1

RESULT 612

US-10-374-686-2
; Sequence 2, Application US/10374686
; Publication No. US20040002089A1
; GENERAL INFORMATION:
; APPLICANT: Dubertret, Benoit
; APPLICANT: Calame, Michel
; APPLICANT: Libchaber, Albert
; TITLE OF INVENTION: Methods Employing Fluorescent Quenching
; TITLE OF INVENTION: by Metal Surfaces
; FILE REFERENCE: 600-1-260PCTUS
; CURRENT APPLICATION NUMBER: US/10/374,686
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: PCT/US01/41941
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/228728
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/280350
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-374-686-2

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 613
US-10-212-993-65/c
; Sequence 65, Application US/10212993
; Publication No. US20040023385A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF REQUIEM EXPRESSION
; FILE REFERENCE: PTS-0031
; CURRENT APPLICATION NUMBER: US/10/212,993
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-212-993-65

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 TTCTTTTCTGGAGTC 73
|||||
Db 19 TTCTTTTCTGGAGTC 5

RESULT 614
US-09-057-351-35/c
; Sequence 35, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-35
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGG 1036
|||||
Db 18 TTGGGGTTGGGTTGGG 1

RESULT 615
US-09-057-351-36/c
; Sequence 36, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-36

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1017 GGTGGGATGGGGCTGG 1034
Db 18 GGTGGGTTGGGGTTGG 1

RESULT 616
US-09-947-659-9
; Sequence 9, Application US/09947659
; Patent No. US20020114797A1
; GENERAL INFORMATION:
; APPLICANT: CHABOT, Benoit
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR MODULATING THE LENGTH OF
; FILE REFERENCE: 13024.2
; CURRENT APPLICATION NUMBER: US/09/947,659
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US 09/214,178
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/CA97/00471
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/020,956
; PRIOR FILING DATE: 1996-07-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-947-659-9

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGG 1036
Db 1 TTGGGGTTGGGGTTGGG 18

RESULT 617
US-09-263-959-716/c
; Sequence 716, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-716

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAGAGAAA 1

RESULT 618
US-10-388-578-28/c
; Sequence 28, Application US/10388578
; Publication No. US20030224411A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Stanton, Lawrence
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; APPLICANT: Shelton, Dawne
; TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of Hun
; TITLE OF INVENTION: Embryonic Stem Cells
; FILE REFERENCE: 135/001
; CURRENT APPLICATION NUMBER: US/10/388,578
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Custom
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-578-28

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 171 CACCTGGCTGCCCCCGAA 188
Db 18 CACCTGGCTGCCCCAAGAA 1

RESULT 619
US-10-188-404-32/c
; Sequence 32, Application US/10188404
; Publication No. US20030105286A1
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; APPLICANT: Coull, James M.
; APPLICANT: Kiely, John
; APPLICANT: Griffith, Michael
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS5042
; CURRENT APPLICATION NUMBER: US/10/188,404
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/275,951

;
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/765,798
; PRIOR FILING DATE: 1997-04-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(10)
; OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
; OTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
US-10-188-404-32

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
||| ||||| |||||
Db 18 AAAAAAAAAAACAAAA 1

RESULT 620

US-10-188-404-33/c
; Sequence 33, Application US/10188404
; Publication No. US20030105286A1
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; APPLICANT: Coull, James M.
; APPLICANT: Kiely, John
; APPLICANT: Griffith, Michael
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS5042
; CURRENT APPLICATION NUMBER: US/10/188,404
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/275,951
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/765,798
; PRIOR FILING DATE: 1997-04-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(10)
; OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
; OTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
US-10-188-404-33

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
||| ||||| |||||
Db 18 AAAAAAAAAAACAAAA 1

RESULT 621

US-10-314-405-44
; Sequence 44, Application US/10314405
; Publication No. US20030108940A1
; GENERAL INFORMATION:
; APPLICANT: Hidetoshi, Inoko
; APPLICANT: Gen, Tamiya
; APPLICANT: Yasunari, Matsuzaka
; TITLE OF INVENTION: NOVEL POLYMORPHIC MICROSATELLITE MARKERS IN THE HUMAN MHC CLASS I
; FILE REFERENCE: 06501-069001
; CURRENT APPLICATION NUMBER: US/10/314,405
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/713,616
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-314-405-44

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 863 GAAGAGGAAGAGGCG 880
||| ||||| |||||
Db 1 GAGGAGGAAGAGGAG 18

RESULT 622

US-10-359-935-35/c
; Sequence 35, Application US/10359935
; Publication No. US20030153076A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; Feng, Junli
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-359-935-35

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGCTGGG 1036
Db 18 TTGGGGTTGGGTTGGG 1

RESULT 623
US-10-359-935-36/c
Sequence 36, Application US/10359935
Publication No. US20030153076A1
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
Feng, Junli
Funk, Walter
Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/359,935
FILING DATE: 07-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-359-935-36

Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1017 GGTGGGATGGGCTGG 1034
Db 18 GGTGGGTTGGGTTGG 1

RESULT 624
US-10-178-325-169
Sequence 169, Application US/10178325
Publication No. US20030199467A1
GENERAL INFORMATION:
APPLICANT: Roberts, M. Luisa
Cowser, Lex M.
TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0404
CURRENT APPLICATION NUMBER: US/10/178,325
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US/09/387,341
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 09/156,424
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 09/156,979
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 09/156,807
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 09/161,015
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 169
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-178-325-169

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1507 CCGCTGGATGGGCATC 1524
Db 1 CAGCAGGATGGGCATC 18

RESULT 625
US-10-089-887-25/c
Sequence 25, Application US/10089887
Publication No. US20030219740A1
GENERAL INFORMATION:
APPLICANT: Bayer Corporation et al.
TITLE OF INVENTION: DNA Sequences Isolated from Human Colonic Epithelial Cells
FILE REFERENCE: 1657/1020
CURRENT APPLICATION NUMBER: US/10/089,887
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US 60/147,933
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-089-887-25

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1617 CTCAGTCCAGTTCAT 1634
Db 18 CTCAGTCCATCCCAT 1

RESULT 626

US-10-455-229-28
; Sequence 28, Application US/10455229
; Publication No. US20040016030A1
; GENERAL INFORMATION:
; APPLICANT: LOWE, BRENDA A.
; APPLICANT: CHOMET, PAUL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF MAIZE LINES
; FILE OF INVENTION: WITH INCREASED TRANSFORMABILITY
; FILE REFERENCE: DEKM:195US
; CURRENT APPLICATION NUMBER: US/10/455,229
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 60/386,522
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-455-229-28

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1649 CTCCTCCCTGACATCCACC 1666
Db 1 CTCCTCCCTGACATCCGCC 18

RESULT 627

US-10-138-674-1471/c
; Sequence 1471, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1471
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1471

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 773 GAGTGAAGTCTGGGGC 790
Db 18 GAGTGTAGTCTGGGGC 1

RESULT 628

US-10-432-962-3/c

; Sequence 3, Application US/10432962
; Publication No. US20040088753A1
; GENERAL INFORMATION:
; APPLICANT: Tsutomu SHIMIZU et al.
; TITLE OF INVENTION: GENE ENCODING ACETOLACTATE SYNTHASE
; FILE REFERENCE: 1254-0225P
; CURRENT APPLICATION NUMBER: US/10/432,962
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2000-362630
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-432-962-3

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1010 AAGATGTGGTGGGATG 1027
Db 18 AAGAGGTGGTGGTGATG 1

RESULT 629

US-10-287-949A-1471/c
; Sequence 1471, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1471
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1471

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 773 GAGTGAAGTCTGGGGC 790
Db 18 GAGTGTAGTCTGGGGC 1

RESULT 630

US-10-251-117-247/c
; Sequence 247, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor Re
; FILE OF INVENTION: Gene Expression Using Short Interfering RNA
; FILE REFERENCE: 900/042 (MBHB02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; CURRENT FILING DATE: 2003-02-24

```
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense x
US-10-251-117-247

Query Match      0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAA 1753
Db      18 AAAAAAAAACAAAACAAAAA 1

RESULT 631
US-10-251-117-496
; Sequence 496, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
; FILE REFERENCE: 900/042 (MBHB02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 496
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-251-117-496

Query Match      0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAAAAA 1753
Db      2 AAAAAAAAACAAAACAAAAA 19

RESULT 632
US-10-636-065-2/c
; Sequence 2, Application US/10636065
```

```
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-10-636-065-2

Query Match      0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      900 CCTGAGCCAGCCTCCAGA 917
Db      18 CCTGAGCCACCCTCTAGA 1

RESULT 633
US-10-665-951-1534/c
; Sequence 1534, Application US/10665951
; Publication No. US20040138163A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/131 (MBHB02-742-F)
; CURRENT APPLICATION NUMBER: US/10/665,951
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1534
; LENGTH: 19
```

```
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-665-951-1534

Query Match          0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 532 CCCCGCCACCTCTGCC 549
    ||| ||||| |||||
Db 19 CCCACACACCTCTGCC 2

RESULT 634
US-10-665-951-1781
; Sequence 1781, Application US/10665951
; Publication No. US20040138163A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/131 (MHB02-742-F)
; CURRENT APPLICATION NUMBER: US/10/665,951
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 10/664,668
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: PCT/US 03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/287,949
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/306,747
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US 02/17674
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1781
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-665-951-1781

Query Match          0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.8e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 532 CCCCGCCACCTCTGCC 549
    ||| ||||| |||||
Db 1 CCCACACACCTCTGCC 18

RESULT 635
US-10-287-919-1636
; Sequence 1636, Application US/10287919
```

```
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1636
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (953569)...(953584)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2082
US-10-287-919-1636

Query Match          0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1325 AGGACTTTTCACAGGAA 1340
    ||||| ||||| |||||
Db 1 AGGACTTTTCGAGGAA 16

RESULT 636
US-10-712-672-1775/c
; Sequence 1775, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1775
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-712-672-1775

Query Match          0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 678 GGTGGCACAGCCAGTG 693
    ||||| ||||| |||||
Db 16 GGTGGCACAGCCACTG 1

RESULT 637
US-09-866-108-7877
; Sequence 7877, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
```

```
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7877
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-7877
```

```
Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      834 GGAAGCTGCTGGGTC 849
          |||||||
Db      2 GGGAGCTGCTGGGTC 17
```

```
RESULT 638
US-09-866-108-7878
; Sequence 7878, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
```

```
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7878
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-7878
```

```
Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      834 GGAAGCTGCTGGGTC 849
          |||||||
Db      1 GGGAGCTGCTGGGTC 16
```

```
RESULT 639
US-09-814-777A-85/c
; Sequence 85, Application US/09814777A
; Patent No. US20020142415A1
; GENERAL INFORMATION:
; APPLICANT: KOOPMAN, Peter Anthony
; APPLICANT: MUSCAT, George Eugene Orlando
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM
; FILE REFERENCE: 21415-0003
; CURRENT APPLICATION NUMBER: US/09/814,777A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: AU PQ6457
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hSOX18 primer A
; US-09-814-777A-85
```

```
Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

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Qy      1470 GCTGCTCTCCTCTGAG 1485
          |||||||
Db      17 GCTGCTCTCCTCTGGG 2
```

```
RESULT 640
US-09-814-777A-87:
; Sequence 87, Application US/09814777A
; Patent No. US20020142415A1
; GENERAL INFORMATION:
; APPLICANT: KOOPMAN, Peter Anthony
; APPLICANT: MUSCAT, George Eugene Orlando
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM
; FILE REFERENCE: 21415-0003
; CURRENT APPLICATION NUMBER: US/09/814,777A
; CURRENT FILING DATE: 2001-03-23
; PRIOR FILING DATE: AU PQ6457
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hSOX18 primer C
US-09-814-777A-87

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1470 GCTGCTCTCCTCTGAG 1485
      |||||
Db 1 GCTGCTCTCCTCTGGG 16

RESULT 641
US-09-864-785-288/c
; Sequence 288, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 288
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-288

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1022 GGGATGGGGCTGGGT 1037
      |||||
Db 16 GGGATAGGGCTGGGT 1

RESULT 642
US-09-864-785-397
; Sequence 397, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 397
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-397

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 704 GCCCACCACCGCGGG 719
      |||||
Db 2 GCCCACCACCGCUGGG 17

RESULT 643
US-09-864-785-398
; Sequence 398, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 398
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-398

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 704 GCCCACCACCGCGGG 719
      |||||
Db 1 GCCCACCACCGCUGGG 16

RESULT 644
US-09-780-533A-2363
; Sequence 2363, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
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; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2363
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2363

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      861 AGGAAGAGGAAGAGGA 876
Db      2 AGGAGGAGGAAGAGGA 17

RESULT 645
US-09-848-754A-2396/c
; Sequence 2396, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2396
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2396

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      239 CCCCGGGCCACCACC 254
Db      17 CCCAGGGCCACCACC 2

RESULT 646
US-09-930-423-856
; Sequence 856, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 856
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-856

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      202 GCCAGAGCCCTCAGG 217
```

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Db      1 GCCAGAGCACCUCAGG 16

RESULT 647
US-09-780-164-800
; Sequence 800, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 800
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-800

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1008 AGAAGATGTGGTTGGG 1023
Db      2 AGAAGAAGUGGUUGGG 17

RESULT 648
US-09-827-395A-272/c
; Sequence 272, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor Ge
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 272
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-272

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      854 GCCCTGCAGGAAGAGG 869
Db      17 GCCGTGCAGGAAGAGG 2

RESULT 649
US-09-827-395A-273/c
; Sequence 273, Application US/09827395A
; Publication No. US20030113891A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-273

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      854 GCCCTGCAGGAAGAGG 869
      ||| ||||| ||||| |||
Db      16 GCCGTGCAGGAAGAGG 1

RESULT 650
US-09-745-237A-856
; Sequence 856, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 856
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-856

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      202 GCCAGAGCCCTCAGG 217
      ||||| ||| ||| |||
Db      1 GCCAGAGCACCUCAGG 16

RESULT 651
US-10-430-882-272/c
; Sequence 272, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haeberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
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```
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 272
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-272

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      854 GCCCTGCAGGAAGAGG 869
      ||| ||||| ||||| |||
Db      17 GCCGTGCAGGAAGAGG 2

RESULT 652
US-10-430-882-273/c
; Sequence 273, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haeberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-273

Query Match          0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      854 GCCCTGCAGGAAGAGG 869
      ||| ||||| ||||| |||
Db      16 GCCGTGCAGGAAGAGG 1

RESULT 653
US-10-163-552-593
; Sequence 593, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; TITLE OF INVENTION: HER2
; FILE REFERENCE: MBHB01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 593
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-593

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 5e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1650 TCTCCCTGACATCCAC 1665
      :||:||||:||||
Db 1 UCUGCCUGACAUCAC 16

RESULT 654
US-10-156-306-520/c
; Sequence 520, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 520
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-520

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1751
      ||| ||||| ||||| ||
Db 17 AAAAAAAAAAAAAAAAAAGA 2

RESULT 655
US-10-156-306-522/c
; Sequence 522, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 522
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-522
```

```
Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1751
      ||| ||||| ||||| ||
Db 16 AAAAAAAAAAAAAAAAAAGA 1

RESULT 656
US-10-156-306-523/c
; Sequence 523, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 523
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-523

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAAAAAAAAAA 1747
      ||| ||||| ||||| ||
Db 17 TTAATAAAAAAAAAAAAAA 2

RESULT 657
US-10-156-306-525/c
; Sequence 525, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-525

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAAAAAAAAAA 1746
      ||| ||||| ||||| ||
Db 16 TTTAAAAAAAAAAAAAAAAA 1

RESULT 658
US-10-156-306-5854/c
; Sequence 5854, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5854
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5854

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1536 CTGCAGCGCCTCGGC 1551
|||||
DB 17 CTGCAGCGCCTCGGC 2

RESULT 659

US-10-238-700-1031/c
; Sequence 1031, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1031
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-1031

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1603 GTACCTGCTGGGTCT 1618
|||
DB 16 GTAACTGCTGGGTCT 1

RESULT 660

US-10-238-700-3484
; Sequence 3484, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3484

; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3484

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 5e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1233 CCACCCCTGGCTTC 1248
|||||
DB 1 CCACCCUGGCUCCUUC 16

RESULT 661

US-10-138-674-8797/c
; Sequence 8797, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8797
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8797

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1621 GTTCCAGTTCCTCCATCC 1636
|||||
DB 16 GTTCCGGTTCCTCCATCC 1

RESULT 662

US-10-287-949A-8797/c
; Sequence 8797, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8797
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8797

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1621 GTTCCAGTTCCCATCC 1636
||||| |||||
Db 16 GTTCCGGTTCCCATCC 1

RESULT 663
US-10-712-672-1234/c
; Sequence 1234, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1234
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1234

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 678 GGTGGCACAGCCAGTG 693
||||| |||||
Db 17 GGTGGCACAGCCACTG 2

RESULT 664
US-10-712-672-2021/c
; Sequence 2021, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2021
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2021

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 531 GCCCCCGCCACCTCCT 546

Db 17 GCCCGCGCGCCTCCT 2
||||| |||||

RESULT 665
US-10-723-361-7877
; Sequence 7877, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7877
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7877

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 834 GGAAGCTGCTGGGTC 849
|| |||||
Db 2 GGGAGCTGCTGGGTC 17

RESULT 666
US-10-723-361-7878
; Sequence 7878, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361

```
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7878
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7878
```

```
Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      834 GGAAGCTGCTGGGGTC 849
      ||| ||||| ||||| |||
Db      1 GGGAGCTGCTGGGGTC 16
```

RESULT 667

```
US-09-969-373-4070
; Sequence 4070, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 4070
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-4070
```

```
Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      862 GGAAGAGGAAGAGGAG 877
      ||||| ||||| ||||| |||
Db      1 GGAAGAGGCAGAGGAG 16
```

RESULT 668

```
US-10-287-919-2609/c
; Sequence 2609, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 2609
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1584335)....(1584352)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3326
US-10-287-919-2609
```

```
Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1325 AGGACTTTCACAGGAA 1340
      ||||| ||||| ||||| |||
Db      17 AGGACTTTCACAGAAA 2
```

RESULT 669

```
US-10-617-334-148
; Sequence 148, Application US/10617334
; Publication No. US20040058869A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-91
; CURRENT APPLICATION NUMBER: US/10/617,334
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 09/526,193
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: PatentIn 3.0
; SEQ ID NO 148
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-617-334-148
```

```
Query Match      0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1184 GCTCCAGCCCATCCT 1199
      ||| ||||| ||||| |||
Db      4 GCTACCAGCCCATCCT 19
```

RESULT 670

```
US-10-287-919-1577
; Sequence 1577, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
```


; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1577
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (884395)...(884412)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2000
US-10-287-919-1577

Query Match 0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1325 AGGACTTTCACAGGAA 1340
|||||
Db 1 AGGACTTTCGAGGAA 16

RESULT 671
US-10-287-919-1860
; Sequence 1860, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1860
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1077945)...(1077963)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2360
US-10-287-919-1860

Query Match 0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1325 AGGACTTTCACAGGAA 1340
|||||
Db 1 AGGACTTTCGAGGAA 16

RESULT 672
US-10-287-941-42/c
; Sequence 42, Application US/10287941
; Publication No. US20030171552A1
; GENERAL INFORMATION:
; APPLICANT: Weidanz, Jon A.
; APPLICANT: Card, Kimberly F.
; APPLICANT: Sherman, Linda A.
; APPLICANT: Klinman, No. US20030171552A1man
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: POLYSPECIFIC BINDING MOLECULES AND USES THEREOF
; FILE REFERENCE: 48531
; CURRENT APPLICATION NUMBER: US/10/287,941
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US/09/422,375
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42

; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-941-42

Query Match 0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 527 ATGAGCCCCCGCCACC 542
|||||
Db 19 ATGAGCCCCCTCCACC 4

RESULT 673
US-10-452-510-148
; Sequence 148, Application US/10452510
; Publication No. US20040005666A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-93
; CURRENT APPLICATION NUMBER: US/10/452,510
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 09/526,193
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-452-510-148

Query Match 0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1184 GCTCCAGCCCCATCCT 1199
|||||
Db 4 GCTACCAGCCCCATCCT 19

RESULT 674
US-10-008-789-31
; Sequence 31, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXP
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-31

Query Match 0.8%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred.No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 462 CACCACGCTGGCCAAA 477
||||| |||||||
Db 5 CACCACACTGGCCAAA 20

RESULT 675
US-09-880-727-7
; Sequence 7, Application US/09880727
; Publication No. US20030064364A1
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; Chee, Mark
; Gunderson, Kevin
; Chaoqiang, Lai
; Wodicka, Lisa
; Cronin, Maureen T.
; Lee, Danny
; Tran, Huu M.
; Matsuzaki, Hajime
; McGall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joe Liebeschuetz
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,727
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,649
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/035,170
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: PCT/US97/01603
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-019410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; (ix) Features:
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-880-727-7

Query Match 0.8%; Score 14.2; DB 1; Length 15;
Best Local Similarity 93.3%; Pred.No. 4.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA 1749
|:|||||

Db 1 CVA 15

RESULT 676
US-09-152-059-65/c
; Sequence 65, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-65

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA 1749
|||||
Db 14 AAAAAA 1

RESULT 677
US-09-152-059-66/c
; Sequence 66, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309

; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-66

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 678
US-09-152-059-67/c
; Sequence 67, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-67

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 679
US-09-152-059-68/c
; Sequence 68, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-68

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 680
US-09-152-059-80/c
; Sequence 80, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19

```
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-80
```

```
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       14 AAAAAAAAAAAAAA 1
```

RESULT 681

```
US-09-152-059-81
; Sequence 81, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-81
```

```
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

```
RESULT 682
US-09-152-059-82
; Sequence 82, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-82
```

```
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

RESULT 683

```
US-09-152-059-83/c
; Sequence 83, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-83
```

```
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-83

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1

RESULT 684
US-09-152-059-84
; Sequence 84, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-84

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 685
US-09-152-059-85
; Sequence 85, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
```

```
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-85

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 686
US-09-152-059-86/c
; Sequence 86, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
```

```
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-86

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 687
US-09-152-059-87
; Sequence 87, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-87

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 14

RESULT 688
US-09-152-059-88
; Sequence 88, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
```

```
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-88

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 14

RESULT 689
US-09-152-059-89/c
; Sequence 89, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-89

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 690
US-09-152-059-90
; Sequence 90, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-90

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 691
US-09-152-059-91
; Sequence 91, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309

; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-91

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 692
US-09-152-059-92/c
; Sequence 92, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-92

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 693
US-09-152-059-93
; Sequence 93, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-93

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 694
US-09-152-059-94
; Sequence 94, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-94

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 695
US-09-152-059-96
; Sequence 96, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-96

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 696
US-09-152-059-97
; Sequence 97, Application US/09152059
; Patent No. US20020068708A1

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; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-97
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
          |||||
Db      1 AAAAAAAAAAAAAA 14
```

```
RESULT 697
US-09-152-059-98/c
; Sequence 98, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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```
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-98
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
          |||||
Db      1 AAAAAAAAAAAAAA 14
```

```
RESULT 698
US-09-152-059-99
; Sequence 99, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-99
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
          |||||
Db      1 AAAAAAAAAAAAAA 14
```

```
RESULT 699
US-09-152-059-100
; Sequence 100, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
```

```
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-100

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       1 AAAAAAAAAAAAAA 14

RESULT 700
US-09-152-059-101/c
; Sequence 101, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-101

Query Match          0.8%; Score 14; DB 1; Length 14;
```

```
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       1 AAAAAAAAAAAAAA 14

RESULT 701
US-09-152-059-102
; Sequence 102, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-102

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       1 AAAAAAAAAAAAAA 14

RESULT 702
US-09-152-059-103
; Sequence 103, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
```

```
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-103

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 703
US-09-152-059-104/c
; Sequence 104, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-104

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14
```

```
Db      14 AAAAAAAAAAAAAA 1

RESULT 704
US-09-152-059-105
; Sequence 105, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-105

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 705
US-09-152-059-106
; Sequence 106, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
```

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; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-106

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 706
US-09-152-059-107/c
; Sequence 107, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-107

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 707
US-09-152-059-108
; Sequence 108, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
```

```
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-108

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 708
US-09-152-059-109
; Sequence 109, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```



```
; OTHER INFORMATION: oligonucleotide
US-09-152-059-109

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 709
US-09-152-059-110/c
; Sequence 110, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,309
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
US-09-152-059-110
; OTHER INFORMATION: oligonucleotide

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1

RESULT 710
US-09-152-059-111
; Sequence 111, Application US/09152059
; Patent No. US20020068708A1
```

```
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,309
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-111

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 711
US-09-152-059-112
; Sequence 112, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,309
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-112

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 712

US-09-152-059-113/c
; Sequence 113, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059

; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 113

LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified base
LOCATION: (1)..(13)

; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-113

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 713

US-09-152-059-114
; Sequence 114, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059

; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 114

LENGTH: 14

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-114

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 714

US-09-152-059-115
; Sequence 115, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:

APPLICANT: WENGEL, JESPER

APPLICANT: NIELSEN, POUL

TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

FILE REFERENCE: 49165 (71994)

CURRENT APPLICATION NUMBER: US/09/152,059

CURRENT FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: 60/058,541

PRIOR FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: 60/068,293

PRIOR FILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/071,682

PRIOR FILING DATE: 1998-01-16

PRIOR APPLICATION NUMBER: 60/076,591

PRIOR FILING DATE: 1998-03-03

PRIOR APPLICATION NUMBER: 60/083,507

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/088,309

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/094,355

PRIOR FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 146

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 115

LENGTH: 14

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-115

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
| | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 715
US-09-152-059-117/c
; Sequence 117, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-117

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
| | | | |
Db 14 AAAAAAAAAAAAAA 1

RESULT 716
US-09-152-059-118
; Sequence 118, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-118

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
| | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 717
US-09-152-059-119
; Sequence 119, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-119

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
| | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 718
US-09-152-059-120/c
; Sequence 120, Application US/09152059

```
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-120
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       14 AAAAAAAAAAAAAA 1
```

```
RESULT 719
US-09-152-059-121
; Sequence 121, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
```

```
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-121
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       1 AAAAAAAAAAAAAA 14
```

```
RESULT 720
US-09-152-059-122
; Sequence 122, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-122
```

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Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       1 AAAAAAAAAAAAAA 14
```

```
RESULT 721
US-09-152-059-123/c
; Sequence 123, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
```

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; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-123

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1

RESULT 722
US-09-152-059-124
; Sequence 124, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

```
; OTHER INFORMATION: oligonucleotide
US-09-152-059-124

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 723
US-09-152-059-125
; Sequence 125, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-125

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 724
US-09-152-059-126/c
; Sequence 126, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
```

```

; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-126

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1
|||||

RESULT 725
US-09-152-059-127
; Sequence 127, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-127

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1
|||||

US-09-152-059-128
; Sequence 128, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-128

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1
|||||

US-09-152-059-129/c
; Sequence 129, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-129/c

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1
|||||
```

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|||||
Db      1 AAAAAAAAAAAAAA 14
|||||

RESULT 726
US-09-152-059-128
; Sequence 128, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-128

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 14
|||||

RESULT 727
US-09-152-059-129/c
; Sequence 129, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-129/c

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 14
|||||
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; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-129

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 728
US-09-152-059-130
; Sequence 130, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-130

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 729
US-09-152-059-131
; Sequence 131, Application US/09152059
; Patent No. US20020068708A1
```

```
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-131

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 730
US-09-152-059-132/c
; Sequence 132, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-132

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 731
US-09-152-059-133:
; Sequence 133, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-133

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 14

RESULT 732
US-09-152-059-134:
; Sequence 134, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
```

```
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-152-059-134

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 14

RESULT 733
US-09-152-059-135/c
; Sequence 135, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
```

US-09-152-059-135

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 14 AAAAAAAAAAAAAA 1

RESULT 734

US-09-152-059-136
; Sequence 136, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 136
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-136

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 735

US-09-152-059-137
; Sequence 137, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-137

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 736

US-09-152-059-138/c
; Sequence 138, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-138

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |

```
Db      14 AAAAAAAAAAAAAA 1
RESULT 737
US-09-152-059-139
; Sequence 139, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-139
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
      |||||
Db      1 AAAAAAAAAAAAAA 14

RESULT 738
US-09-152-059-140/c
; Sequence 141, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-09-152-059-141
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
      |||||
Db      1 AAAAAAAAAAAAAA 14

RESULT 738
US-09-152-059-140
; Sequence 140, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
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Db 14 AAAAAAAAAAAAAA 1

RESULT 740

US-09-152-059-142

; Sequence 142, Application US/09152059

; Patent No. US20020068708A1

; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER

; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

; FILE REFERENCE: 49165 (71994)

; CURRENT APPLICATION NUMBER: US/09/152,059

; CURRENT FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12

; PRIOR APPLICATION NUMBER: 60/068,293

; PRIOR FILING DATE: 1997-12-19

; PRIOR APPLICATION NUMBER: 60/071,682

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03

; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/094,355

; PRIOR FILING DATE: 1998-07-28

; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 142

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: LNA modified

; OTHER INFORMATION: oligonucleotide

US-09-152-059-142

Query Match 0.8%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749

Db 1 AAAAAAAAAAAAAA 14

RESULT 741

US-09-152-059-143

; Sequence 143, Application US/09152059

; Patent No. US20020068708A1

; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER

; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

; FILE REFERENCE: 49165 (71994)

; CURRENT APPLICATION NUMBER: US/09/152,059

; CURRENT FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12

; PRIOR APPLICATION NUMBER: 60/068,293

; PRIOR FILING DATE: 1997-12-19

; PRIOR APPLICATION NUMBER: 60/071,682

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03

; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/094,355

; PRIOR FILING DATE: 1998-07-28

; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 143

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide

US-09-152-059-143

Query Match 0.8%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749

Db 1 AAAAAAAAAAAAAA 14

RESULT 742

US-09-152-059-144/c

; Sequence 144, Application US/09152059

; Patent No. US20020068708A1

; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER

; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

; FILE REFERENCE: 49165 (71994)

; CURRENT APPLICATION NUMBER: US/09/152,059

; CURRENT FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12

; PRIOR APPLICATION NUMBER: 60/068,293

; PRIOR FILING DATE: 1997-12-19

; PRIOR APPLICATION NUMBER: 60/071,682

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03

; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/094,355

; PRIOR FILING DATE: 1998-07-28

; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 144

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: modified base

; LOCATION: (1)..(13)

; OTHER INFORMATION: LNA monomer

; OTHER INFORMATION: Description of Artificial Sequence: LNA modified

; OTHER INFORMATION: oligonucleotide

US-09-152-059-144

Query Match 0.8%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 743

US-09-152-059-145

; Sequence 145, Application US/09152059

; Patent No. US20020068708A1

```
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-145

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 744
US-09-152-059-146
; Sequence 146, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-20

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 746
US-10-208-357-20
; Sequence 20, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-20

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 745
US-10-096-075-11
; Sequence 11, Application US/10096075
; Publication No. US20030225247A1
; GENERAL INFORMATION:
; APPLICANT: STAVRIANOPOULOS, JANNIS G.
; APPLICANT: RABBANI, ELAZAR
; TITLE OF INVENTION: LABELING REAGENTS AND LABELED TARGETS, TARGET LABELING
; TITLE OF INVENTION: PROCESSES AND OTHER PROCESSES FOR USING SAME IN NUCLEIC
; TITLE OF INVENTION: ACID DETERMINATIONS AND ANALYSES
; FILE REFERENCE: ENZ-61
; CURRENT APPLICATION NUMBER: US/10/096,075
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-096-075-11

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 745
US-10-096-075-11
; Sequence 11, Application US/10096075
; Publication No. US20030225247A1
; GENERAL INFORMATION:
; APPLICANT: STAVRIANOPOULOS, JANNIS G.
; APPLICANT: RABBANI, ELAZAR
; TITLE OF INVENTION: LABELING REAGENTS AND LABELED TARGETS, TARGET LABELING
; TITLE OF INVENTION: PROCESSES AND OTHER PROCESSES FOR USING SAME IN NUCLEIC
; TITLE OF INVENTION: ACID DETERMINATIONS AND ANALYSES
; FILE REFERENCE: ENZ-61
; CURRENT APPLICATION NUMBER: US/10/096,075
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-096-075-11

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 746
US-10-208-357-20
; Sequence 20, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-20

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 744
US-09-152-059-146
; Sequence 146, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165 (71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```



```
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14
RESULT 747
US-10-301-844-20
; Sequence 20, Application US/10301844
; Publication No. US20030100747A1
; GENERAL INFORMATION:
; APPLICANT: Ruddy, David A.
; Wolff, Roger K.
; TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
; HEMOCHROMATOSIS GENE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/301,844
; FILING DATE: 20-No. US20030100747A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,495C
; FILING DATE: 07-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0057-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-301-844-20
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14
RESULT 748
US-10-008-029-65/c
; Sequence 65, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
```

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; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; US-10-008-029-65
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1
RESULT 749
US-10-008-029-66/c
; Sequence 66, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
US-10-008-029-66

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 750

US-10-008-029-67/c
; Sequence 67, Application US/10008029
; Publication No. US20030134808A1

; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-67

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 751

US-10-008-029-68/c
; Sequence 68, Application US/10008029
; Publication No. US20030134808A1

; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
US-10-008-029-68

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 752

US-10-008-029-80/c
; Sequence 80, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-80

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 753
US-10-008-029-81
; Sequence 81, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-81

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 754
US-10-008-029-82
; Sequence 82, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-82

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 755
US-10-008-029-83/c
; Sequence 83, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-81

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; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
US-10-008-029-83

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 756
US-10-008-029-84
; Sequence 84, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-84

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 757
US-10-008-029-85
```

```
; Sequence 85, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-85

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 758
US-10-008-029-86/c
; Sequence 86, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-86
```

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
US-10-008-029-86

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1

RESULT 759
US-10-008-029-87
; Sequence 87, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-87

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 760
US-10-008-029-88
; Sequence 88, Application US/10008029
; Publication No. US20030134808A1
```

```
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-88

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 761
US-10-008-029-89/c
; Sequence 89, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
```

```
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-89

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 762
US-10-008-029-90
; Sequence 90, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-008-029-90

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 763
US-10-008-029-91
; Sequence 91, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
```

```
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-008-029-91

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 764
US-10-008-029-92/c
; Sequence 92, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 14
; TYPE: DNA
```


; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
US-10-008-029-92

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 765
US-10-008-029-93
; Sequence 93, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

US-10-008-029-93
; Sequence 93, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 766
US-10-008-029-94
; Sequence 94, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 767
US-10-008-029-96
; Sequence 96, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05

```
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-96
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

RESULT 768

```
US-10-008-029-97
; Sequence 97, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-97
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

RESULT 769

```
US-10-008-029-98/c
; Sequence 98, Application US/10008029
; Publication No. US20030134808A1
```

```
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: LNA monomer
US-10-008-029-98
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       14 AAAAAAAAAAAAAA 1
```

RESULT 770

```
US-10-008-029-99
; Sequence 99, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
```

```
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-99
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
        |||||
Db      1 AAAAAAAAAAAAAA 14
```

```
RESULT 771
US-10-008-029-100.
; Sequence 100, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-100
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
        |||||
Db      1 AAAAAAAAAAAAAA 14
```

```
RESULT 772
US-10-008-029-101/c
; Sequence 101, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
```

```
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
US-10-008-029-101
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
        |||||
Db      14 AAAAAAAAAAAAAA 1
```

```
RESULT 773
US-10-008-029-102
; Sequence 102, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
```

; SEQ ID NO 102

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide

US-10-008-029-102

Query Match

Best Local Similarity 0.8%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 1 AAAAAAAAAAAAAA 14

RESULT 774

US-10-008-029-103

; Sequence 103, Application US/10008029

; Publication No. US20030134808A1

; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER

; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

; FILE REFERENCE: 49165-C2(71994)

; CURRENT APPLICATION NUMBER: US/10/008,029

; CURRENT FILING DATE: 2001-11-05

; PRIOR APPLICATION NUMBER: 09/152,059

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12

; PRIOR APPLICATION NUMBER: 60/068,293

; PRIOR FILING DATE: 1997-12-19

; PRIOR APPLICATION NUMBER: 60/071,682

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03

; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/094,355

; PRIOR FILING DATE: 1998-07-28

; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 103

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide

US-10-008-029-103

Query Match

Best Local Similarity 0.8%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 1 AAAAAAAAAAAAAA 14

RESULT 775

US-10-008-029-104/c

; Sequence 104, Application US/10008029

; Publication No. US20030134808A1

; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER

; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

; FILE REFERENCE: 49165-C2(71994)

; CURRENT APPLICATION NUMBER: US/10/008,029

; CURRENT FILING DATE: 2001-11-05

; PRIOR APPLICATION NUMBER: 09/152,059

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12

; PRIOR APPLICATION NUMBER: 60/068,293

; PRIOR FILING DATE: 1997-12-19

; PRIOR APPLICATION NUMBER: 60/071,682

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03

; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/094,355

; PRIOR FILING DATE: 1998-07-28

; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 104

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: LNA modified

; OTHER INFORMATION: oligonucleotide

; NAME/KEY: modified_base

; LOCATION: (7)

; OTHER INFORMATION: LNA monomer

; NAME/KEY: modified_base

; LOCATION: (9)

; OTHER INFORMATION: LNA monomer

US-10-008-029-104

Query Match

Best Local Similarity 0.8%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 776

US-10-008-029-105

; Sequence 105, Application US/10008029

; Publication No. US20030134808A1

; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER

; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

; FILE REFERENCE: 49165-C2(71994)

; CURRENT APPLICATION NUMBER: US/10/008,029

; CURRENT FILING DATE: 2001-11-05

; PRIOR APPLICATION NUMBER: 09/152,059

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12

; PRIOR APPLICATION NUMBER: 60/068,293

; PRIOR FILING DATE: 1997-12-19

; PRIOR APPLICATION NUMBER: 60/071,682

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03

; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/094,355

; PRIOR FILING DATE: 1998-07-28

; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-105

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 777
US-10-008-029-106
; Sequence 106, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-106

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 778
US-10-008-029-107/c
; Sequence 107, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-107

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 779
US-10-008-029-108
; Sequence 108, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108

; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-108

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 780

US-10-008-029-109
; Sequence 109, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-109

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 781

US-10-008-029-110/c
; Sequence 110, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)

; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
US-10-008-029-110

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 782

US-10-008-029-111
; Sequence 111, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-111

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 783
US-10-008-029-112
; Sequence 112, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-112

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 784
US-10-008-029-113/c

; Sequence 113, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified base
; LOCATION: (1)..(13)
; OTHER INFORMATION: LNA monomer
US-10-008-029-113

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 14 AAAAAAAAAAAAAA 1

RESULT 785
US-10-008-029-114
; Sequence 114, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05

```
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-114
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

RESULT 786

```
US-10-008-029-115
; Sequence 115, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-115
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

RESULT 787

```
US-10-008-029-117/c
; Sequence 117, Application US/10008029
; Publication No. US20030134808A1
```

```
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: LNA monomer
US-10-008-029-117
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       14 AAAAAAAAAAAAAA 1
```

RESULT 788

```
US-10-008-029-118
; Sequence 118, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
```

```
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-118
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
         |||||
Db       1 AAAAAAAAAAAAAA 14
```

```
RESULT 789
US-10-008-029-119
; Sequence 119, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-119
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
         |||||
Db       1 AAAAAAAAAAAAAA 14
```

```
RESULT 790
US-10-008-029-120/c
; Sequence 120, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
```

```
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
US-10-008-029-120
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
         |||||
Db       14 AAAAAAAAAAAAAA 1
```

```
RESULT 791
US-10-008-029-121
; Sequence 121, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 121
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-121
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14
```

RESULT 792

```
US-10-008-029-122
; Sequence 122, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
```

```
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-122
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14
```

RESULT 793

```
US-10-008-029-123/c
; Sequence 123, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
```

```
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-123
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1
```

RESULT 794

```
US-10-008-029-124
; Sequence 124, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-124

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 795
US-10-008-029-125
; Sequence 125, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-125

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 796
US-10-008-029-126/c
; Sequence 126, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-126

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 14 AAAAAAAAAAAAAA 1

RESULT 797
US-10-008-029-127
; Sequence 127, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127

```
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-127
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

RESULT 798

```
US-10-008-029-128
; Sequence 128, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver..2.1
; SEQ ID NO 128
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-128
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

RESULT 799

```
US-10-008-029-129/c
; Sequence 129, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
```

```
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified.
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: LNA monomer
US-10-008-029-129
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       14 AAAAAAAAAAAAAA 1
```

RESULT 800

```
US-10-008-029-130
; Sequence 130, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 14
; TYPE: DNA
```


; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-130

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 801

US-10-008-029-131
; Sequence 131, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-131

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 802

US-10-008-029-132/c
; Sequence 132, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05

; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: LNA monomer
US-10-008-029-132

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 803

US-10-008-029-133
; Sequence 133, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-133.

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 804

US-10-008-029-134
; Sequence 134, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029

; CURRENT FILING DATE: 2001-11-05

; PRIOR APPLICATION NUMBER: 09/152,059

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: 60/058,541

; PRIOR FILING DATE: 1997-09-12

; PRIOR APPLICATION NUMBER: 60/068,293

; PRIOR FILING DATE: 1997-12-19

; PRIOR APPLICATION NUMBER: 60/071,682

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03

; PRIOR APPLICATION NUMBER: 60/083,507

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/094,355

; PRIOR FILING DATE: 1998-07-28

; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 134

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide

US-10-008-029-134

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 805

US-10-008-029-135/c
; Sequence 135, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER

; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

; FILE REFERENCE: 49165-C2(71994)

; CURRENT APPLICATION NUMBER: US/10/008,029

; CURRENT FILING DATE: 2001-11-05

; PRIOR APPLICATION NUMBER: 09/152,059

; PRIOR FILING DATE: 1998-09-11

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-136

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 807

US-10-008-029-137
; Sequence 137, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide

US-10-008-029-137

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 808

US-10-008-029-138/c
; Sequence 138, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059

; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-008-029-138

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 809

US-10-008-029-139
; Sequence 139, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:

; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```
; OTHER INFORMATION: oligonucleotide
US-10-008-029-139

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 810
US-10-008-029-140
; Sequence 140, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-140

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 811
US-10-008-029-141/c
; Sequence 141, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
```

```
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
; OTHER INFORMATION: LNA monomer
US-10-008-029-141

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1

RESULT 812
US-10-008-029-142
; Sequence 142, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-10-008-029-142

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 813
US-10-008-029-143
; Sequence 143, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-143

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAA 14

RESULT 814
US-10-008-029-144/c
; Sequence 144, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL

; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified base
; LOCATION: (1)..(13)
; OTHER INFORMATION: LNA monomer
US-10-008-029-144

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
| | | | | | | | | | | | | | | |
Db 14 AAAAAAAAAAAAAA 1

RESULT 815
US-10-008-029-145
; Sequence 145, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES

; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145

```

; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-145

```

```

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14

```

RESULT 816

```

US-10-008-029-146
; Sequence 146, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-146

```

```

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14

```

RESULT 817

```

US-10-208-650-65/c
; Sequence 65, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)

```

```

; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
US-10-208-650-65

```

```

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       14 AAAAAAAAAAAAAA 1

```

RESULT 818

```

US-10-208-650-66/c
; Sequence 66, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28

```


; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
US-10-208-650-66

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 819
US-10-208-650-67/c
; Sequence 67, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-67

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA.1749

Db 14 AAAAAAAAAAAAAA 1
RESULT 820
US-10-208-650-68/c
; Sequence 68, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
US-10-208-650-68

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 821
US-10-208-650-80/c
; Sequence 80, Application US/10208650
; Publication No. US20030144231A1

```
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-80
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       14 AAAAAAAAAAAAAA 1
```

```
RESULT 822
US-10-208-650-81
; Sequence 81, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
```

```
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-81
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

```
RESULT 823
US-10-208-650-82
; Sequence 82, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-82
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1749
          |||||
Db       1 AAAAAAAAAAAAAA 14
```

```
RESULT 824
US-10-208-650-83/c
; Sequence 83, Application US/10208650
```

; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
US-10-208-650-83

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 825
US-10-208-650-84
; Sequence 84, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03

; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-84

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 826
US-10-208-650-85
; Sequence 85, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-85

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 827
US-10-208-650-86/c
; Sequence 86, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
US-10-208-650-86

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 828
US-10-208-650-87
; Sequence 87, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293

; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-87

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 829
US-10-208-650-88
; Sequence 88, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-88

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;

```
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 830
US-10-208-650-89/c
; Sequence 89, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-89

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 831
US-10-208-650-90
; Sequence 90, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
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; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-90

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 832
US-10-208-650-91
; Sequence 91, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

OTHER INFORMATION: oligonucleotide
US-10-208-650-91

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 833

US-10-208-650-92/c
; Sequence 92, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified

OTHER INFORMATION: oligonucleotide

NAME/KEY: modified_base
LOCATION: (5)
OTHER INFORMATION: LNA monomer

NAME/KEY: modified_base
LOCATION: (7)
OTHER INFORMATION: LNA monomer

NAME/KEY: modified_base
LOCATION: (9)
OTHER INFORMATION: LNA monomer

NAME/KEY: modified_base
LOCATION: (11)
OTHER INFORMATION: LNA monomer

US-10-208-650-92

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749

Db 14 AAAAAAAAAAAAAA 1

RESULT 834

US-10-208-650-93
; Sequence 93, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: oligonucleotide

NAME/KEY: modified_base
LOCATION: (5)
OTHER INFORMATION: LNA monomer

NAME/KEY: modified_base
LOCATION: (7)
OTHER INFORMATION: LNA monomer

NAME/KEY: modified_base
LOCATION: (9)
OTHER INFORMATION: LNA monomer

NAME/KEY: modified_base
LOCATION: (11)
OTHER INFORMATION: LNA monomer

US-10-208-650-93

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 835

US-10-208-650-94
; Sequence 94, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682

OTHER INFORMATION: oligonucleotide

NAME/KEY: modified_base
LOCATION: (5)
OTHER INFORMATION: LNA monomer

NAME/KEY: modified_base
LOCATION: (7)
OTHER INFORMATION: LNA monomer

NAME/KEY: modified_base
LOCATION: (9)
OTHER INFORMATION: LNA monomer

NAME/KEY: modified_base
LOCATION: (11)
OTHER INFORMATION: LNA monomer

US-10-208-650-94

; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-94

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 836
US-10-208-650-96
; Sequence 96, Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-96

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 837
US-10-208-650-97
; Sequence 97, Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-97

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 838
US-10-208-650-98/c
; Sequence 98, Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: LNA monomer
US-10-208-650-98

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1

RESULT 839
US-10-208-650-99
; Sequence 99, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-99
```

```
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 840
US-10-208-650-100
; Sequence 100, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-100

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 841
US-10-208-650-101/c
; Sequence 101, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
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; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
; US-10-208-650-101

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1

RESULT 842
US-10-208-650-102
; Sequence 102, Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 14
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-102

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 843
US-10-208-650-103
; Sequence 103, Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-103

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 844
US-10-208-650-104/c
; Sequence 104, Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
```

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; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-104

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1

RESULT 845
US-10-208-650-105
; Sequence 105, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-106

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1
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```
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-105

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 846
US-10-208-650-106
; Sequence 106, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-106

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14
```

RESULT 847
US-10-208-650-107/c
; Sequence 107, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-107

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 848
US-10-208-650-108
; Sequence 108, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682

; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-108

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 849
US-10-208-650-109
; Sequence 109, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-109

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 850
US-10-208-650-110/c
; Sequence 110, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
US-10-208-650-110

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 851
US-10-208-650-111
; Sequence 111, Application US/10208650
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; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-111

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 852
US-10-208-650-112
; Sequence 112, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
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; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-112

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 853
US-10-208-650-113/c
; Sequence 113, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(13)
; OTHER INFORMATION: LNA monomer
US-10-208-650-113

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 854
US-10-208-650-114
; Sequence 114, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-114

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 855
US-10-208-650-115
; Sequence 115, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591

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; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-115

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 856
US-10-208-650-117/c
; Sequence 117, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: LNA monomer
US-10-208-650-117

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
```

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 857
US-10-208-650-118
; Sequence 118, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-118

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 858
US-10-208-650-119
; Sequence 119, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
```

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; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-119

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 859
US-10-208-650-120/c
; Sequence 120, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
```

```
; OTHER INFORMATION: LNA monomer
US-10-208-650-120

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 860
US-10-208-650-121
; Sequence 121, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-121

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 861
US-10-208-650-122
; Sequence 122, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
```

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; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-123

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       1 AAAAAAAAAAAAAA 14

RESULT 862
US-10-208-650-123/c
; Sequence 123, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-124

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       1 AAAAAAAAAAAAAA 14

RESULT 864
US-10-208-650-125
; Sequence 125, Application US/10208650
```

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; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-123

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       1 AAAAAAAAAAAAAA 14

RESULT 863
US-10-208-650-124
; Sequence 124, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-124

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1749
        |||||
Db       1 AAAAAAAAAAAAAA 14

RESULT 864
US-10-208-650-125
; Sequence 125, Application US/10208650
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; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-125

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
        |||||
Db      1 AAAAAAAAAAAAAA 14

RESULT 865
US-10-208-650-126/c
; Sequence 126, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
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; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-126

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
        |||||
Db      1 AAAAAAAAAAAAAA 14

RESULT 866
US-10-208-650-127
; Sequence 127, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-127

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
        |||||
Db      1 AAAAAAAAAAAAAA 14
```

RESULT 867
US-10-208-650-128
; Sequence 128, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-128

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 868
US-10-208-650-129/c
; Sequence 129, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591

; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)
; OTHER INFORMATION: LNA monomer
US-10-208-650-129

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 869
US-10-208-650-130
; Sequence 130, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-130

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;


```
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 870
US-10-208-650-131
; Sequence 131, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-208-650-131

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 871
US-10-208-650-132/c
; Sequence 132, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
```

```
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(8)
; OTHER INFORMATION: LNA monomer
US-10-208-650-132

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 872
US-10-208-650-133
; Sequence 133, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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```
; OTHER INFORMATION: oligonucleotide
US-10-208-650-133

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 873
US-10-208-650-134
; Sequence 134, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 874
US-10-208-650-135/c
; Sequence 135, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029

; OTHER INFORMATION: oligonucleotide
US-10-208-650-134

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 875
US-10-208-650-136
; Sequence 136, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 1

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 136
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-136

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 876
US-10-208-650-137
; Sequence 137, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-137

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 877
US-10-208-650-138/c
; Sequence 138, Application US/10208650

; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(9)
; OTHER INFORMATION: LNA monomer
US-10-208-650-138

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 878
US-10-208-650-139
; Sequence 139, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03

; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-139.

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 879
US-10-208-650-140
; Sequence 140, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-140

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 880
US-10-208-650-141/c
; Sequence 141, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: LNA monomer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (11)
; OTHER INFORMATION: LNA monomer
; US-10-208-650-141

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 881
US-10-208-650-142
; Sequence 142, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER

```
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
US-10-208-650-142
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
        |||||
Db      1 AAAAAAAAAAAAAA 14
```

```
RESULT 882
US-10-208-650-143
; Sequence 143; Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-143
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
        |||||
Db      1 AAAAAAAAAAAAAA 14
```

```
RESULT 883
US-10-208-650-144/c
; Sequence 144; Application US/10208650
; Publication No. US2003014231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LNA modified
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(13)
; OTHER INFORMATION: LNA monomer
US-10-208-650-144
```

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1736 AAAAAAAAAAAAAA 1749
        |||||
Db      14 AAAAAAAAAAAAAA 1
```

RESULT 884

US-10-208-650-145
; Sequence 145, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-145

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 885
US-10-208-650-146
; Sequence 146, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-146

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 886
US-10-106-749-4
; Sequence 4, Application US/10106749
; Publication No. US20030165879A1
; GENERAL INFORMATION:
; APPLICANT: Inscent, Inc.
; APPLICANT: Woods, Daniel
; APPLICANT: Dimitratos, Spiros
; TITLE OF INVENTION: EFFICIENT METHODS FOR ISOLATING FUNCTIONAL G-PROTEIN COUPLED RECEPTORS
; TITLE OF INVENTION: AND IDENTIFYING ACTIVE EFFECTORS AND EFFICIENT METHODS TO ISOLATE
; TITLE OF INVENTION: INVOLVED IN OLFACTION AND IDENTIFYING ACTIVE EFFECTORS
; FILE REFERENCE: INS-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/106,749
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/279,168
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/353,392
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-106-749-4

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 887
US-10-151-061-16
; Sequence 16, Application US/10151061
; Publication No. US20030219751A1
; GENERAL INFORMATION:
; APPLICANT: Lao, Kai Qin
; APPLICANT: Chen, Caifu
; APPLICANT: Coehler, Ryan
; APPLICANT: Scafe, Charles
; APPLICANT: Schroth, Gary
; TITLE OF INVENTION: THE WHOLE GENOME AMPLIFICATION USING
; TITLE OF INVENTION: SHORT, UNIVERSAL-TAGGED, OLIGO PRIMERS


```
; FILE REFERENCE: ABIOS.004A
; CURRENT APPLICATION NUMBER: US/10/151,061
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A site in a synthetic oligonucleotide template
; OTHER INFORMATION: having no significant homology to the human genome.
US-10-151-061-16

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 888
US-10-324-409B-17/c
; Sequence 17, Application US/10324409B
; Publication No. US20040086880A1
; GENERAL INFORMATION:
; APPLICANT: Sampson, et al.
; TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced
; TITLE OF INVENTION: Secondary Structure
; FILE REFERENCE: 2003309-0028
; CURRENT APPLICATION NUMBER: US/10/324,409B
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Incubate with
; OTHER INFORMATION: DNA Polymerases.
US-10-324-409B-17

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      14 AAAAAAAAAAAAAA 1

RESULT 889
US-10-468-753-42
; Sequence 42, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
```

```
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-42

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      1 AAAAAAAAAAAAAA 14

RESULT 890
US-10-468-753-47/c
; Sequence 47, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-47

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1734 AAAAAAAAAAAAAA 1747
Db      14 AAAAAAAAAAAAAA 1

RESULT 891
US-10-468-753-50/c
; Sequence 50, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
```

```
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-50

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
DB 14 CAAAAAAAAAAAAA 1

RESULT 892
US-10-468-753-51/c
; Sequence 51, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-51

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
DB 14 AAAAAAAAAAAAAA 1

RESULT 893
US-10-056-414-16
; Sequence 16, Application US/10056414
; Publication No. US20030003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; RELATED TO LEVELS OF
; RELATED TO LEVELS OF
; NF-KB
; NUMBER OF SEQUENCES: 830
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; SUITE: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,414
; FILING DATE: 23-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-056-414-16

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 5.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 727 CAGGCTTCTGGGCC 740
DB 1 CAGGCUUCUGGGCC 14

RESULT 894
US-10-227-001-24/c
; Sequence 24, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
; APPLICANT: Dempcy, Robert O.
; APPLICANT: Afonina, Irina Aleksandrovna
; APPLICANT: Vermeulen, Nicolaas M.J.
; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: Hybridization-Triggered Fluorescent
; TITLE OF INVENTION: Detection of Nucleic Acids
; FILE REFERENCE: 17682A-004210US
; CURRENT APPLICATION NUMBER: US/10/227,001
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 09/428,236
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```

;
; FEATURE:
;
; OTHER INFORMATION: 15-mer poly dT-MGB-
;
; OTHER INFORMATION: (2-dimethylaminonaphthalene-6-sulfonamide)
;
; OTHER INFORMATION: conjugate, poly(dT)-15-MGB-dansyl conjugate
;
; FEATURE:
;
; NAME/KEY: modified_base
;
; LOCATION: (1)
;
; OTHER INFORMATION: n = thymine modified by MGB-
;
; OTHER INFORMATION: (2-dimethylaminonaphthalene-6-sulfonamide)
;
; OTHER INFORMATION: (dansyl group)
;
US-10-227-001-24

```

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 15 AAAAAAAAAAAAAA 2

RESULT 895

```

US-09-894-159-64
; Sequence 64, Application US/09894159
; Publication No. US20030149237A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar
; APPLICANT: Patturjan, Meera
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Herrmann, John L
; APPLICANT: MacDougall, John R
; APPLICANT: Rastelli, Luca
; APPLICANT: Zhong, Haihong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Shenoy, Suresh
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Gangolli, Esha A
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 21402-033
; CURRENT APPLICATION NUMBER: US/09/894,159
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: U.S.S.N 60/261,014
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: U.S.S.N 60/214,759
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: U.S.S.N 60/263,215
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: U.S.S.N 60/244,546
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-894-159-64

```

```
Query Match      0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1736	AAAAAAAAAAAAA	1749
D _b	1	AAAAAAAAAAAAA	14

RESULT 896

```

US-09-880-727-8/c
; Sequence 8, Application US/09880727
; Publication No. US20030064364A1
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; Chee, Mark
; Gunderson, Kevin
; Chaoqiang, Lai
; Modicka, Lisa
; Cronin, Maureen T.
; Lee, Danny
; Tran, Huu M.
; Matsuzaki, Hajime
; McGall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joe Liebeschuetz
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,727
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,649
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/035,170
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: PCT/US97/01603
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-019410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; (ix) Features:
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-880-727-8

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Query Match          0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3

RESULT 897
US-10-324-409B-33/c
; Sequence 33, Application US/10324409B
; Publication No. US20040086880A1
; GENERAL INFORMATION:
; APPLICANT: Sampson, et al.

;
; TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced
; FILE REFERENCE: Secondary Structure
; CURRENT APPLICATION NUMBER: US/10/324,409B
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Poly T Prime.
; NAME/KEY: misc_feature
; LOCATION: (15)..(16)
; OTHER INFORMATION: N = any nucleotide.
US-10-324-409B-33

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
|||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 898
US-09-848-754A-905
; Sequence 905, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 905
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-905

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.7e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 907 CAGCCTCCAGAGGA 920
|||||
Db 4 CAGCCUCCAGAGGA 17

RESULT 899
US-10-061-201-1502/c
; Sequence 1502, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669

;
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1502
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1502

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 898 CCCCTGAGCCAGCC 911
|||||
Db 17 CCCCTGAGCCAGCC 4

RESULT 900
US-10-061-201-1506/c
; Sequence 1506, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1506
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1506

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 897 GCCCCTGAGCCAGC 910

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Db      14 GCCCCTGAGCCAGC 1
|||||
RESULT 901
US-10-338-777-196
; Sequence 196, Application US/10338777
; Publication No. US20030188343A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: United States Department of Agriculture
; APPLICANT: Bowen, Benjamin A
; APPLICANT: Haudenschild, Christian D
; APPLICANT: Buckler, Edward S
; TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants
; FILE REFERENCE: 37-000510US
; CURRENT APPLICATION NUMBER: US/10/338,777
; CURRENT FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-338-777-196

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA
Db      4 CAAAAA

RESULT 902
US-10-138-674-1072/c
; Sequence 1072, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1072
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1072

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAA
Db      17 AAAAAA

RESULT 903
US-10-138-674-1077/c
; Sequence 1077, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1077
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1077

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAA
Db      14 AAAAAA

RESULT 904
US-10-287-949A-1072/c
; Sequence 1072, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1072
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1072

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAA
Db      17 AAAAAA

RESULT 905
US-10-287-949A-1077/c
; Sequence 1077, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
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; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1077
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1077

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 906
US-10-712-672-2015/c
; Sequence 2015, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MEHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2015
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2015

Query Match      0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 325 CAGCCCCCAGGGG 338
Db 14 CAGCCCCCAGGGG 1

RESULT 907
US-09-823-887C-7/c
; Sequence 7, Application US/09823887C
; Publication No. US20030180723A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sanjay
; APPLICANT: Lal, Lakhvir
; APPLICANT: Ahuja, Paramvir
; TITLE OF INVENTION: Cloning of No. US20030180723A1e1 Gene Sequences Expressed and Rep
; FILE REFERENCE: Dormancy in the Apical Buds of Tea (Camellia Sinensis L. (O.) Ku
; CURRENT APPLICATION NUMBER: US/09/823,887C
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: primer_bind
US-09-823-887C-7

Query Match      0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
Db 18 CAAAAAAAAAAAAA 5

RESULT 908
US-10-328-578-142/c
; Sequence 142, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen F.
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-III
; FILE REFERENCE: 377882002020
; CURRENT APPLICATION NUMBER: US/10/328,578
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 10/176,883
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/375,253
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 10/177,826
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-328-578-142

Query Match      0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 18 AAAAAAAAAAAAAA 5

RESULT 909
US-10-407-089-22
; Sequence 22, Application US/10407089
; Publication No. US20030224419A1
; GENERAL INFORMATION:
; APPLICANT: Corcoran, Kevin C.
; APPLICANT: Eletri, Sam
; TITLE OF INVENTION: System for Determining a Signature of a
; TITLE OF INVENTION: Nucleotide Sequence
; FILE REFERENCE: 55525-8040.US00
; CURRENT APPLICATION NUMBER: US/10/407,089
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/654,187
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/182,454
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/US98/11224
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 08/862,610
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: adaptor
US-10-407-089-22

Query Match      0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1749
Db      5 AAAAAAAAAAAAAA 18

RESULT 910
US-10-106-799-3/c
; Sequence 3, Application US/10106799
; Publication No. US20030140379A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: No. US20030140379A1el DNA sequence in plants Caragana jubata with
; TITLE OF INVENTION: method thereof
; FILE REFERENCE: US 673
; CURRENT APPLICATION NUMBER: US/10/106,799
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T11G (anchored) primer for differential display
US-10-106-799-3

Query Match      0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAAAAAAAAAA 1748
Db      18 CAAAAAAAAAAAAA 5

RESULT 911
US-10-056-908-11/c
; Sequence 11, Application US/10056908
; Publication No. US20030165865A1
; GENERAL INFORMATION:
; APPLICANT: Hinkel, Christopher A.
; APPLICANT: Kimmerly, William J.
; APPLICANT: Yang, Li
; TITLE OF INVENTION: METHODS OF ANALYSIS OF NUCLEIC ACIDS
; FILE REFERENCE: TM0141-UT
; CURRENT APPLICATION NUMBER: US/10/056,908
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 60/264,972
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/266,186
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/295,986
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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```
; OTHER INFORMATION: Hybridization Tag
US-10-056-908-11

Query Match      0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1122 CGTGGAGAGGAGGG 1135
Db      15 CGTGGAGAGGAGGG 2

RESULT 912
US-10-109-363-18/c
; Sequence 18, Application US/10109363
; Publication No. US20030196214A1
; GENERAL INFORMATION:
; APPLICANT: SHARMA, PRITI
; APPLICANT: KUMAR, SANJAY
; APPLICANT: AHUJA, PARAMVIR SINGH
; TITLE OF INVENTION: NOVEL GENES FROM DROUGHT STRESS TOLERANT TEA PLANT AND A
; TITLE OF INVENTION: METHOD OF INTRODUCING WATER-STRESS TOLERANCE
; FILE REFERENCE: 3097-4009
; CURRENT APPLICATION NUMBER: US/10/109,363
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Camellia sinensis
US-10-109-363-18

Query Match      0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAAAAAAAAAA 1748
Db      18 CAAAAAAAAAAAAA 5

RESULT 913
US-10-623-371-142/c
; Sequence 142, Application US/10623371
; Publication No. US20040132677A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; APPLICANT: TUCK, Stephen F.
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-IV
; FILE REFERENCE: 377882002021
; CURRENT APPLICATION NUMBER: US/10/623,371
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/328,578
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 10/176,883
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/177,826
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
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US-10-623-371-142

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 18 AAAAAAAAAAAAAA 5

RESULT 914

US-09-866-108-896
; Sequence 896, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 896
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-896

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1020 TGGGGATGGGCTGGG 1036
Db 1 TGGGGAAGGGCTTGG 17

RESULT 915

US-09-866-108-7879
; Sequence 7879, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7879
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7879

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 835 GAAGCTGCTGGGCTCTC 851
Db 1 GGAGCTGCTGGGCTCAC 17

RESULT 916

US-09-866-108-10022
; Sequence 10022, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.

```

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10022
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10022

```

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 132 CGCTGCTCGAGTCCC 148
|||
Db 1 CGGTGCTCGGAGTCCTC 17

RESULT 917
US-09-866-108-10502
; Sequence 10502, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6

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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10502
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10502

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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15: Conservative 0; Mismatches 2; Indels

QY 805 CAGAGAGAGCCAGGGCC 821
Db 1 CGGAGAGAGCCAGGGAC 17

RESULT 918
US-09-108-10504
; Sequence 10504, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 10504
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10504

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02; Indels 2; Mismatches 0; Gaps 0;
Matches 15; Conservative 0;

QY 807 GAGAGCCAGGCGCAG 823
Db 1 GAGAGCCAGGCGG 17

RESULT 919

US-09-866-108-10505
; Sequence 10505, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 10505
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10505

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02; Indels 2; Mismatches 0; Gaps 0;
Matches 15; Conservative 0;

QY 808 AGAGAGCCAGGCGCAGG 824
Db 1 AGAGAGCCAGGCGG 17

RESULT 920

US-09-866-108-10506
; Sequence 10506, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 10506

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;
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10506

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      809 GAGAGCCAGGCCAGGG 825
Db      1 GAGAGCCAGGCCAGGG 17

RESULT 921
US-09-827-998-484
; Sequence 484, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMPF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 484
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-484

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      37 AAAAAAAAAAGCCAGAAA 53
Db      1 AAAAAAAAAAGAAAGAAA 17

RESULT 922
US-09-263-959-744
; Sequence 744, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 744:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-744

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1752
Db      1 AAAAAAAAAAAAAAAAAATAAA 17

RESULT 923
US-09-864-785-2145/c
; Sequence 2145, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2145
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2145

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1634 TCCTTTGATTGATCACT 1650
Db      17 TGCTTTGATTGTTCACT 1

RESULT 924
US-09-825-805-466
; Sequence 466, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti
; FILE REFERENCE: MBHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
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; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 466
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-466

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 6e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1151 GCTACGTGGCCACCCCTG 1167
Db 1 GCUACGUUGCCCCCUG 17

RESULT 925
US-09-825-805-563/c
; Sequence 563, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
; FILE REFERENCE: MBH00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 563
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-563

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 232 CGCGGCACCCCGGGGCC 248
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Db 17 CGCGGCTGCCCGGGGCC 1

RESULT 926
US-09-961-077-881/c
; Sequence 881, Application US/09961077
; Publication No. US20030014775A1
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; Edington, Brent E.
; McSwiggen, James A.
; Merlo, Patricia Ann Owens
; Guo, Lining
; Skokut, Thomas A.
; Young, Scott A.
; Folkerts, Otto
; Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; MODULATION OF GENE EXPRESSION
; IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/961,077
; FILING DATE: 21-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/679,645
; FILING DATE: July 12, 1996
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 881:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 881:
US-09-961-077-881

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1733 TACAAAAAATAAAAAA 1749
Db 17 TACAAAAAATAAAAAA 1
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RESULT 927
US-09-780-533A-1375/c
; Sequence 1375, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1375
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1375

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1329 CTTTCACAGGAAGTTTG 1345
Db      17 CTTTCACAGAAGACTTTG 1

RESULT 928
US-09-780-533A-2357
; Sequence 2357, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2357
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2357

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      861 AGGAAGAGGAAGAGGAG 877
Db      1 AGGAGGAAGAAGAGGAG 17

RESULT 929
US-09-780-533A-2358
; Sequence 2358, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
```

```

; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2358
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2358

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      861 AGGAAGAGGAAGAGGAG 877
Db      1 AGGAAGAGAGGAGGAG 17

RESULT 930
US-09-780-533A-2367
; Sequence 2367, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2367
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2367

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      861 AGGAAGAGGAAGAGGAG 877
Db      1 AGGAAGAGGAGGAGGAG 17

RESULT 931
US-09-848-754A-2551
; Sequence 2551, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2551
```

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; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2551

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 6e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 959 TGAACACCCGCCCCGAGC 975
Db 1 UGAACCCCGCCGCCGAGC 17

RESULT 932
US-09-848-754A-3385/c
; Sequence 3385, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3385
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3385

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 240 CCCGGGCCACCCACCGG 256
Db 17 CCCAGGGCCACCCACGAG 1

RESULT 933
US-09-930-423-1448
; Sequence 1448, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1448

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 AAAAAAAGCCAGAAAA 54
Db 1 AAAAAAAGAACUAGAAAA 17

RESULT 934
US-09-780-164-1043
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```
; Sequence 1043, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1043
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-1043

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 860 CAGGAAGAGGAGAGGA 876
Db 1 CAAGAAGAGGAGAGGA 17

RESULT 935
US-09-827-395A-646/c
; Sequence 646, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 646
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-646

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 852 TGGCCCTGCAGGAGAG 868
Db 17 TTGCCGTGCAGGAGAG 1

RESULT 936
US-09-740-332-106
; Sequence 106, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
```

; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-106

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 6e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 880 GAGCAGGGGCCCCAGGT 896
| ||| ||||| ||||| :
Db 1 GCGCAGGGGCCCCAGGU 17

RESULT 937
US-09-740-332-2617
; Sequence 2617, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2617
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2617

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 6e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1005 CGGAGAAGATGTGTTG 1021
| |||| ||||| ||||| :
Db 1 CGGAGCGGAUGUGGUUG 17

RESULT 938
US-09-740-332-3100/c
; Sequence 3100, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3100
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-3100

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1212 GCGGGCTATGGGAAGG 1228
| ||||| ||||| ||||| :
Db 17 GCGGGCTATGGAGCAGG 1

RESULT 939
US-09-792-818-92
; Sequence 92, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insert
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-92

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 203 CCAGAGCCCCCTCAGGGG 219
| ||||| ||||| ||||| :
Db 1 CCAGAGCUCCCCAGGGG 17

RESULT 940
US-09-792-818-275
; Sequence 275, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insert
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 275
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-275

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 202 GCCAGAGCCCTCAGGG 218
| | | | |
Db 1 GCCAGAGCUCCCGAGGG 17

RESULT 941

US-09-792-818-276
; Sequence 276, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insertion
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 276
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-792-818-276

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 CAGAGCCCTCAGGGGA 220
| | | | |
Db 1 CAGAGCUCCCGAGGGGA 17

RESULT 942

US-09-792-818-373/c
; Sequence 373, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insertion
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 373
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-792-818-373

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1133 GGCATATTCGAGGCG 1149
| | | | |
Db 17 GGCATATTCGAGGCG 1

RESULT 943

US-09-792-818-521/c
; Sequence 521, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insertion
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 521
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-792-818-521

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1135 GCATATTCGAGGGCTG 1151
| | | | |
Db 17 GCATATTCGAGGGCTG 1

RESULT 944

US-09-745-237A-1448
; Sequence 1448, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-745-237A-1448

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 AAAAAAAAAAGCCAGAAAA 54
| | | | |
Db 1 AAAAAAAAAACUAGAAAA 17

RESULT 945

US-09-817-879-106
; Sequence 106, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1133 GGCATATTCGAGGCG 1149
| | | | |
Db 17 GGCATATTCGAGGCG 1

RESULT 943

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-106

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 6e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 880 GAGCAGCGGCCCCAGGT 896
| ||| ||||| |||||
Db 1 GCGCAGCGGCCCCAGGU 17

RESULT 946
US-09-817-879-2617
; Sequence 2617, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2617
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2617

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 6e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1005 CGGAGAGATGTGTTG 1021
| |||| |:::|
Db 1 CGGAGCGGAUGGUUG 17

RESULT 947
US-09-817-879-3100/c
; Sequence 3100, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3100
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate

US-09-817-879-3100

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1212 GCGGCTATGGGAAG 1228
| ||||| |||||
Db 17 GCGGCTATGGAGCAGG 1

RESULT 948
US-10-675-685-484
; Sequence 484, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 484
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-484

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 37 AAAAAAAAAAGCCAGAAA 53
| ||||| |||||
Db 1 AAAAAAAAAAGAGAAA 17

RESULT 949
US-09-915-152-31/c
; Sequence 31, Application US/09915152
; Publication No. US20020082298A1
; GENERAL INFORMATION:
; APPLICANT: Fluehmann, Beat
; APPLICANT: Helm, Manuel
; APPLICANT: Hunziker, Willi
; APPLICANT: Weber, Peter
; TITLE OF INVENTION: PHYTANIC ACID DERIVATIVE COMPOSITIONS AND METHOD OF TREATING AND/OR PREVENTING DIABETES MELLITUS
; FILE REFERENCE: 20722 US/Mez (C038435/0119491)
; CURRENT APPLICATION NUMBER: US/09/915,152
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: EPO 00116848.3
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide used for the amplification of LDLR.

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 694 AGGGCTGCGCCACC 710
Db 17 AGGGCTGCTGACCACC 1
RESULT 950
US-10-430-882-646/c
; Sequence 646, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor

; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 646
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-646

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 852 TGGCCCTGCAGGAAGAG 868
Db 17 TTGCCGTGCAGGAAGAG 1

RESULT 951
US-10-060-756A-384.
; Sequence 384, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804

; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 384
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-384

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 855 CCCTGCAGGAAGAGAA 871
Db 1 CCCTGCCGAGGAGGAA 17

RESULT 952
US-10-060-756A-647/c
; Sequence 647, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 647
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-647

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 852 TGGCCCTGCAGGAAGAG 868
Db 17 TGGCCCTGCAGGAAGCG 1

RESULT 953
US-10-060-895A-228/c
; Sequence 228, Application US/10060895A
; Publication No. US20030104403A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 10
; FILE REFERENCE: PB0158
; CURRENT APPLICATION NUMBER: US/10/060,895A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/315,984
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 1682
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 228
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-895A-228

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1025 ATGGGGCTGGGTTGTG 1041
Db 17 ATGGGGCTGGCGCTGTG 1

RESULT 954
US-10-060-895A-229/c
; Sequence 229, Application US/10060895A
; Publication No. US2003010403A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 10
; FILE REFERENCE: PB0158
; CURRENT APPLICATION NUMBER: US/10/060,895A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/315,984
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 1682
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 229
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-060-895A-229

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1024 GATGGGCTGGGTTGT 1040
Db 17 GATGGGCTGGCGCTGT 1

RESULT 955
US-10-060-895A-230/c
; Sequence 230, Application US/10060895A
; Publication No. US2003010403A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 10
; FILE REFERENCE: PB0158
; CURRENT APPLICATION NUMBER: US/10/060,895A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/315,984
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 1682
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 230
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-895A-230

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1023 GGATGGGCTGGGTTG 1039
Db 17 GGATGGGCTGGCGCTG 1

RESULT 956
US-10-060-895A-257
; Sequence 257, Application US/10060895A
; Publication No. US2003010403A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 10
; FILE REFERENCE: PB0158
; CURRENT APPLICATION NUMBER: US/10/060,895A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/315,984
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 1682
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 257
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-895A-257

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1535 CCTGCAGCGCCTGGCGC 1551
||||| ||||| |||||
Db 1 CCTGAAGCGCCTGTGCG 17

RESULT 957
US-10-163-552-6/c
; Sequence 6, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; TITLE OF INVENTION: HER2
; FILE REFERENCE: MBHB01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-6

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 232 CGCGCACCCCGGGGCC 248
||||| ||||| |||||
Db 17 CGCGCGTGTCCCGGGGCC 1

RESULT 958
US-10-163-552-826
; Sequence 826, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level

; TITLE OF INVENTION: HER2
; FILE REFERENCE: MBHB01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 826
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-826

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 6e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1151 GCTACGTGGCCACCCTG 1167
||:||||: ||||| |||||
Db 1 GCUACGUUGCCCCCUG 17

RESULT 959
US-10-081-646-23/c
; Sequence 23, Application US/10081646
; Publication No. US20030108884A1
; GENERAL INFORMATION:
; APPLICANT: Rice, Robert No. US20030108884Alman
; APPLICANT: Harrison, Bruce Thomas
; TITLE OF INVENTION: A Method and Kit
; FILE REFERENCE: 37921-2
; CURRENT APPLICATION NUMBER: US/10/081,646
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 60/316,308
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Primer
US-10-081-646-23

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1357 TCAGTGTGGGTGGGGC 1373
||||| ||||| |||||
Db 17 TCAGTGTGGGAGGGGC 1

RESULT 960
US-10-156-306-517/c
; Sequence 517, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 517
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-517

```
Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAGATAA 1

RESULT 961
US-10-156-306-518/c
; Sequence 518, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 518
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-518

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAGATAA 1

RESULT 962
US-10-156-306-519/c
; Sequence 519, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 519
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-519

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAGATAA 1

RESULT 963
US-10-189-956-62/c
; Sequence 62, Application US/10189956
; Publication No. US20030152951A1
; GENERAL INFORMATION:
; APPLICANT: Mirel, Daniel B
```

```
; APPLICANT: Erlich, Henry A
; APPLICANT: Bugawan, Teodorica L
; APPLICANT: No. US20030152951A1, Janelle A
; APPLICANT: Valdes, Ana M
; TITLE OF INVENTION: IL-4 RECEPTOR SEQUENCE VARIATION ASSOCIATED WITH TYPE 1
; TITLE OF INVENTION: DIABETES
; FILE REFERENCE: 1803-295-999
; CURRENT APPLICATION NUMBER: US/10/189,956
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: allele specific PCR primer
US-10-189-956-62

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 898 CCCCTGAGCCAGCCTCC 914
Db 17 CCCCTGAGCCAGTCACC 1

RESULT 964
US-10-238-700-2807/c
; Sequence 2807, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2807
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-2807

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 736 GGGCCCTCCCGGCCCC 752
Db 17 GGGCCCGCGCCCGGCCCC 1

RESULT 965
US-10-238-700-2872
; Sequence 2872, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
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```
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2872
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-2872

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 6e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      730 GCTTCTGGGCCCCCTCCC 746
Db      1 GCUCUCGGCCCCCUCC 17

RESULT 966
US-10-339-782-67
; Sequence 67, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-000110US
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-67

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      320 GTTACCAGGCCCCAGGG 336
Db      1 GATCCAGGCCCCAGGG 17

RESULT 967
US-10-061-201-1507/c
; Sequence 1507, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence.Listing Engine
; SEQ ID NO 1507
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1507

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      893 AGGTGCCCTGAGCCAG 909
Db      17 AGACGCCCTGAGCCAG 1

RESULT 968
US-10-230-006-523/c
; Sequence 523, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 523
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-523

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      529 GAGCCCCCGCCACCTCC 545
Db      17 GAGCCCCCGGCAGCTCC 1

RESULT 969
US-10-230-006-1288/c
; Sequence 1288, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1288
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

US-10-230-006-1288

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 263 GAGCAGCACTCCAGCCC 279
||||| ||||| ||||| |||||
Db 17 GAGCACCACCCAGCCC 1

RESULT 970

US-10-230-006-2124/c
; Sequence 2124, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2124
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-2124

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 264 AGCAGCACTCCAGCCC 280
||||| ||||| ||||| |||||
Db 17 AGCACCACCCAGCCC 1

RESULT 971

US-10-138-674-675/c
; Sequence 675, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 675
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-675

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 771 CCGAGGTGAAGTCTGGG 787
||||| ||||| ||||| |||||
Db 17 CCGAGTTGTAGTCTGGG 1

RESULT 972

US-10-138-674-1078/c
; Sequence 1078, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1078
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1078

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1748
|| ||||| ||||| |||||
Db 17 TTGGAAAAA 1

RESULT 973

US-10-138-674-1079/c
; Sequence 1079, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1079

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1747
||| ||||| ||||| |||||
Db 17 TTGGAAAAA 1

RESULT 974

US-10-138-674-3602/c
; Sequence 3602, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3602

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
||| ||||| |||||
Db 17 AAAAAAAAAACAAAAA 1

RESULT 975

US-10-138-674-3603/c
; Sequence 3603, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3603
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3603

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
||| ||||| |||||
Db 17 AAAAAAAAAACAAAAA 1

RESULT 976

US-10-138-674-3604/c
; Sequence 3604, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3604
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3604

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1751
||| ||||| |||||
Db 17 CAAAAACAAAAACAAA 1

RESULT 977

US-10-138-674-3605/c
; Sequence 3605, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3605
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3605

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAA 1750
||| ||||| |||||
Db 17 CAAAAACAAAAACAAA 1

RESULT 978

US-10-138-674-3607/c
; Sequence 3607, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3607
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3607

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 675
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-675

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      771 CCGAGGTGAAGTCTGGG 787
Db      17 CCGAGTGTAGTCTGGG 1

RESULT 984
US-10-287-949A-1078/c
; Sequence 1078, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1078
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1078

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1732 TTACAAAAA 1748
Db      17 TTGGA 1

RESULT 985
US-10-287-949A-1079/c
; Sequence 1079, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
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```
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1079

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1731 TTTACAAAAA 1747
Db      17 TTTGGA 1

RESULT 986
US-10-287-949A-3602/c
; Sequence 3602, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3602

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1736 AAAAAA 1752
Db      17 AAACAA 1

RESULT 987
US-10-287-949A-3603/c
; Sequence 3603, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3603
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3603

Query Match      0.8%; Score 13.8; DB 1; Length 17;
```

Best Local Similarity 88.2%; Pred. No. 6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAACAAAAA 1

RESULT 988

US-10-287-949A-3604/c
; Sequence 3604, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3604
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3604

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAA 1751
Db 17 CAAAAACAAAAACAAA 1

RESULT 989

US-10-287-949A-3605/c
; Sequence 3605, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3605
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3605

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1734 AAAAAAAAAAAAAAAAAA 1750
Db 17 AAAAAACAAAAACAAA 1

RESULT 990

US-10-287-949A-3607/c
; Sequence 3607, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3607
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3607

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1734 AAAAAAAAAAAAAAAAAA 1750
Db 17 AAAAAACAAAAACAAA 1

RESULT 991

US-10-287-949A-5015/c
; Sequence 5015, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5015
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5015

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 772 CGAGTGAAGTCTGGG 788
Db 17 CGAGTTGTAGTCTGGG 1

RESULT 992

US-10-287-949A-7840/c
; Sequence 7840, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

```

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7840
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7840

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      774 AGGTGAAGTCTGGGGGC 790
      ||| ||||| |||||
Db      17 AGTTGTAGTCTGGGGGC 1

RESULT 993
US-10-712-672-637/c
; Sequence 637, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 637
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-637

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      345 GGATCGGGGGCCCGCGT 361
      ||| ||||| |||||
Db      17 GGATGGGGGGCCCGCGT 1

RESULT 994
US-10-712-672-902
; Sequence 902, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31

```

; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2044
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2044

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 6e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 734 CTGGGCCCTCCCGGC 750
Db 1 CUGGCCCAACCGGC 17

RESULT 997
US-10-712-672-2080
; Sequence 2080, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2080
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2080

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 640 AGCACCCCGCTGGCC 656
Db 1 AGCACCCAGCGGGCC 17

RESULT 998
US-10-669-841-2699
; Sequence 2699, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; FILE REFERENCE: 400/042US (MBH02-249-E)

; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2699
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-2699

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 6e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 880 GAGCAGGGCCCCAGGT 896
Db 1 GCGCAGGGCCCCAGGU 17

RESULT 999
US-10-669-841-5210
; Sequence 5210, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05

; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5210
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-5210

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 4;

QY 1005 CGGAGAAGATGTGGTTG 1021
||||| |:|:|:|:
Db 1 CGGAGCGGAUGUGGUUG 17

RESULT 1000
US-10-669-841-5693/c
; Sequence 5693, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5693
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-5693

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1212 GCGGGCTATGGGAAGG 1228
||||| |:|:|:|:
Db 17 GCGGGCTATGGAGCAGG 1

RESULT 1001
US-10-723-361-896
; Sequence 896, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 896
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-896

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1020 TGGGGATGGGGCTGGG 1036
||||| ||||| |||

Db 1 TGGGGAAGGGCTTGGG 17

RESULT 1002

US-10-723-361-7879
; Sequence 7879, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7879
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7879

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 835 GAAGCTGCTGGGGTCTC 851
| ||||| ||||| |||

Db 1 GGAGCTGCTGGGGTCTC 17

RESULT 1003

US-10-723-361-10022
; Sequence 10022, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10022
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10022

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 132 CGTGTCTGGAGTCCCC 148
|| ||||| ||||| |

Db 1 CGGTGTCTGGAGTCTC 17

RESULT 1004

US-10-723-361-10502
; Sequence 10502, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7879
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7879

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 835 GAAGCTGCTGGGGTCTC 851
| ||||| ||||| |||

Db 1 GGAGCTGCTGGGGTCTC 17

RESULT 1003

US-10-723-361-10022
; Sequence 10022, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

;
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10502
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10502

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 805 CAGAGAGCCAGGCC 821
Db 1 CGGAGAGCCAGGGAC 17

RESULT 1005
US-10-723-361-10504
; Sequence 10504, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10504
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10504

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 807 GAGAGAGCCAGGCCAG 823

Db 1 GAGAGAGCCAGGGACGG 17
RESULT 1006
US-10-723-361-10505
; Sequence 10505, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10505
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10505

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 808 AGAGAGCCAGGCCAGG 824
Db 1 AGAGAGCCAGGGACGGG 17

RESULT 1007
US-10-723-361-10506
; Sequence 10506, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361

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; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10506
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10506

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      809 GAGAGCCAGGCGCAGGG 825
Db      1 GAGAGCCAGGCGCAGGG 17

RESULT 1008
US-10-766-118-31/c
; Sequence 31, Application US/10766118
; Publication No. US20040138181A1
; GENERAL INFORMATION:
; APPLICANT: Fluehmann, Beat
; APPLICANT: Heim, Manuel
; APPLICANT: Hunziker, Willi
; APPLICANT: Weber, Peter
; TITLE OF INVENTION: PHYTANIC ACID DERIVATIVE COMPOSITIONS AND METHOD OF TREATING
; TITLE OF INVENTION: AND/OR PREVENTING DIABETES MELLITUS
; FILE REFERENCE: 20722 US/Mez (C038435/0119491)
; CURRENT APPLICATION NUMBER: US/10/766,118
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US/09/915,152
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: EPO 00116848.3
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide used for the amplification of LDLR.
US-10-766-118-31

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      694 AGGGGCTGGGCCACC 710
Db      1 AGGGGCTGGGCCACC 710

; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10506
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10506

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      809 GAGAGCCAGGCGCAGGG 825
Db      1 GAGAGCCAGGCGCAGGG 17

RESULT 1008
US-10-766-118-31/c
; Sequence 31, Application US/10766118
; Publication No. US20040138181A1
; GENERAL INFORMATION:
; APPLICANT: Fluehmann, Beat
; APPLICANT: Heim, Manuel
; APPLICANT: Hunziker, Willi
; APPLICANT: Weber, Peter
; TITLE OF INVENTION: PHYTANIC ACID DERIVATIVE COMPOSITIONS AND METHOD OF TREATING
; TITLE OF INVENTION: AND/OR PREVENTING DIABETES MELLITUS
; FILE REFERENCE: 20722 US/Mez (C038435/0119491)
; CURRENT APPLICATION NUMBER: US/10/766,118
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US/09/915,152
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: EPO 00116848.3
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide used for the amplification of LDLR.
US-10-766-118-31

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      694 AGGGGCTGGGCCACC 710
Db      1 AGGGGCTGGGCCACC 710
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Db      17 AGGGGCTGCTGACCACC 1

RESULT 1009
US-09-942-588A-22
; Sequence 22, Application US/09942588A
; Patent No. US20020106667A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Screening method for gene variation
; FILE REFERENCE: CFO 15717
; CURRENT APPLICATION NUMBER: US/09/942,588A
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263396
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 67
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-588A-22

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      482 ATGGGGCTCGGGTTCAT 498
Db      2 ATGGGGCTCGGGTTCAT 18

RESULT 1010
US-09-764-420A-23
; Sequence 23, Application US/09764420A
; Patent No. US20020115072A1
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Yamamoto, No. US20020115072A1uko
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Probe Bound Substrate, Process For
; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of
; TITLE OF INVENTION: Detecting Target Substance, Method Of
; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-
; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; TITLE OF INVENTION: In Sample
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-23

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      482 ATGGGGCTCGGGTTCAT 498
Db      2 ATGGGGCTCGGGTTCAT 18

RESULT 1011
US-09-764-420A-23
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; Sequence 23, Application US/09764420A
; Publication No. US20030198952A9
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Yamamoto, No. US20030198952A9uko
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Probe Bound Substrate, Process For
; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of
; TITLE OF INVENTION: Detecting Target Substance, Method Of
; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-
; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; TITLE OF INVENTION: In Sample
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-23

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGGTCTCGGGTTCAT 498
||||| ||||| |||||
Db 2 ATGGGGGTCTCGGGTTCAT 18

RESULT 1012

US-09-969-373-2606/c
; Sequence 2606, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2606
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2606

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 862 GGAAGAGGAGGAGGAGG 878
||||| ||||| |||||
Db 18 GGAAGAGGAGGAGGAGG 2

RESULT 1013

US-09-969-373-3605
; Sequence 3605, Application US/09969373
; Patent No. US20020133852A1

; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3605
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3605

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1569 CACCGTCACCACTGACT 1585
||||| ||||| |||||
Db 1 CACCGTCACCACTGCT 17

RESULT 1014

US-09-728-574-2
; Sequence 2, Application US/09728574
; Patent No. US20020137036A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; TITLE OF INVENTION: Methods for Detection of a Target Nucleic Acid By Capture
; FILE REFERENCE: 25436/1660
; CURRENT APPLICATION NUMBER: US/09/728,574
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 09/728574
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cleavage product of oligonucleotide Heltest4
; NAME/KEY: cleavage product of oligonucleotide Heltest4
; LOCATION: (1)..(18)
US-09-728-574-2

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
||||| ||||| |||||
Db 1 AAATAAATAAAAAAAAAA 17

RESULT 1015

US-09-942-596A-22
; Sequence 22, Application US/09942596A
; Patent No. US20020168648A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Method of analyzing base sequence of nucleic acid
; FILE REFERENCE: CFO 15718
; CURRENT APPLICATION NUMBER: US/09/942,596A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 263506/2000

; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-596A-22

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 482 ATGGGGTCGGGGTTCAT 498
Db 2 ATGGGGTCGGGGTTCAT 18

RESULT 1016

US-09-988-873A-22
; Sequence 22, Application US/09988873A
; Publication No. US20030027160A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Terminal labelled probe array and method of making it
; FILE REFERENCE: CF015961
; CURRENT APPLICATION NUMBER: US/09/988,873A
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: JP2000-357446
; PRIOR FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized
US-09-988-873A-22

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 482 ATGGGGTCGGGGTTCAT 498
Db 2 ATGGGGTCGGGGTTCAT 18

RESULT 1017

US-09-925-388-30
; Sequence 30, Application US/09925388
; Publication No. US20030054523A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/925,388
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/306,595
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of 5'-adjacent region of MVK gene
US-09-925-388-30

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 28 GGAAGAGAGAAAAAAA 44
Db 1 GGAAGAGAGAGAAAAA 17

RESULT 1018

US-09-942-662A-22
; Sequence 22, Application US/09942662A
; Publication No. US20030190612A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: An assay of many samples for multiple items at the same time
; FILE REFERENCE: 3912041
; CURRENT APPLICATION NUMBER: US/09/942,662A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263395
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263505
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-662A-22

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 482 ATGGGGTCGGGGTTCAT 498
Db 2 ATGGGGTCGGGGTTCAT 18

RESULT 1019

US-10-463-549-23
; Sequence 23, Application US/10463549
; Publication No. US20040053308A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Kumi
; TITLE OF INVENTION: Probe Immobilized Substrate and Method for Manufacturing the Same,
; FILE REFERENCE: 03560.003309
; CURRENT APPLICATION NUMBER: US/10/463,549
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 2002-190009
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 2002-189836
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-463-549-23

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 482 ATGGGGTCGGGGTTCAT 498
Db 2 ATGGGGTCGGGGTTCAT 18

```
RESULT 1020
US-10-231-302-22
; Sequence 22, Application US/10231302
; Publication No. US20030082602A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, No. US20030082602A1uko
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Method for analyzing base sequence of nucleic acid
; FILE REFERENCE: 03500.015203
; CURRENT APPLICATION NUMBER: US/10/231,302
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/JP00/07244
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-231-302-22
Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      482 ATGGGGTCTGGGGTCAT 498
      ||||| ||||| |||||
Db      2 ATGGGGCTCGGGTTCAT 18

RESULT 1021
US-10-153-401-52/c
; Sequence 52, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; Foon, Kenneth A.
; Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
```

```
TELEFAX: (415) 494-0792
TELEX: 706141
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-153-401-52
Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      297 TTGCCCCCTTCCATCTG 313
      ||| ||||| |||||
Db      17 TTGGGCCCTTCCATCTG 1

RESULT 1022
US-10-082-502-15
; Sequence 15, Application US/10082502
; Publication No. US20030171542A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jelinek, Laura J.
; TITLE OF INVENTION: Mammalian Secretory Protein - 9
; FILE REFERENCE: 97-11C2
; CURRENT APPLICATION NUMBER: US/10/082,502
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/318,028
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/109,808
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/089,899
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/085,983
; PRIOR FILING DATE: 1998-05-19
; PRIOR APPLICATION NUMBER: 60/051,704
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-082-502-15
Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1570 ACCGTCACCACTGACTG 1586
      ||| ||||| |||||
Db      2 ACCTCCACCACTGACTG 18

RESULT 1023
US-10-306-878-18/c
; Sequence 18, Application US/10306878
; Publication No. US20030175819A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Guo, Bin
; TITLE OF INVENTION: Methods for Identifying Modulators of
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: P-LJ 5535
; CURRENT APPLICATION NUMBER: US/10/306,878
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US 60/334,149
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 28
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-306-878-18

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1123 GTGGAGAGGAGGGCATA 1139
Db      18  GTGAAGAGGCGGCATA 2

RESULT 1024
US-10-025-145A-60
; Sequence 60, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Corresponding to Conserved Amino Acid Sequence Se
; OTHER INFORMATION: t Forth in SEQ ID NO:49
US-10-025-145A-60

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      749 GCCCCCCACTTTCCTCTC 765
Db      1  GCCACCACCTTCCTCTC 17

RESULT 1025
US-10-431-846-30
; Sequence 30, Application US/10431846
; Publication No. US20030190734A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/10/431,846
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US/09/925,388
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/306,595
; PRIOR FILING DATE: 1999-05-06
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```
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sense primer
; OTHER INFORMATION: for cloning of 5'-adjacent region of MVK gene
US-10-431-846-30

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      28  GGAAGAGGAAAAAAA 44
Db      1  GGAAGAGGAGAGAAAA 17

RESULT 1026
US-10-608-804-22
; Sequence 22, Application US/10608804
; Publication No. US20040014124A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, No. US20040014124A1uko
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Shimizu, Satoshi
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Method for Examining Reactivity and Method for Detecting a Complex
; FILE REFERENCE: 03500.015716.1
; CURRENT APPLICATION NUMBER: US/10/608,804
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US/09/942,662
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263395
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263505
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-10-608-804-22

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      482 ATGGGGGTCGGGGTCAT 498
Db      2  ATGGGGCTCGGGTTCAT 18

RESULT 1027
US-10-634-510-22
; Sequence 22, Application US/10634510
; Publication No. US20040018552A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Terminal labelled probe array and method of making it
; FILE REFERENCE: CF015961
; CURRENT APPLICATION NUMBER: US/10/634,510
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: JP2000-357446
; PRIOR FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthesized
US-10-634-510-22

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGGTCGGGGTCAT 498
Db      ||||| ||||| |||||
2 ATGGGGCTCGGGTTCAT 18

RESULT 1028
US-10-138-674-4028/c
; Sequence 4028, Application US/10138674
; Publication No. US2004007565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4028
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-4028

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 773 GAGGTGAAGTCTGGGG 789
Db      ||||| ||||| |||||
18 GAGTTGTAGTCTGGGG 2

RESULT 1029
US-10-287-949A-4028/c
; Sequence 4028, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4028
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-4028

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 773 GAGGTGAAGTCTGGGG 789
Db      ||||| ||||| |||||
18 GAGTTGTAGTCTGGGG 2

RESULT 1030
US-10-716-824-15
; Sequence 15, Application US/10716824
; Publication No. US20040110927A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jelinek, Laura J.
; TITLE OF INVENTION: Mammalian Secretory Protein - 9
; FILE REFERENCE: 97-11C2
; CURRENT APPLICATION NUMBER: US/10/716,824
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/10/082,502
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/318,028
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/109,808
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/089,899
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/085,983
; PRIOR FILING DATE: 1998-05-19
; PRIOR APPLICATION NUMBER: 60/051,704
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-716-824-15

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1570 ACCGTCACCACACTGACTG 1586
Db      ||||| ||||| |||||
2 ACCTCCACCACACTGACTG 18

RESULT 1031
US-10-481-044-8
; Sequence 8, Application US/10481044
; Publication No. US20040152101A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Novel polypeptide and use thereof
; FILE REFERENCE: P02-0068PCT
; CURRENT APPLICATION NUMBER: US/10/481,044
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: JP 2001-182275
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: JP 2001-233532
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
US-10-481-044-8

Query Match          0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1121 CCGTGGAGAGGAGGGCA 1137
Db      ||||| ||||| |||||
2-CCGTGAAGAGGCGGGCA 18
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RESULT 1032
US-09-805-296D-12/c
; Sequence 12, Application US/09805296D
; Patent No. US20020155989A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1US
; CURRENT APPLICATION NUMBER: US/09/805,296D
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-09-805-296D-12
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAGAAAAAA 1
RESULT 1033
US-09-880-313A-143
; Sequence 143, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-880-313A-143
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1530 CAAGGCCTGCAGCGC 1544
Db 1 CATGGCCTGCAGCGC 15

RESULT 1034
US-09-848-754A-9214/c
; Sequence 9214, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9214
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-9214
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1313 TCCACTGTATTGAGG 1327
Db 15 TCCACTGTGTGAGG 1
RESULT 1035
US-09-848-754A-9265
; Sequence 9265, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9265
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-9265
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 6.3e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 834 GGAAGCTGCTGGGT 848
Db 1 GGGAGCUGCUGGGU 15
RESULT 1036
US-10-339-674-267/c
; Sequence 267, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary

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; SEQ ID NO 267
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (319590)...(319604)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 362
US-10-339-674-267

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 577 CCAGCCTCGCCGCTC 591
Db 15 CCAGCTTCGCCGCTC 1

RESULT 1037
US-10-339-674-3455/c
; Sequence 3455, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 3455
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (4552785)...(4552799)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 4572
US-10-339-674-3455

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 577 CCAGCCTCGCCGCTC 591
Db 15 CCAGCTTCGCCGCTC 1

RESULT 1038
US-10-072-975-12/c
; Sequence 12, Application US/10072975
; Publication No. US20030059789A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakhecheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/10/072,975
; CURRENT FILING DATE: 2002-02-09
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/805,296
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/0811
```

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; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-072-975-12

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAGAAAAAA 1

RESULT 1039
US-10-051-436-12/c
; Sequence 12, Application US/10051436
; Publication No. US20030138045A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakhecheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1US
; CURRENT APPLICATION NUMBER: US/10/051,436
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-051-436-12

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAGAAAAAA 1

RESULT 1040
US-10-360-275-12/c
; Sequence 12, Application US/10360275
; Publication No. US20040014644A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
```

```
; APPLICANT: Archdeacon, John
; APPLICANT: Choob, Mikhail
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: AM102.P.1.1.IUS
; CURRENT APPLICATION NUMBER: US/10/360,275
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/072,975
; PRIOR FILING DATE: 2002-02-09
; PRIOR APPLICATION NUMBER: US 09/805,296
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-360-275-12

Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAA 1750
Db      15 AAAAAAAGAAAAAAA 1

RESULT 1041
US-10-287-919-2610
; Sequence 2610, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 2610
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1584335)...(1584350)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3325
US-10-287-919-2610

Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1325 AGGACTTTTCACAGGA 1339
Db      2 AGGACTTTTCACAGAA 16

RESULT 1042
US-10-164-915-3
; Sequence 3, Application US/10164915
; Publication No. US20030148391A1
; GENERAL INFORMATION:
; APPLICANT: Salafsky, Joshua S.
; TITLE OF INVENTION: Method Using a Surface-Selective No. US20030148391A1linear Optica
; TITLE OF INVENTION: for Detection of Interactions Involving a Conformational Change
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; FILE REFERENCE: 11100-035-999
; CURRENT APPLICATION NUMBER: US/10/164,915
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/253,862
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/260,249
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/265,775
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/278,941
; PRIOR FILING DATE: 2001-01-27
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Aritificial Sequence: Oligonucleotide structure for
; OTHER INFORMATION: molecular beacon
US-10-164-915-3

Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAA 1750
Db      2 AAAAAAACAAAAAAA 16

RESULT 1043
US-10-191-997-38/c
; Sequence 38, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.
; APPLICANT: ARROW, Amy
; APPLICANT: THOMPSON, Terry
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
; FILE REFERENCE: 54800-5019
; CURRENT APPLICATION NUMBER: US/10/191,997
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,820
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Ghre oligonucleotide
US-10-191-997-38

Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      167 GGCCACACCTGGCTGC 181
Db      16 GGCCACACCTGTCTGC 2

RESULT 1044
US-10-321-039-561
; Sequence 561, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
```

; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 561
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-321-039-561

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 6.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1533 GGCTGCGAGCGCCTG 1547
||| ||||| ||||| ||
Db 1 GGCTGCGAGCGCCAG 15

RESULT 1045

US-10-712-672-1517
; Sequence 1517, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1517
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1517

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1461 GTGTGGGTGCTGCTG 1475
|:| ||||| |:| ||:
Db 2 GUGGGGCGUCGUCGU 16

RESULT 1046

US-10-712-672-1655
; Sequence 1655, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1655
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1655

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 6.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 692 TCAGGGGCTGCGGCC 706
:| ||||| |||||
Db 2 UGACGGGCGCGGCC 16

RESULT 1047

US-10-230-006-2124
; Sequence 2124, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2124
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-2124

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1027 GGGGCTGGGTTGTG 1041
|||||:|||||:|:
Db 1 GGGGCGUGGGUGGUG 15

RESULT 1048

US-09-866-108-6390
; Sequence 6390, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6390
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-6390

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1177 GCCACGTGCTCCCG 1191
||| |||||
Db 3 GCCCGTGTCTCCCG 17

RESULT 1049

US-09-866-108-6391
; Sequence 6391, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6391
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-6391

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1177 GCCACGTGCTCCCG 1191
||| |||||
Db 2 GCCCGTGTCTCCCG 16

RESULT 1050

US-09-866-108-6392
; Sequence 6392, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 6392
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6392

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1177 GCCACGTGCTCCAG 1191
||| |||||
Db 1 GCCCGTGCTCCAG 15

RESULT 1051

US-09-866-108-7876
; Sequence 7876, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 6392
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6392

; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7876
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7876

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 834 GGAAGCTGCTGGGT 848
||| |||||
Db 3 GGGAGCTGCTGGGT 17

RESULT 1052

US-09-866-108-7880
; Sequence 7880, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7880
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7880

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 AGCTGCTGGGTCTC 851
Db 2 AGCTGCTGGGTAC 16

RESULT 1053

US-09-866-108-7881
; Sequence 7881, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7881
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7881

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 AGCTGCTGGGTCTC 851
Db 1 AGCTGCTGGGTAC 15

RESULT 1054

US-09-866-108-10020
; Sequence 10020, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10020
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10020

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 132 CGCTGTCTGGAGTCC 146
Db 3 CGGTGTCTGGAGTCC 17

RESULT 1055

US-09-866-108-10021
; Sequence 10021, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng

```
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10021
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10021
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Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 132 CGCTGTCTGGAGTCC 146
Db 2 CGGTGCTGGAGTCC 16
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RESULT 1056
US-09-866-108-10281/c
; Sequence 10281, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10281
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10281
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Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1288 TTCACAGTGGATGCT 1302
Db 17 TTCAAAGTGGATGCT 3
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RESULT 1057
US-09-866-108-10282/c
; Sequence 10282, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10282
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10282

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1288 TTCACAGTGGATGCT 1302
|||||
Db 16 TTCAAAGTGGATGCT 2

RESULT 1058

US-09-866-108-10283/c
; Sequence 10283, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10283
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10283

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1288 TTCACAGTGGATGCT 1302
|||||
Db 15 TTCAAAGTGGATGCT 1

RESULT 1059

US-09-866-108-10500
; Sequence 10500, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10500
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-866-108-10500

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 805 CAGAGAGCCAGGG 819
Db 3 CGGAGAGCCAGGG 17

RESULT 1060

US-09-866-108-10501
; Sequence 10501, Application US/09866108
; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 10501

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108-10501

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 805 CAGAGAGCCAGGG 819
Db 2 CGGAGAGCCAGGG 16

RESULT 1061

US-09-866-108-10503

; Sequence 10503, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 10503

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108-10503

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 807 GAGAGAGCCAGGCC 821
Db 2 GAGAGAGCCAGGAC 16

RESULT 1062

US-09-417-386-8

; Sequence 8, Application US/09417386

; Patent No. US20020090612A1

; GENERAL INFORMATION:

; APPLICANT: Rothberg, et al.

; TITLE OF INVENTION: METHOD OF IDENTIFYING NUCLEIC ACIDS

; FILE REFERENCE: 15966-539

; CURRENT APPLICATION NUMBER: US/09/417,386
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/115,109
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-09-417-386-8

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 613 CCCACTCCAGCCTCT 627
Db 3 CACACTCCAGCCTCT 17

RESULT 1063

US-09-864-785-289/c
; Sequence 289, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 289
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-289

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1022 GGGATGGGCTGGGG 1036
Db 15 GGGATAGGGCTGGGG 1

RESULT 1064

US-09-864-785-396
; Sequence 396, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 396

; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-396

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 704 GCCCACCAGGCGG 718
Db 3 GCCCACCAGGCGG 17

RESULT 1065

US-09-864-785-694/c
; Sequence 694, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 694
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-694

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1636 CTTTGATGATCACT 1650
Db 16 CTTTGATGATCACT 2

RESULT 1066

US-09-864-785-1439
; Sequence 1439, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1439
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1439

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Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1445 GTTACAAGTGCAGG 1459
Db 2 GCUACAAGUCGAGG 16

RESULT 1067
US-09-864-785-1440
; Sequence 1440, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1440
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1440

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1447 TACAAGTGCAGGAG 1461
Db 2 UACAAGUCGAGGG 16

RESULT 1068
US-09-864-785-1552/c
; Sequence 1552, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1552
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1552

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1023 GGATGGGGTGGGGT 1037
Db 17 GGATAGGGCTGGGGT 3
```

```
RESULT 1069
US-09-864-785-2828
; Sequence 2828, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2828
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2828

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 705 CCCACCCAGCGGGG 719
Db 1 CCCACCCAGCGUGGG 15

RESULT 1070
US-09-818-875-3406/c
; Sequence 3406, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3406
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-3406

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 CAGTTCAGTCCCA 1633
Db 16 CAGTCCAGTCCCA 2
```

RESULT 1071
US-09-818-875-3407
; Sequence 3407, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3407
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-3407

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1619 CAGTTCAGTCCCA 1633
|||||
Db 2 CAGTGCCAGTCCCA 16

RESULT 1072
US-09-780-533A-2365
; Sequence 2365, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2365
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2365

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 864 AAGAGGAAGAGGAGG 878
|||||
Db 1 AGGAGGAAGAGGAGG 15

RESULT 1073
US-09-848-754A-931/c

; Sequence 931, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 931
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-931

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1313 TCCACTGTATTGAGG 1327
|||||
Db 16 TCCACTGTATTGAGG 2

RESULT 1074
US-09-848-754A-999
; Sequence 999, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 999
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-999

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 834 GGAAGCTGCTGGGT 848
|||||
Db 3 GGGAGCUCUGGGGU 17

RESULT 1075
US-09-848-754A-1327/c
; Sequence 1327, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1327
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-1327

```
Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 239 CCCCGGGGCCACCAC 253
Db 15 CCCAGGGCCACCAC 1

RESULT 1076
US-09-848-754A-2220
; Sequence 2220, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2220
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2220

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 834 GGAAGCTGCTGGGT 848
Db 2 GGGAGCUGCUGGGGU 16

RESULT 1077
US-09-930-423-27
; Sequence 27, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-27

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1145 AGGGCTGCTACGTGG 1159
Db 3 AGGGCUACUACGUGG 17

RESULT 1078
US-09-930-423-497
; Sequence 497, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
```

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; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-497

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1145 AGGGCTGCTACGTGG 1159
Db 1 AGGGCUACUACGUGG 15

RESULT 1079
US-09-930-423-1320
; Sequence 1320, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1320
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1320

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 6.8e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 202 GCCAGAGCCCCCTCAG 216
Db 3 GCCAGAGCACCUCAG 17

RESULT 1080
US-09-780-164-1035
; Sequence 1035, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1035
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-1035
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Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1009 GAAGATGTGGTGGG 1023
Db 1 GAAGAGUGGUUGGG 15

RESULT 1081
US-09-827-395A-37/c
; Sequence 37, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-37

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 855 CCCTGCAGGAAGAGG 869
Db 17 CCGTGCAGGAAGAGG 3

RESULT 1082
US-09-827-395A-559/c
; Sequence 559, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 559
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-559

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1528 TGCAAGGCGCTGCAGC 1542

Db 16 TGCCAGGCGCTGCAGC 2

RESULT 1083
US-09-827-395A-856/c
; Sequence 856, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 856
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-856

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1528 TGCAAGGCGCTGCAGC 1542
Db 17 TGCCAGGCGCTGCAGC 3

RESULT 1084
US-09-740-332-4449/c
; Sequence 4449, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4449
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4449

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 882 GCACGGGCCCCCAGGT 896
Db 16 GCAGGGGCCCCCAGGT 2

RESULT 1085
US-09-745-237A-27
; Sequence 27, Application US/09745237A

```
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-27

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1145 AGGGCTGCTACTGG 1159
Db 3 AGGGCUACUACGUGG 17

RESULT 1086
US-09-745-237A-497
; Sequence 497, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-497

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1145 AGGGCTGCTACTGG 1159
Db 1 AGGGCUACUACGUGG 15

RESULT 1087
US-09-745-237A-1320
; Sequence 1320, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1320
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-09-745-237A-1320

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 6.8e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 202 GCCAGAGCCCTCAG 216
Db 3 GCCAGAGCACCUACAG 17

RESULT 1088
US-09-817-879-4449/c
; Sequence 4449, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4449
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4449

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 882 GCACGGGCCCCAGGT 896
Db 16 GCAGGGGCCCCAGGT 2

RESULT 1089
US-10-426-179-8
; Sequence 8, Application US/10426179
; Publication No. US20040029155A1
; GENERAL INFORMATION:
; APPLICANT: Curagen Corporation
; APPLICANT: Rothberg, Jonathan
; APPLICANT: et al.,
; TITLE OF INVENTION: Method for Identifying a Biomolecule
; FILE REFERENCE: 15966-539 CIP CON (Cura-39 CIP CON)
; CURRENT APPLICATION NUMBER: US/10/426,179
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: USSN 09/614505
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: USSN 09/417386
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: USSN 60/115109
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: PCR primer and adaptor
US-10-426-179-8

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
```


Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 613 CCCACTCCAGCCTCT 627
| | | | | | | | | |
Db 3 CACACTCCAGCCTCT 17

RESULT 1090

US-09-927-046-403/c
; Sequence 403, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 403
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-403

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 908 AGCCTCCAGAGGATG 922
| | | | | | | | | |
Db 17 AGCCTCCCGAGGATG 3

RESULT 1091

US-09-927-046-2136/c
; Sequence 2136, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2136
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-2136

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 908 AGCCTCCAGAGGATG 922
| | | | | | | | | |
Db 16 AGCCTCCCGAGGATG 2

RESULT 1092
US-09-927-046-2137/c
; Sequence 2137, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2137
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-2137

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 908 AGCCTCCAGAGGATG 922
| | | | | | | | | |
Db 15 AGCCTCCCGAGGATG 1

RESULT 1093

US-10-430-882-37/c
; Sequence 37, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor Gene
; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-37

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 855 CCCTGCAGGAGG 869

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/327,898
;; PRIOR FILING DATE: 2001-10-09
;; NUMBER OF SEQ ID NOS: 4804
;; SOFTWARE: Aeomica Sequence Listing Engine
;; SEQ ID NO 649
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-756A-649

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 852 TGGCCCTGCAGGAAG 866
||| ||||| |||||
Db 15 TGGCCCTGCAGGAAG 1

RESULT 1098
US-10-156-306-526/c
; Sequence 526, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 526
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-526

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1731 TTACAAAAA 1745
||| ||||| |||||
Db 15 TTAAAAA 1

RESULT 1099
US-10-156-306-5855/c
; Sequence 5855, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5855
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-10-156-306-5855
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1536 CTGACGCCCTGGCG 1550
||||| ||||| |||||
Db 15 CTGACGCCCTGGCG 1
RESULT 1100
US-10-156-306-5868/c
; Sequence 5868, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5868
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5868

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 849 CTCTGCCCTGCAGG 863
||||| ||||| |||||
Db 15 CTCTGCCCTGCATG 1

RESULT 1101
US-10-156-306-6933/c
; Sequence 6933, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6933
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-6933

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1537 TGCAGGCCCTGGCGC 1551
||||| ||||| |||||
Db 17 TGCAGGCCCTGGCGC 3

RESULT 1102
US-10-156-306-6937/c
; Sequence 6937, Application US/10156306
; Publication No. US20030119017A1

```

; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6937
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-6937

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      849 CTCTGGCCCTGCAGG 863
Db      17 CTCTGGCCCTGCATG 3

RESULT 1103
US-10-156-306-6938/c
; Sequence 6938, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6938
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-6938

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      849 CTCTGGCCCTGCAGG 863
Db      16 CTCTGGCCCTGCATG 2

RESULT 1104
US-10-238-700-18/c
; Sequence 18, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-18
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-18

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      529 GAGCCCCCGCCACCT 543
Db      15 GAGCCGCGCCACCT 1

RESULT 1105
US-10-238-700-2977/c
; Sequence 2977, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2977
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-2977

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1529 GCAAGGCGCTGCAGCG 1543
Db      16 GCAAGGACTGCAGCG 2

RESULT 1106
US-10-238-700-3413
; Sequence 3413, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3413
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3413

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      888 GCCCCAGGTGCCCT 902
```

Db 2 GCGGCGGGGCGCCCU 16
||||| ||:|||||:

RESULT 1107

US-10-407-519-8
; Sequence 8, Application US/10407519
; Publication No. US20030162217A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, et al.
; TITLE OF INVENTION: METHOD OF IDENTIFYING NUCLEIC ACIDS
; FILE REFERENCE: 15966-539
; CURRENT APPLICATION NUMBER: US/10/407,519
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/417,386
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/115,109
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-10-407-519-8

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 613 CCCACTCCAGCTCT 627
| ||||| |||||
Db 3 CACACTCCAGCTCT 17

RESULT 1108

US-10-314-321A-51/c
; Sequence 51, Application US/10314321A
; Publication No. US20030190648A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi, Ltd.
; TITLE OF INVENTION: Gene Predicting Method
; FILE REFERENCE: 310101185US1
; CURRENT APPLICATION NUMBER: US/10/314,321A
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: JP 2002-103333
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: partial sequence of AL365356
US-10-314-321A-51

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 884 ACGGCCCCCAGGTGC 898
| ||||| |||||
Db 17 ACAGGCCCCAGGTGC 3

RESULT 1109

US-10-230-006-2122
; Sequence 2122, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2122
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-2122

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1027 GGGGCTGGGTTGTG 1041
| ||||| |||||
Db 3 GGGGCGGGGUGGUG 17

RESULT 1110

US-10-230-006-2123
; Sequence 2123, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2123
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-2123

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 6.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1027 GGGGCTGGGTTGTG 1041
| ||||| |||||
Db 2 GGGGCGGGGUGGUG 16

RESULT 1111

US-10-209-787-3406/c
; Sequence 3406, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176

; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3406
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-3406

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 CAGTTCAGTTCCCA 1633
|||||
Db 16 CAGTGCCAGTTCCCA 2

RESULT 1112

US-10-209-787-3407
; Sequence 3407, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:

; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30

; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3407
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-3407

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 CAGTTCAGTTCCCA 1633
|||||
Db 2 CAGTGCCAGTTCCCA 16

RESULT 1113

US-10-261-185-3406/c
; Sequence 3406, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:

; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single

; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3406
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-3406

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 CAGTTCAGTTCCCA 1633
|||||
Db 16 CAGTGCCAGTTCCCA 2

RESULT 1114

US-10-261-185-3407
; Sequence 3407, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:

; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3407
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-3407

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 CAGTTCAGTTCCCA 1633
|||||
Db 2 CAGTGCCAGTTCCCA 16

RESULT 1115

US-10-138-674-1300/c


```
; Sequence 1300, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1300
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1301

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      33 AGGAAAAAAGC 47
      |||||
Db      17 AGGAAAAAAGC 3

RESULT 1116
US-10-138-674-1301/c
; Sequence 1301, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1301
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1301

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      33 AGGAAAAAAGC 47
      |||||
Db      17 AGGAAAAAAGC 3

RESULT 1117
US-10-138-674-1302/c
; Sequence 1302, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
```

```
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1302
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1302

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      33 AGGAAAAAAGC 47
      |||||
Db      15 AGGAAAAAAGC 1

RESULT 1118
US-10-138-674-5090
; Sequence 5090, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5090
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5090

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 6.8e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      530 AGCCCCGCCACCTC 544
      |||||
Db      3 AACCCCCGCCACCUC 17

RESULT 1119
US-10-138-674-7735/c
; Sequence 7735, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7735
; LENGTH: 17
; TYPE: RNA
```

```

; ORGANISM: Homo sapiens
US-10-138-674-7735

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAGGAGCTCTCAGCC 1569
Db 15 CAGGAGCTCTCATCC 1

RESULT 1120
US-10-138-674-7887
; Sequence 7887, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7887
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7887

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 6.8e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 530 AGCCCCCGCCACCTC 544
Db 2 AACCCCCGCCACCUC 16

RESULT 1121
US-10-138-674-8938
; Sequence 8938, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8938
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8938

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 830 AAGAGGAAGCTGCTG 844
      |||||||:|:
```

```

Db 1 AAGAGGAAGCUCCUG 15

RESULT 1122
US-10-287-949A-1300/c
; Sequence 1300, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1300
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1300

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 AGGAAAAAAAAGC 47
      |||||||:|
Db 17 AGGAAAAAAAAGC 3

RESULT 1123
US-10-287-949A-1301/c
; Sequence 1301, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1301
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1301

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 AGGAAAAAAAAGC 47
      |||||||:|
Db 16 AGGAAAAAAAAGC 2

RESULT 1124
US-10-287-949A-1302/c
; Sequence 1302, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1302
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1302
```

```
Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      33 AGGAAAAAAGAGC 47
          |||||
Db      15 AGGAAAAAAGAGC 1
```

RESULT 1125

```
US-10-287-949A-5090
; Sequence 5090, Application US/10287949A
; Publication No. US20040102389A1
```

GENERAL INFORMATION:

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: Pavco, Pam
```

```
; APPLICANT: McSwiggen, Jim
```

```
; APPLICANT: Stinchcomb, Dan
```

```
; APPLICANT: Escobedo, Jaime
```

```
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
```

```
; FILE REFERENCE: MBHB00-876-N (400/049)
```

```
; CURRENT APPLICATION NUMBER: US/10/287,949A
```

```
; CURRENT FILING DATE: 2003-04-11
```

```
; NUMBER OF SEQ ID NOS: 20822
```

```
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 5090
```

```
; LENGTH: 17
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-10-287-949A-5090
```

```
Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 6.8e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      530 AGCCCCGCCACCTC 544
          | |||||
Db      3 AACCCCCGCCACCUC 17
```

RESULT 1126

```
US-10-287-949A-7735/c
; Sequence 7735, Application US/10287949A
; Publication No. US20040102389A1
```

GENERAL INFORMATION:

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: Pavco, Pam
```

```
; APPLICANT: McSwiggen, Jim
```

```
; APPLICANT: Stinchcomb, Dan
```

```
; APPLICANT: Escobedo, Jaime
```

```
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
```

```
; FILE REFERENCE: MBHB00-876-N (400/049)
```

```
; CURRENT APPLICATION NUMBER: US/10/287,949A
```

```
; CURRENT FILING DATE: 2003-04-11
```

```
; NUMBER OF SEQ ID NOS: 20822
```

```
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 8938
```

```
; LENGTH: 17
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-10-287-949A-8938
```

```
Query Match
```

```
0.8%; Score 13.4; DB 1; Length 17;
```

```
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7735
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7735
```

```
Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1555 CAGGAGCTCTCAGCC 1569
          |||||
Db      15 CAGGAGCTCTCATCC 1
```

RESULT 1127

```
US-10-287-949A-7887
; Sequence 7887, Application US/10287949A
; Publication No. US20040102389A1
```

GENERAL INFORMATION:

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: Pavco, Pam
```

```
; APPLICANT: McSwiggen, Jim
```

```
; APPLICANT: Stinchcomb, Dan
```

```
; APPLICANT: Escobedo, Jaime
```

```
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
```

```
; FILE REFERENCE: MBHB00-876-N (400/049)
```

```
; CURRENT APPLICATION NUMBER: US/10/287,949A
```

```
; CURRENT FILING DATE: 2003-04-11
```

```
; NUMBER OF SEQ ID NOS: 20822
```

```
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 7887
```

```
; LENGTH: 17
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-10-287-949A-7887
```

```
Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 6.8e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      530 AGCCCCGCCACCTC 544
          | |||||
Db      2 AACCCCCGCCACCUC 16
```

RESULT 1128

```
US-10-287-949A-8938
; Sequence 8938, Application US/10287949A
; Publication No. US20040102389A1
```

GENERAL INFORMATION:

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: Pavco, Pam
```

```
; APPLICANT: McSwiggen, Jim
```

```
; APPLICANT: Stinchcomb, Dan
```

```
; APPLICANT: Escobedo, Jaime
```

```
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
```

```
; FILE REFERENCE: MBHB00-876-N (400/049)
```

```
; CURRENT APPLICATION NUMBER: US/10/287,949A
```

```
; CURRENT FILING DATE: 2003-04-11
```

```
; NUMBER OF SEQ ID NOS: 20822
```

```
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 8938
```

```
; LENGTH: 17
```

```
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
```

```
US-10-287-949A-8938
```

Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 830 AAGAGGAAGCTGCTG 844
|||||:|:
Db 1 AAGAGGAAGCUCCUG 15

RESULT 1129
US-10-712-672-506
; Sequence 506, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 506
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-506.

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 6.8e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1461 GTGTGGGCTGCTGCT 1475
|:|:|:|:|:|:
Db 1 GUGGGGCGUCUGCU 15

RESULT 1130
US-10-712-672-636
; Sequence 636, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 636
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-636

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 460 AGCACCAACGCTGGCC 474
|||||:|:
Db 3 AGCACCAACGCGGCC 17

RESULT 1131
US-10-712-672-1902/c
; Sequence 1902, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1902
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1902

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 350 GGGGGCGCGCTGGG 364
|||||:|:
Db 15 GGGGGCGCGCGGGG 1

RESULT 1132
US-10-712-672-2563/c
; Sequence 2563, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2563
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2563

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1240 GGCTGCTTCACCTGC 1254
Db 15 GGCTGTTTCACCTGC 1

RESULT 1133

US-10-669-841-7042/c
; Sequence 7042, Application US/10669841
; Publication No. US20040127446A1

GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7042
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-7042

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 882 GCACGGGCCCCAGGT 896
Db 16 GCAGGGGCCCCAGGT 2

RESULT 1134

US-10-723-361-6390
; Sequence 6390, Application US/10723361
; Publication No. US20040137589A1

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6390
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6390

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1177 GCCACGTGCTCCAG 1191
Db 3 GCCCGTGTCTCCAG 17

RESULT 1135

US-10-723-361-6391
; Sequence 6391, Application US/10723361
; Publication No. US20040137589A1

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6391
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-6391

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1177 GCCACGTGCTCCCG 1191
||| |||||
Db 2 GCCCGTGTCTCCCG 16

RESULT 1136
US-10-723-361-6392
; Sequence 6392, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 6392
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-723-361-6392
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1177 GCCACGTGCTCCCG 1191
||| |||||
Db 1 GCCCGTGTCTCCCG 15
RESULT 1137
US-10-723-361-7876
; Sequence 7876, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7876
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7876

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 834 GGAAGCTGTGGGT 848
||| |||||
Db 3 GGAGCTGTGGGT 17
RESULT 1138
US-10-723-361-7880
; Sequence 7880, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7880
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7880

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 837 AGCTGCTGGGCTCTC 851
|||||
Db 2 AGCTGCTGGGTCAC 16

RESULT 1139
US-10-723-361-7881
; Sequence 7881, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7880
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7880

; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7881
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7881

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 837 AGCTGCTGGGCTCTC 851
|||||
Db 1 AGCTGCTGGGTCAC 15

RESULT 1140
US-10-723-361-10020
; Sequence 10020, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10020
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10020

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 132 CGTGTCTGGAGTCC 146
|| |||||
Db 3 CGGTGTCTGGAGTCC 17

RESULT 1141

US-10-723-361-10021
; Sequence 10021, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10021
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10021

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 132 CGTGTCTGGAGTCC 146
|| |||||
Db 2 CGGTGTCTGGAGTCC 16

RESULT 1142

US-10-723-361-10281/c
; Sequence 10281, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10281
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10281

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1288 TTCACAGTGGATGCT 1302
||| |||||
Db 17 TTCAAAGTGGATGCT 3

RESULT 1143

US-10-723-361-10282/c
; Sequence 10282, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10282
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10282

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1288 TTCACAGTGGATGCT 1302
Db 16 TTCAAAGTGGATGCT 2

RESULT 1144
US-10-723-361-10283/c
; Sequence 10283, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10283
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10283

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1288 TTCACAGTGGATGCT 1302
Db 15 TTCAAAGTGGATGCT 1

RESULT 1145
US-10-723-361-10500
; Sequence 10500, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10500
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10500

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 805 CAGAGAGAGCCAGGG 819
Db 3 CGGAGAGAGCCAGGG 17

RESULT 1146
US-10-723-361-10501
; Sequence 10501, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI

```

; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10501
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10501

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Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. NO. 6.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 805 CAGAGAGAGCCAGG 819
Db 2 CGGAGAGAGCCAGG 16

RESULT 1147
US-10-723-361-10503
; Sequence 10503, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POL
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10503
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10503

```

Query Match	0.8%;	Score 13.4;	DB 1;	Length 17;
Best Local Similarity	93.3%;	Pred. No. 6.8e+02;		
Matches 14; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 807 GAGAGAGCCAGGGCC 821
Db 2 GAGAGAGCCAGGGAC 16

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RESULT 1148
US-10-008-789-21
; Sequence 21, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF T
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-21

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Query Match 0.8%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 986 TTGGCCAGTGTGGTG 1000
pb 1 TTGGCCAGCGTGGTG 15

RESULT 1149
US-10-291-808-65/c
; Sequence 65, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-65

Query Match          0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.3e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA1748
Db 14 BAAAAA1748

RESULT 1150
US-10-006-430-26
; Sequence 26, Application US/10006430
; Publication No. US20030113914A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD81 EXPRESSION
; FILE REFERENCE: RTS-0341
; CURRENT APPLICATION NUMBER: US/10/006,430
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-430-26

Query Match          0.8%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 177 GCTGCCCCGAGCAGCC 194
Db 1 GATGCCCCCGTAGCAGCC 18

RESULT 1151
US-09-862-101-2/c
; Sequence 2, Application US/09862101
; Patent No. US20020061526A1
; GENERAL INFORMATION:
; APPLICANT: Ju, Jingfang
; APPLICANT: Simons, Jan Fredrik
; TITLE OF INVENTION: Method for Analyzing a Nucleic Acid
; FILE REFERENCE: 21402-017 US
; CURRENT APPLICATION NUMBER: US/09/862,101
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,385
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/265,394
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/282,982
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-862-101-2

Query Match          0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-65

Query Match          0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.3e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA1748
Db 14 BAAAAA1748

RESULT 1150
US-10-006-430-26
; Sequence 26, Application US/10006430
; Publication No. US20030113914A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD81 EXPRESSION
; FILE REFERENCE: RTS-0341
; CURRENT APPLICATION NUMBER: US/10/006,430
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-430-26

Query Match          0.8%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 177 GCTGCCCCGAGCAGCC 194
Db 1 GATGCCCCCGTAGCAGCC 18

RESULT 1151
US-09-862-101-2/c
; Sequence 2, Application US/09862101
; Patent No. US20020061526A1
; GENERAL INFORMATION:
; APPLICANT: Ju, Jingfang
; APPLICANT: Simons, Jan Fredrik
; TITLE OF INVENTION: Method for Analyzing a Nucleic Acid
; FILE REFERENCE: 21402-017 US
; CURRENT APPLICATION NUMBER: US/09/862,101
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,385
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/265,394
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/282,982
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-862-101-2

Query Match          0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA 1748
Db 13 AAAAAAAAAA 1

RESULT 1152
US-09-919-345-2/c
; Sequence 2, Application US/09919345
; Patent No. US20020061530A1
; GENERAL INFORMATION:
; APPLICANT: Belotserkovskii, Boris P.
; APPLICANT: Reddy, Gurucharan
; APPLICANT: Zarling, David
; TITLE OF INVENTION: Enhanced Targeting of DNA Sequences by Recombinase and Single-Strand Annealing
; FILE REFERENCE: A-69625-1/RFT/DLR
; CURRENT APPLICATION NUMBER: US/09/919,345
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/222,272
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-345-2

Query Match          0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAA 1748
Db 13 AAAAAAAAAA 1

RESULT 1153
US-09-888-326-835/c
; Sequence 835, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 835
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: phosphodiester backbone
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: FITC labeled
US-09-888-326-835

Query Match          0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1736 AAAAAAAAAAAAAA 1748
      |||||||
Db      13 AAAAAAAAAAAAAA 1
      |||||||

RESULT 1154
US-09-888-326-836/c
; Sequence 836, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 836
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; NAME/KEY: misc_difference
; LOCATION: (13)...(13)
; OTHER INFORMATION: FITC labeled
US-09-888-326-836

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
      |||||||
Db      13 AAAAAAAAAAAAAA 1
      |||||||

RESULT 1155
US-09-776-479-867/c
; Sequence 867, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 867
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(13)
; OTHER INFORMATION: Conjugated to FITC moiety.
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphodiester backbone.
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-867

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
      |||||||
Db      13 AAAAAAAAAAAAAA 1
      |||||||

RESULT 1157
US-09-776-479-868/c
; Sequence 868, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 868
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(13)
; OTHER INFORMATION: Conjugated to FITC moiety.
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
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; OTHER INFORMATION: Has phosphodiester backbone.
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-867

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
      |||||||
Db      13 AAAAAAAAAAAAAA 1
      |||||||

RESULT 1156
US-09-776-479-867/c
; Sequence 867, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 867
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(13)
; OTHER INFORMATION: Conjugated to FITC moiety.
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphodiester backbone.
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-867

Query Match      0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1748
      |||||||
Db      13 AAAAAAAAAAAAAA 1
      |||||||

RESULT 1157
US-09-776-479-868/c
; Sequence 868, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 868
```


; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(13)
; OTHER INFORMATION: Conjugated to biotin moiety.
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphorothioate and phosphodiester chimeric
; OTHER INFORMATION: backbone with phosphodiester on 3' end.
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-868

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1158
US-09-776-479-868/c
; Sequence 868, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 868
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(13)
; OTHER INFORMATION: Conjugated to biotin moiety.
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphorothioate and phosphodiester chimeric
; OTHER INFORMATION: backbone with phosphodiester on 3' end.
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-868

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1159
US-10-314-578-867/c
; Sequence 867, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian

; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 867
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(13)
; OTHER INFORMATION: Conjugated to FITC moiety.
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphodiester backbone.
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-867

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1160
US-10-314-578-868/c
; Sequence 868, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 868
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(13)
; OTHER INFORMATION: Conjugated to biotin moiety.
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphorothioate and phosphodiester chimeric
; OTHER INFORMATION: backbone with phosphodiester on 3' end.
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-868

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 1161

US-10-094-183-19
; Sequence 19, Application US/10094183
; Publication No. US20020168631A1
; GENERAL INFORMATION:
; APPLICANT: Wegene, Inc.
; TITLE OF INVENTION: Random Gene Unidirectional Antisense Library
; FILE REFERENCE: 57354.00003
; CURRENT APPLICATION NUMBER: US/10/094,183
; CURRENT FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Sequence: Synthetic Primer
US-10-094-183-19

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
Db 1 CAAAAAAAAAAAAA 13

RESULT 1162

US-10-208-357-19
; Sequence 19, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-19

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 1163

US-10-112-653-838/c
; Sequence 838, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 838
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (13)...(13)
; OTHER INFORMATION: fluorescein isothiocyanate conjugate
US-10-112-653-838

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 1164

US-10-112-653-839/c
; Sequence 839, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 839
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (13)...(13)
; OTHER INFORMATION: fluorescein isothiocyanate conjugate
US-10-112-653-839

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 1165

US-10-017-995-867/c
; Sequence 867, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 867
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(13)
; OTHER INFORMATION: Conjugated to FITC moiety.
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphodiester backbone.
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-867

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
|||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1166
US-10-017-995-868/c
; Sequence 868, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 868
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(13)
; OTHER INFORMATION: Conjugated to biotin moiety.
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Has phosphorothioate and phosphodiester chimeric
; OTHER INFORMATION: backbone with phosphodiester on 3' end.
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-868

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
|||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1167
US-10-149-121-6/c
; Sequence 6, Application US/10149121
; Publication No. US20030097678A1
; GENERAL INFORMATION:
; APPLICANT: KUVSHINOV, VIKTOR
; APPLICANT: KANERVA, ANNE
; APPLICANT: KOIVU, KIMMO
; APPLICANT: PEHU, EIJA
; TITLE OF INVENTION: A PROCESS FOR CONVERTING STORAGE RESERVES OF DICOT
; TITLE OF INVENTION: SEEDS INTO COMPOSITIONS COMPRISING ONE OR MORE GENE
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: BRN-003
; CURRENT APPLICATION NUMBER: US/10/149,121
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: FI 19992659
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: PCT/FI00/01081
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 3' primer
US-10-149-121-6

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAA 1746
|||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1168
US-10-180-196-6/c
; Sequence 6, Application US/10180196
; Publication No. US20030124562A1
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl
; APPLICANT: Tan, Ruoying
; APPLICANT: Rose, Michael J.
; TITLE OF INVENTION: Methods and Compositions for Producing
; TITLE OF INVENTION: Full Length cDNA Libraries
; FILE REFERENCE: 06514-087US1
; CURRENT APPLICATION NUMBER: US/10/180,196
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US/09/352,540
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized Primer
US-10-180-196-6

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
|||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1169
US-10-371-600-13
; Sequence 13, Application US/10371600
; Publication No. US20030180776A1
; GENERAL INFORMATION:
; APPLICANT: WU, MING
; APPLICANT: ULLMAN, EDWIN F.
; TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION
; FILE REFERENCE: 3817.10-2
; CURRENT APPLICATION NUMBER: US/10/371,600
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/359,223
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/379,360
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-371-600-13

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 1170
US-10-361-028-56
; Sequence 56, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361,028
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US/09/704,525
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: JP 316133/1999
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 13
; TYPE: DNA/RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: poly(A) oligo
US-10-361-028-56

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 1171
US-10-324-409B-15/c

; Sequence 15, Application US/10324409B
; Publication No. US20040086880A1
; GENERAL INFORMATION:
; APPLICANT: Sampson, et al.
; TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced
; FILE REFERENCE: 2003309-0028
; CURRENT APPLICATION NUMBER: US/10/324,409B
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: The DNA primer
; OTHER INFORMATION: and temp seqs used to test the effect of the
; OTHER INFORMATION: polynucleotide secondary structure on the
; OTHER INFORMATION: polymerase ext reaction.
US-10-324-409B-15

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1172
US-10-343-710-151/c
; Sequence 151, Application US/10343710
; Publication No. US20040087478A1
; GENERAL INFORMATION:
; APPLICANT: GILLEN, Clemens
; APPLICANT: WETZELS, Ingrid
; APPLICANT: WENNDT, Stephan
; APPLICANT: WEIHE, E.
; APPLICANT: SCHAEFER, M., K.-H.
; TITLE OF INVENTION: SCREENING METHOD
; FILE REFERENCE: 029310.52022US
; CURRENT APPLICATION NUMBER: US/10/343,710
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP01/09011
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-10-343-710-151

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAA 1746
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1173
US-10-335-573-4
; Sequence 4, Application US/10335573
; Publication No. US20040126770A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Gyanendra
; APPLICANT: Abarzua, Patricia

; TITLE OF INVENTION: ROLLING CIRCLE AMPLIFICATION OF RNA
; FILE REFERENCE: 13172.0021U1
; CURRENT APPLICATION NUMBER: US/10/335,573
; CURRENT FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Note =
; OTHER INFORMATION: synthetic construct
US-10-335-573-4

Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 1174
US-09-504-231A-1370
; Sequence 1370, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1370
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1370

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 700 TCGGCGCCACCCA 712
Db 2 UGCGGCCACCCA 14

RESULT 1175
US-09-274-553D-1370
; Sequence 1370, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1370
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1370

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 6.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 700 TCGGCGCCACCCA 712
Db 2 UGCGGCCACCCA 14

RESULT 1176
US-10-103-614A-1/c
; Sequence 1, Application US/10103614A
; Publication No. US20030059796A1
; GENERAL INFORMATION:
; APPLICANT: SALMAN AL-MAHMOOD
; TITLE OF INVENTION: METHOD FOR IDENTIFYING NOVEL GENES INVOLVED IN THE
; TITLE OF INVENTION: REGULATION OF ANGIOGENESIS, STUDY OF SAID GENES AND USE
; TITLE OF INVENTION: THEREOF FOR THERAPEUTIC PURPOSES
; FILE REFERENCE: 1071-02
; CURRENT APPLICATION NUMBER: US/10/103,614A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: PCT/FR00/02607
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: FR 99/11790
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-103-614A-1

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1

RESULT 1177
US-10-301-844-23/c
; Sequence 23, Application US/10301844
; Publication No. US20030100747A1
; GENERAL INFORMATION:

APPLICANT: Ruddy, David A.
Wolff, Roger K.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
HEMOCHROMATOSIS GENE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-301-844-23

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
| | | | | | | | | | | | | | | | | |
Db 14 AAAAAAAAAAAAAA 2

RESULT 1178
US-10-385-450-18/c
; Sequence 18, Application US/10385450
; Publication No. US20030157683A1
; GENERAL INFORMATION:
; APPLICANT: Lehar, et al., Sophie M.
; TITLE OF INVENTION: APOPTOSIS GENE EI24, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 104322.170DIV
; CURRENT APPLICATION NUMBER: US/10/385,450
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/151,771B
; PRIOR FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer sequence
; NAME/KEY: unsure
; LOCATION: (13)

; OTHER INFORMATION: any nucleotide can be used
US-10-385-450-18

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
| | | | | | | | | | | | | | | | | |
Db 14 CAAAAAAAAAAAAA 1

RESULT 1179
US-10-385-450-20/c
; Sequence 20, Application US/10385450
; Publication No. US20030157683A1
; GENERAL INFORMATION:
; APPLICANT: Lehar, et al., Sophie M.
; TITLE OF INVENTION: APOPTOSIS GENE EI24, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 104322.170DIV
; CURRENT APPLICATION NUMBER: US/10/385,450
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/151,771B
; PRIOR FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer sequence
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: any nucleotide can be used
US-10-385-450-20

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAA 1747
| | | | | | | | | | | | | | | | | |
Db 14 ANAAAAAAAAAAAAA 1

RESULT 1180
US-10-468-753-43
; Sequence 43, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JF02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:


```
; OTHER INFORMATION: synthetic DNA
US-10-468-753-43

Query Match          0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 1181
US-10-468-753-44
; Sequence 44, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-44

Query Match          0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 1182
US-10-468-753-45
; Sequence 45, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-45

Query Match          0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 1183
US-10-468-753-48/c
; Sequence 48, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-48

Query Match          0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 1184
US-10-468-753-49/c
; Sequence 49, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-49
```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-468-753-49

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1748
|||||
Db 13 AAAAAAAAAAAAA 1

RESULT 1185

US-10-787-958-1/c
; Sequence 1, Application US/10787958
; Publication No. US20040154053A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Paul
; APPLICANT: Roberts, Jeremy A.
; APPLICANT: Whitelaw, Catherine
; TITLE OF INVENTION: Signal Transduction Protein Involved in Plant Dehiscence
; FILE REFERENCE: 0623.089000
; CURRENT APPLICATION NUMBER: US/10/787,958
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: GB9806113.8
; PRIOR FILING DATE: 1998-03-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligo dt primer 7
US-10-787-958-1

Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAA 1747
|||||
Db 13 CAAAAAAAAAAAA 1

RESULT 1186

US-10-287-919-2595/c
; Sequence 2595, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 2595
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1576469)...(1576482)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3307
US-10-287-919-2595

Query Match 0.7%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1325 AGGACTTTCACAG 1337
|||||
Db 13 AGGACTTTCACAG 1

RESULT 1187

US-10-333-068-114/c
; Sequence 114, Application US/10333068
; Publication No. US20040101863A1
; GENERAL INFORMATION:
; APPLICANT: HATTORI, Hiroaki
; TITLE OF INVENTION: METHOD OF DETECTING ABNORMALITY OF LIPID METABOLISM
; FILE REFERENCE: Q73807
; CURRENT APPLICATION NUMBER: US/10/333,068
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: PCT/JP01/06153
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JPA 2000-218039
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Hominidae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n is a, c, g, or t
US-10-333-068-114

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 7.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1021 GGGGATGGGCTGG 1034
|||||
Db 15 GGGGATGGGCTGG 2

RESULT 1188

US-10-432-803-4/c
; Sequence 4, Application US/10432803
; Publication No. US20040029199A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Jin Woo
; TITLE OF INVENTION: HUMAN CERVICAL CANCER 2 PROTOONCOGENE AND PROTEIN ENCODED THEREIN
; FILE REFERENCE: KJW-0613
; CURRENT APPLICATION NUMBER: US/10/432,803
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: KOPATIN 1.5
; SEQ ID NO 4
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: H-T11G anchored oligo-dt primer
US-10-432-803-4

Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAA 1747
|||||
Db 16 CAAAAAAAAAAAA 4

RESULT 1189

```
US-10-287-919-785/c
; Sequence 785, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 785
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (291860)...(291875)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 962
US-10-287-919-785
Query Match      0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1325 AGGACTTTTCACAG 1337
      |||||||
Db      16 AGGACTTTTCACAG 4

RESULT 1190
US-10-287-919-1256/c
; Sequence 1256, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1256
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (573509)...(573524)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1543
US-10-287-919-1256
Query Match      0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1325 AGGACTTTTCACAG 1337
      |||||||
Db      16 AGGACTTTTCACAG 4

RESULT 1191
US-10-287-919-1775/c
; Sequence 1775, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1775
; LENGTH: 16
```

```
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1045875)...(1045890)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2257
US-10-287-919-1775
Query Match      0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1325 AGGACTTTTCACAG 1337
      |||||||
Db      16 AGGACTTTTCACAG 4

RESULT 1192
US-10-287-919-2598
; Sequence 2598, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 2598
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1576549)...(1576564)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3310
US-10-287-919-2598
Query Match      0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1325 AGGACTTTTCACAG 1337
      |||||||
Db      3 AGGACTTTTCACAG 15

RESULT 1193
US-10-188-404-42/c
; Sequence 42, Application US/10188404
; Publication No. US20030105286A1
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; APPLICANT: Coull, James M.
; APPLICANT: Kiely, John
; APPLICANT: Griffith, Michael
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS5042
; CURRENT APPLICATION NUMBER: US/10/188,404
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/275,951
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/765,798
; PRIOR FILING DATE: 1997-04-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: N is Pseudoisocytosine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(6)
; OTHER INFORMATION: N is Pseudoisocytosine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(9)
; OTHER INFORMATION: Ethylene Glycol, Ethylene Glycol,
; OTHER INFORMATION: Ethylene Glycol Linkage
US-10-188-404-42
```

```
Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 30 AAGAGGAAAAA 45
Db 16 AAGAGGAAANANAA 1
```

RESULT 1194

```
US-09-866-108-1381/c
; Sequence 1381, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
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; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1381
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1381
```

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Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1244 GCTTCACCTGCGT 1256
Db 17 GCTTCACCTGCGT 5
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RESULT 1195

```
US-09-866-108-1382/c
; Sequence 1382, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1382
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1382
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```
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1244 GCTTCACCTGCGT 1256
 Db 16 GCTTCACCTGCGT 4

RESULT 1196

US-09-866-108-1383/c
 ; Sequence 1383, Application US/09866108
 ; Patent No. US20020048800A1

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
 ; APPLICANT: JI, Yonggang
 ; APPLICANT: PENN, Sharron G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng
 ; APPLICANT: SHANNON, Mark
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 ; FILE REFERENCE: AEOMICA-7
 ; CURRENT APPLICATION NUMBER: US/09/866,108
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 60/266,860
 ; PRIOR FILING DATE: 2001-02-05
 ; NUMBER OF SEQ ID NOS: 15752
 ; SOFTWARE: Aeomica Sequence Listing Engine
 ; SEQ ID NO 1383
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-866-108-1383

Qy 1244 GCTTCACCTGCGT 1256
 Db 15 GCTTCACCTGCGT 3

RESULT 1197

US-09-866-108-1384/c
 ; Sequence 1384, Application US/09866108
 ; Patent No. US20020048800A1

; GENERAL INFORMATION:
 ; APPLICANT: GU, Yizhong
 ; APPLICANT: JI, Yonggang
 ; APPLICANT: PENN, Sharron G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng
 ; APPLICANT: SHANNON, Mark
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 ; FILE REFERENCE: AEOMICA-7
 ; CURRENT APPLICATION NUMBER: US/09/866,108
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 60/266,860
 ; PRIOR FILING DATE: 2001-02-05
 ; NUMBER OF SEQ ID NOS: 15752
 ; SOFTWARE: Aeomica Sequence Listing Engine
 ; SEQ ID NO 1384
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-866-108-1384

Qy 1244 GCTTCACCTGCGT 1256
 Db 14 GCTTCACCTGCGT 2

Query Match 0.7%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred.No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1244 GCTTCACCTGCGT 1256
 Db 15 GCTTCACCTGCGT 3

Query Match 0.7%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred.No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1244 GCTTCACCTGCGT 1256
 Db 15 GCTTCACCTGCGT 3

Query Match 0.7%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred.No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1244 GCTTCACCTGCGT 1256
 Db 15 GCTTCACCTGCGT 3

Query Match 0.7%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred.No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1244 GCTTCACCTGCGT 1256
 Db 15 GCTTCACCTGCGT 3

Query Match 0.7%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred.No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1244 GCTTCACCTGCGT 1256
 Db 15 GCTTCACCTGCGT 3

Query Match 0.7%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred.No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1244 GCTTCACCTGCGT 1256
 Db 15 GCTTCACCTGCGT 3

Query Match 0.7%; Score 13; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred.No. 7.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1385
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1385

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1244 GCTTCACCTGCGT 1256
Db 13 GCTTCACCTGCGT 1

RESULT 1199
US-09-969-373-3467/c
; Sequence 3467, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3467

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 GGACGGAAGAGGG 100
Db 15 GGACGGAAGAGGG 3

RESULT 1200
US-09-780-533A-2366
; Sequence 2366, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: MCSwiggan, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2366
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2366

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GAGGAAGAGGAGG 878
Db 1 GAGGAAGAGGAGG 13

RESULT 1201
US-09-848-754A-904
; Sequence 904, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 904
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-904

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 907 CAGCCTCCAGAGG 919
Db 5 CAGCCUCCAGAGG 17

RESULT 1202
US-09-848-754A-1461
; Sequence 1461, Application US/09848754A


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; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1461
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-1461

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 84.6%; Pred. No. 7.7e+02;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      468 GCTGGCCCAAACTG 480
      ||:|||||:|
Db      3 GCUGGCCCAACUG 15

RESULT 1203
US-09-848-754A-1462
; Sequence 1462, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1462
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-1462

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 84.6%; Pred. No. 7.7e+02;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      468 GCTGGCCCAAACTG 480
      ||:|||||:|
Db      2 GCUGGCCCAACUG 14

RESULT 1204
US-09-848-754A-2472
; Sequence 2472, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2472
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2472

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 84.6%; Pred. No. 7.7e+02;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      468 GCTGGCCCAAACTG 480
      ||:|||||:|
Db      2 GCUGGCCCAACUG 14

RESULT 1205
US-09-848-754A-3120
; Sequence 3120, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3120

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 84.6%; Pred. No. 7.7e+02;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      910 CCTCCAGAGGATG 922
      ||:|||||:|
Db      1 CCUCCAGAGGAUG 13

RESULT 1206
US-09-792-818-152
; Sequence 152, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insertion of Grb-2-related with Insertion
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 152
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-152

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 53.8%; Pred. No. 7.7e+02;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1666 CTGTATGACTTTG 1678
      ||:||||:|
Db      5 CUGAUGACUUUG 17

RESULT 1207
US-09-792-818-539
; Sequence 539, Application US/09792818
; Publication No. US20030134806A1
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; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 539
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-539

Query Match          0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 53.8%; Pred. No. 7.7e+02;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1666 CTGTATGACTTTG 1678
|:|:|:|:|:|:|
Db 3 CUGAUGACUUUG 15

RESULT 1208
US-09-792-818-720
; Sequence 720, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 720
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-720

Query Match          0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 53.8%; Pred. No. 7.7e+02;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1666 CTGTATGACTTTG 1678
|:|:|:|:|:|:|
Db 2 CUGAUGACUUUG 14

RESULT 1209
US-09-949-298-4
; Sequence 4, Application US/09949298
; Publication No. US20020104107A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: LESTER, Henry A.
; APPLICANT: LABARCA, Cesar
; APPLICANT: SCHWARZ, Johannes
; APPLICANT: Fonck, Carlos
; TITLE OF INVENTION: POINT MUTANT MICE WITH HYPERSENSITIVE ALPHA 4 NICOTINIC RECEPTORS
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; TITLE OF INVENTION: DOPAMINERGIC PATHOLOGY AND INCREASED ANXIETY
; FILE REFERENCE: CITI400-1
; CURRENT APPLICATION NUMBER: US/09/949,298
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230,757
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Mouse
US-09-949-298-4

Query Match          0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TGCTGTCTTCTCT 1699
|||||
Db 3 TGCTGTCTTCTCT 15

RESULT 1210
US-10-163-552-197
; Sequence 197, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; FILE REFERENCE: MBHB01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 197
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-197

Query Match          0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 76.9%; Pred. No. 7.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1577 CCACTGACTGCTG 1589
||||:|:|:|:|
Db 3 CCACUGACUGCUG 15

RESULT 1211
US-10-156-306-4928/c
; Sequence 4928, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4928
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-4928

Query Match          0.7%; Score 13; DB 1; Length 17;
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Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 849 CTCTGGCCCTGCA 861
Db 13 CTCTGGCCCTGCA 1

RESULT 1212
US-10-061-201-1501/c
; Sequence 1501, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1501
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1501

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 899 CCCTGAGCCAGCC 911
Db 17 CCCTGAGCCAGCC 5

RESULT 1213
US-10-138-674-1071/c
; Sequence 1071, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1071
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; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1071

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 17 AAAAAAAAAAAAAA 5

RESULT 1214
US-10-138-674-5091
; Sequence 5091, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5091
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5091

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 532 CCCCCGCCACCTC 544
Db 2 CCCCCGCCACCUC 14

RESULT 1215
US-10-138-674-5092
; Sequence 5092, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5092
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5092

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 532 CCCCCGCCACCTC 544
|||||
Db 1 CCCCCGCCACCUC 13

RESULT 1216

US-10-287-949A-1071/c
; Sequence 1071, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1071
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1071

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1748
|||||
Db 17 AAAAAAAAAAAAA 5

RESULT 1217

US-10-287-949A-5091
; Sequence 5091, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5091
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5091

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 532 CCCCCGCCACCTC 544
|||||
Db 2 CCCCCGCCACCUC 14

RESULT 1218

US-10-287-949A-5092
; Sequence 5092, Application US/10287949A
; Publication No. US20040102389A1

; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5092
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5092

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 7.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 532 CCCCCGCCACCTC 544
|||||
Db 1 CCCCCGCCACCUC 13

RESULT 1219

US-10-723-361-1381/c
; Sequence 1381, Application US/107233361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1381
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-1381

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Query Match          0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1244 GCTTCACCTGCGT 1256
Db       17 GCTTCACCTGCGT 5

RESULT 1220
US-10-723-361-1382/c
; Sequence 1382, Application US/107233361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1382
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-1382

Query Match          0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1244 GCTTCACCTGCGT 1256
Db       16 GCTTCACCTGCGT 4

RESULT 1221
US-10-723-361-1383/c
; Sequence 1383, Application US/107233361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
```

```
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1383
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-1383

Query Match          0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1244 GCTTCACCTGCGT 1256
Db       15 GCTTCACCTGCGT 3

RESULT 1222
US-10-723-361-1384/c
; Sequence 1384, Application US/107233361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1384
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-1384

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1244 GCTTCACCTGCGT 1256
Db 14 GCTTCACCTGCGT 2

RESULT 1223
US-10-723-361-1385/c
; Sequence 1385, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1385
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-1385

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1244 GCTTCACCTGCGT 1256
Db 13 GCTTCACCTGCGT 1
Search completed: August 16, 2004, 15:30:37
Job time : 26 secs